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(54) Title: COMPOSITIONS ISOLATED FROM SKIN CELLS AND METHODS FOR THEIR USE

(57) Abstract: Isolated polynucleotides encoding polypeptides expressed in mammalian skin cells are provided, together with expression vectors and host cells comprising such isolated polynucleotides. Methods for the use of such polynucleotides and polypeptides are also provided.

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COMPOSITIONS ISOLATED FROM SKIN CELLS
AND METHODS FOR THEIR USE

5

Technical Field of the Invention

This invention relates to polynucleotides, polypeptides, polypeptides expressed in skin cells, and various methods for treating a patient involving administration of a polypeptide or polynucleotide of the present invention.

10

Background of the Invention

The skin is the largest organ in the body and serves as a protective cover. The loss of skin, as occurs in a badly burned person, may lead to death owing to the absence of a barrier against infection by external microbial organisms, as well as loss of body temperature and body fluids.

Skin tissue is composed of several layers. The outermost layer is the epidermis which is supported by a basement membrane and overlies the dermis. Beneath the dermis is loose connective tissue and fascia which cover muscles or bony tissue. The skin is a self-renewing tissue in that cells are constantly being formed and shed. The deepest cells of the epidermis are the basal cells, which are enriched in cells capable of replication. Such replicating cells are called progenitor or stem cells. Replicating cells in turn give rise to daughter cells called 'transit amplifying cells'. These cells undergo differentiation and maturation into keratinocytes (mature skin cells) as they move from the basal layer to the more superficial layers of the epidermis. In the process, keratinocytes become cornified and are ultimately shed from the skin surface. Other cells in the epidermis include melanocytes which synthesize melanin, the pigment responsible for protection against sunlight. The Langerhans cell also resides in the epidermis and functions as a cell which processes foreign proteins for presentation to the immune system.

The dermis contains nerves, blood and lymphatic vessels, fibrous and fatty tissue. Within the dermis are fibroblasts, macrophages and mast cells. Both the epidermis and dermis are penetrated by sweat, or sebaceous glands and hair follicles. Each strand of hair is derived from a hair follicle. When hair is plucked out, the hair re-grows from epithelial cells directed by the dermal papillae of the hair follicle.

When the skin surface is breached, for example in a wound, the stem cells proliferate and daughter keratinocytes migrate across the wound to reseal the tissues. The skin cells therefore possess genes activated in response to trauma. The products of these genes include several growth factors, such as epidermal growth factor, which mediate the proliferation of skin cells. The genes that are activated in the skin, and the protein products of such genes, may be developed as agents for the treatment of skin wounds. Additional growth factors derived from skin cells may also influence growth of other cell types. As skin cancers are a disorder of the growth of skin cells, proteins derived from skin that regulate cellular growth may be developed as agents for the treatment of skin cancers. Skin derived proteins that regulate the production of melanin may be useful as agents, which protect skin against unwanted effects of sunlight.

Keratinocytes are known to secrete cytokines and express various cell surface proteins. Cytokines and cell surface molecules are proteins, which play an important role in the inflammatory response against infection, and also in autoimmune diseases affecting the skin. Genes and their protein products that are expressed by skin cells may thus be developed into agents for the treatment of inflammatory disorders affecting the skin.

Hair is an important part of a person's individuality. Disorders of the skin may lead to hair loss. Alopecia areata is a disease characterized by the patchy loss of hair over the scalp. Total baldness is a side effect of drug treatment for cancer. The growth and development of hair is mediated by the effects of genes expressed in skin and dermal papillae. Such genes and their protein products may be usefully developed into agents for the treatment of disorders of the hair follicle.

New treatments are required to hasten the healing of skin wounds, to prevent the loss of hair, enhance the re-growth of hair or removal of hair, and to treat autoimmune

and inflammatory skin diseases more effectively and without adverse effects. More effective treatments of skin cancers are also required. There thus remains a need in the art for the identification and isolation of genes encoding proteins expressed in the skin, for use in the development of therapeutic agents for the treatment of disorders including those associated with skin.

Summary of the Invention

The present invention provides polypeptides and functional portions of polypeptides, which may be expressed in skin cells, together with polynucleotides encoding such polypeptides or functional portions thereof, expression vectors and host cells comprising such polynucleotides, and methods for their use.

In specific embodiments, isolated polynucleotides are provided that comprise a polynucleotide selected from the group consisting of: (a) sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623; (b) complements of the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623; (c) reverse complements of the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623; (d) reverse sequences of the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623; (e) sequences having a 99% probability of being the same as a sequence of (a)-(d); and (f) sequences having at least 50%, 75%, 90% or 95% identity to a sequence of (a)-(d).

In further embodiments, the present invention provides isolated polypeptides comprising an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725; and (b) sequences having at least 50%, 75%, 90% or 95% identity to a sequence provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725, together with isolated polynucleotides encoding such polypeptides. Isolated polypeptides which

comprise at least a functional portion of a polypeptide comprising an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725; and (b) sequences having 50%, 75% or 90% identity to a sequence of SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725, are also provided.

In related embodiments, the present invention provides expression vectors comprising the above polynucleotides, together with host cells transformed with such vectors.

10 In a further aspect, the present invention provides a method of stimulating keratinocyte growth and motility, inhibiting the growth of epithelial-derived cancer cells, inhibiting angiogenesis and vascularization of tumors, or modulating the growth of blood vessels in a subject, comprising administering to the subject a composition comprising an isolated polypeptide, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398; and (b) sequences having at least 50%, 75%, 90% or 95% identity to a sequence provided in SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398.

20 Methods for modulating skin inflammation in a subject are also provided, the methods comprising administering to the subject a composition comprising an isolated polypeptide, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 338 and 347; and (b) sequences having at least 50%, 75%, 90% or 95% identity to a sequence provided in SEQ ID NOS: 338 and 347. In an additional aspect, the present invention provides methods for stimulating the growth of epithelial cells in a subject. Such methods 25 comprise administering to the subject a composition comprising an isolated polypeptide including an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 129 and 348; and (b) sequences having at least 50%, 75%, 90% or 95% identity to a sequence provided in SEQ ID NOS: 129 and 348.

In yet a further aspect, methods for inhibiting the binding of HIV-1 to leukocytes, for the treatment of an inflammatory disease or for the treatment of cancer in a subject are provided, the methods comprising administering to the subject a composition comprising an isolated polypeptide including an amino acid sequence selected from the group
5 consisting of: (a) sequences provided in SEQ ID NOS: 340, 344, 345 and 346; and (b) sequences having at least 50%, 75%, 90% or 95% identity to a sequence provided in SEQ ID NOS: 340, 344, 345 and 346.

As detailed below, the isolated polynucleotides and polypeptides of the present invention may be usefully employed in the preparation of therapeutic agents for the
10 treatment of skin disorders.

The above-mentioned and additional features of the present invention, together with the manner of obtaining them, will be best understood by reference to the following more detailed description. All references disclosed herein are incorporated herein by reference in their entirety as if each was incorporated individually.

15

Brief Description of the Drawings

Fig. 1 shows the results of a Northern analysis of the distribution of huTR1 mRNA in human tissues. Key: He, Heart; Br, Brain; Pl, Placenta; Lu, Lung; Li, Liver; SM, Skeletal muscle; Ki, Kidney; Sp, Spleen; Th, Thymus; Pr, Prostate; Ov, Ovary.

20 Fig. 2 shows the results of a MAP kinase assay of muTR1a and huTR1a. MuTR1a (500ng/ml), huTR1a (100ng/ml) or LPS (3pg/ml) were added as described in the text.

Fig. 3 shows the stimulation of growth of neonatal foreskin keratinocytes by muTR1a.

25 Fig. 4 shows the stimulation of growth of the transformed human keratinocyte cell line HaCaT by muTR1a and huTR1a.

Fig. 5 shows the inhibition of growth of the human epidermal carcinoma cell line A431 by muTR1a and huTR1a.

Fig. 6 shows the inhibition of IL-2 induced growth of concanavalin A-stimulated

murine splenocytes by KS2a.

Fig. 7 shows the stimulation of growth of rat intestinal epithelial cells (IEC-18) by a combination of KS3a plus apo-transferrin.

Fig. 8 illustrates the oxidative burst effect of TR-1 (100 ng/ml), muKS1 (100 ng/ml), SDF1 α (100 ng/ml), and fMLP (10 μ M) on human PBMC.

Figure 9 shows the chemotactic effect of muKS1 and SDF-1 α on THP-1 cells.

Figure 10 shows the induction of cellular infiltrate in C3H/HeJ mice after intraperitoneal injections with muKS1 (50 μ g), GV14B (50 μ g) and PBS.

Figure 11 demonstrates the induction of phosphorylation of ERK1 and ERK2 in CV1/EBNA and HeLa cell lines by huTR1a.

Figure 12 shows the huTR1 mRNA expression in HeLa cells after stimulation by muTR1, huTR1, huTGF α and PBS (100 ng/ml each).

Figure 13 shows activation of the SRE by muTR1a in PC-12 (Fig. 13A) and HaCaT (Fig. 13B) cells.

Figure 14 shows the inhibition of huTR1a mediated growth on HaCaT cells by an antibody to the EGF receptor.

Figure 15A shows the nucleotide sequence of KS1 cDNA (SEQ ID NO: 464) along with the deduced amino acid sequence (SEQ ID NO: 465) using single letter code. The 5' UTR is indicated by negative numbers. The underlined NH₂-terminal amino acids represent the predicted leader sequence and the stop codon is denoted by ***. The polyadenylation signal is marked by a double underline. Figure 15B shows a comparison of the complete open reading frame of KS1 (referred to in Fig. 15B as KLF-1) with its human homologue BRAK and with the mouse α -chemokines mCrg-2, mMig, mSDF-1, mBLC, mMIP2, mKC and mLIX. An additional five residues are present in KS1 and BRAK between cysteine 3 and cysteine 4 that have not previously been described for chemokines.

Detailed Description of the Invention

In one aspect, the present invention provides polynucleotides that were isolated from mammalian skin cells. As used herein, the term "polynucleotide" means a single or

double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes DNA and RNA molecules, both sense and anti-sense strands. The term comprehends cDNA, genomic DNA, recombinant DNA and wholly or partially synthesized nucleic acid molecules. A polynucleotide may consist of an entire gene, or a portion thereof. A
5 gene is a DNA sequence that codes for a functional protein or RNA molecule. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all operable anti-sense fragments. Anti-sense polynucleotides and techniques involving anti-sense polynucleotides are well known in the art and are described, for example, in Robinson-
10 Benion et al., "Anti-sense Techniques," *Methods in Enzymol.* 254(23):363-375, 1995; and Kawasaki et al., *Artific. Organs* 20(8):836-848, 1996.

Identification of genomic DNA and heterologous species DNAs can be accomplished by standard DNA/DNA hybridization techniques, under appropriately stringent conditions, using all or part of a cDNA sequence as a probe to screen an
15 appropriate library. Alternatively, PCR techniques using oligonucleotide primers that are designed based on known genomic DNA, cDNA and protein sequences can be used to amplify and identify genomic and cDNA sequences. Synthetic DNAs corresponding to the identified sequences and variants may be produced by conventional synthesis methods. All the polynucleotides provided by the present invention are isolated and
20 purified, as those terms are commonly used in the art.

In specific embodiments, the polynucleotides of the present invention comprise a sequence selected from the group consisting of sequences provided in SEQ ID NOS: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511, and 514-623, and variants of the sequences of SEQ ID NOS: 1-119, 198-274, 349-372, 399-
25 405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623. Polynucleotides that comprise complements of such sequences, reverse complements of such sequences, or reverse sequences of such sequences, together with variants of such sequences, are also provided.

The definition of the terms "complement," "reverse complement," and "reverse sequence," as used herein, is best illustrated by the following example. For the sequence 5' AGGACC 3', the complement, reverse complement, and reverse sequence are as follows:

5	complement	3' TCCTGG 5'
	reverse complement	3' GGTCCT 5'
	reverse sequence	5' CCAGGA 3'.

As used herein, the term "complement" refers to sequences that are fully complementary to a sequence disclosed herein.

In another aspect, the present invention provides isolated polypeptides and functional portions of polypeptides encoded, or partially encoded, by the above polynucleotides. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. The term "polypeptide encoded by a polynucleotide" as used herein, includes polypeptides encoded by a polynucleotide which comprises a partial isolated DNA sequence provided herein. In specific embodiments, the inventive polypeptides comprise an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725, as well as variants of such sequences.

Polypeptides of the present invention may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the polypeptide in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, insect, yeast, or a mammalian cell line such as COS or CHO. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In a related aspect, polypeptides are provided that comprise at least a functional portion of a polypeptide having an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512-513 and 624-725, and variants thereof. As
5 used herein, the "functional portion" of a polypeptide is that portion which contains the active site essential for affecting the function of the polypeptide, for example, the portion of the molecule that is capable of binding one or more reactants. The active site may be made up of separate portions present on one or more polypeptide chains and will generally exhibit high binding affinity.

10 Functional portions of a polypeptide may be identified by first preparing fragments of the polypeptide by either chemical or enzymatic digestion of the polypeptide, or by mutation analysis of the polynucleotide that encodes the polypeptide and subsequent expression of the resulting mutant polypeptides. The polypeptide fragments or mutant polypeptides are then tested to determine which portions retain
15 biological activity, using, for example, the representative assays provided below.

Portions and other variants of the inventive polypeptides may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such
20 polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems, Inc.
25 (Foster City, California), and may be operated according to the manufacturer's instructions. Variants of a native polypeptide may be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (Kunkel, T., *Proc. Natl. Acad. Sci. USA* 82:488-492, 1985). Sections of DNA sequence

may also be removed using standard techniques to permit preparation of truncated polypeptides.

In general, the polypeptides disclosed herein are prepared in an isolated, substantially pure, form. Preferably, the polypeptides are at least about 80% pure, more preferably at least about 90% pure, and most preferably at least about 99% pure. In certain preferred embodiments, described in detail below, the isolated polypeptides are incorporated into pharmaceutical compositions or vaccines for use in the treatment of skin disorders.

As used herein, the term "variant" comprehends nucleotide or amino acid sequences different from the specifically identified sequences, wherein one or more nucleotides or amino acid residues is deleted, substituted, or added. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. In certain preferred embodiments, variants of the inventive sequences retain certain, or all, of the functional characteristics of the inventive sequence. Variant sequences (polynucleotide or polypeptide) preferably exhibit at least 50%, more preferably at least 75%, and most preferably at least 90% or 95% identity to a sequence of the present invention. The percentage identity is determined by aligning the two sequences to be compared as described below, determining the number of identical residues in the aligned portion, dividing that number by the total number of residues in the inventive (queried) sequence, and multiplying the result by 100.

Polynucleotide or polypeptide sequences may be aligned, and percentages of identical nucleotides in a specified region may be determined against another polynucleotide or polypeptide, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. The alignment and similarity of polypeptide sequences may be examined using the BLASTP and algorithm. BLASTX and FASTX algorithms compare nucleotide query sequences translated in all reading frames against polypeptide sequences. The BLASTN, BLASTP and BLASTX algorithms are available on the NCBI anonymous FTP server (<ftp://ncbi.nlm.nih.gov>).

under /blast/executables/ and are available from the National Center for Biotechnology Information (NCBI), National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894 USA.

The FASTA and FASTX algorithms are available on the Internet at the ftp site
5 ftp://ftp.Virginia.edu/pub/. The FASTA software package is also available from the University of Virginia by contacting David Hudson, Assistant Provost for Research, University of Virginia, PO Box 9025, Charlottesville, VA 22906-9025. The FASTA algorithm, set to the default parameters described in the documentation and distributed with the algorithm, may be used in the determination of polynucleotide variants. The
10 readme files for FASTA and FASTX v1.0x that are distributed with the algorithms describe the use of the algorithms and describe the default parameters. The use of the FASTA and FASTX algorithms is also described in Pearson, and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988; and Pearson, *Methods in Enzymol.* 183:63-98, 1990.

15 The BLASTN algorithm version 2.0.4 [Feb-24-1998], 2.0.6 [Sept-16-1998] and 2.0.11 [Jan-20-2000], set to the default parameters described in the documentation and distributed with the algorithm, is preferred for use in the determination of polynucleotide variants according to the present invention. The BLASTP algorithm version 2.0.4, 2.0.6 and 2.0.11, set to the default parameters described in the documentation and distributed
20 with the algorithm, is preferred for use in the determination of polypeptide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP and BLASTX is described in the publication of Altschul, *et al.*, *Nucleic Acids Res.* 25:3389-3402, 1997.

The following running parameters are preferred for determination of alignments
25 and similarities using BLASTN that contribute to the E values and percentage identity for polynucleotides: Unix running command with default parameters thus: blastall -p blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i queryseq -o results; and parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero

invokes default behavior) [Integer]; -r Reward for a nucleotide match (blastn only) [Integer]; -v Number of one-line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; -o BLAST report Output File [File Out] Optional. The following running parameters are preferred for determination of
 5 alignments and similarities using BLASTP that contribute to the E values and percentage identity for polypeptides: blastall -p blastp -d swissprot db -e 10 -G 1 -E 11 -r 1 -v 30 -b 30 -i queryseq -o results; and the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior)
 10 [Integer]; -v Number of one-line descriptions (v) [Integer]; -b Number of alignments to show (b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out] Optional.

The "hits" to one or more database sequences by a queried sequence produced by BLASTN, BLASTP, FASTA, or a similar algorithm, align and identify similar portions
 15 of sequences. The hits are arranged in order of the degree of similarity and the length of sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence.

As noted above, the percentage identity of a polynucleotide or polypeptide sequence is determined by aligning polynucleotide and polypeptide sequences using
 20 appropriate algorithms, such as BLASTN or BLASTP, respectively, set to default parameters; identifying the number of identical nucleic or amino acids over the aligned portions; dividing the number of identical nucleic or amino acids by the total number of nucleic or amino acids of the polynucleotide or polypeptide of the present invention; and then multiplying by 100 to determine the percentage identity. By way of example, a
 25 queried polynucleotide having 220 nucleic acids has a hit to a polynucleotide sequence in the EMBL database having 520 nucleic acids over a stretch of 23 nucleotides in the alignment produced by the BLASTN algorithm using the default parameters. The 23 nucleotide hit includes 21 identical nucleotides, one gap and one different nucleotide. The percentage identity of the queried polynucleotide to the hit in the EMBL database is

thus 21/220 times 100, or 9.5%. The identity of polypeptide sequences may be determined in a similar fashion.

The BLASTN and BLASTX algorithms also produce "Expect" values for polynucleotide and polypeptide alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database indicates true similarity. For example, an E value of 0.1 assigned to a polynucleotide hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the sequences then have a probability of 90% of being the same. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN algorithm. E values for polypeptide sequences may be determined in a similar fashion using various polypeptide databases, such as the SwissProt database.

According to one embodiment, "variant" polynucleotides and polypeptides, with reference to each of the polynucleotides and polypeptides of the present invention, preferably comprise sequences having the same number or fewer nucleic or amino acids than each of the polynucleotides or polypeptides of the present invention and producing an E value of 0.01 or less when compared to the polynucleotide or polypeptide of the present invention. That is, a variant polynucleotide or polypeptide is any sequence that has at least a 99% probability of being the same as the polynucleotide or polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or BLASTX algorithms set at the default parameters. According to a preferred embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of the present invention that has at least a 99% probability of being the same as the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN algorithm set at the default

parameters. Similarly, according to a preferred embodiment, a variant polypeptide is a sequence having the same number or fewer amino acids than a polypeptide of the present invention that has at least a 99% probability of being the same as the polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTP
 5 algorithm set at the default parameters.

Variant polynucleotide sequences will generally hybridize to the recited polynucleotide sequences under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X
 10 SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

As used herein, the term "x-mer," with reference to a specific value of "x," refers to a polynucleotide or polypeptide, respectively, comprising at least a specified number ("x") of contiguous residues of: any of the polynucleotides provided in SEQ ID NO:
 15 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623; or any of the polypeptides set out in SEQ ID NO: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725. The value of x may be from about 20 to about 600, depending upon the specific sequence.

Polynucleotides of the present invention comprehend polynucleotides comprising
 20 at least a specified number of contiguous residues (x-mers) of any of the polynucleotides identified as SEQ ID NO: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623, or their variants. Polypeptides of the present invention comprehend polypeptides comprising at least a specified number of contiguous residues (x-mers) of any of the polypeptides identified as SEQ ID NO: 120-197, 275-348,
 25 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725. According to preferred embodiments, the value of x is at least 20, more preferably at least 40, more preferably yet at least 60, and most preferably at least 80. Thus, polynucleotides of the present invention include polynucleotides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a

250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polynucleotide provided in SEQ ID NOS: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623, or of a variant of one of the polynucleotides provided in SEQ ID NO: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511
5 and 514-623. Polypeptides of the present invention include polypeptides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polypeptide provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725, or of a variant of one of the polypeptides provided
10 in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463, 465, 488-509, 512, 513 and 624-725.

The inventive polynucleotides may be isolated by high throughput sequencing of cDNA libraries prepared from mammalian skin cells as described below in Example 1. Alternatively, oligonucleotide probes based on the sequences provided in SEQ ID NOS:
15 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623 can be synthesized and used to identify positive clones in either cDNA or genomic DNA libraries from mammalian skin cells by means of hybridization or polymerase chain reaction (PCR) techniques. Probes can be shorter than the sequences provided herein but should be at least about 10, preferably at least about 15 and most
20 preferably at least about 20 nucleotides in length. Hybridization and PCR techniques suitable for use with such oligonucleotide probes are well known in the art (see, for example, Mullis, *et al.*, *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich, ed., *PCR Technology*, Stockton Press: NY, 1989; (Sambrook, J, Fritsch, EF and Maniatis, T, eds., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor
25 Laboratory Press, Cold Spring Harbor: New York, 1989). Positive clones may be analyzed by restriction enzyme digestion, DNA sequencing or the like.

In addition, DNA sequences of the present invention may be generated by synthetic means using techniques well known in the art. Equipment for automated synthesis of oligonucleotides is commercially available from suppliers such as Perkin

Elmer/Applied Biosystems Division (Foster City, California) and may be operated according to the manufacturer's instructions.

Since the polynucleotide sequences of the present invention have been derived from skin, they likely encode proteins that have important roles in growth and development of skin, and in responses of skin to tissue injury and inflammation as well as disease states. Some of the polynucleotides contain sequences that code for signal sequences, or transmembrane domains, which identify the protein products as secreted molecules or receptors. Such protein products are likely to be growth factors, cytokines, or their cognate receptors. Several of the polypeptide sequences have more than 25% similarity to known biologically important proteins and thus are likely to represent proteins having similar biological functions.

In particular, the inventive polypeptides have important roles in processes such as: induction of hair growth; differentiation of skin stem cells into specialized cell types; cell migration; cell proliferation and cell-cell interaction. The polypeptides are important in the maintenance of tissue integrity, and thus are important in processes such as wound healing. Some of the disclosed polypeptides act as modulators of immune responses, especially since immune cells are known to infiltrate skin during tissue insult causing growth and differentiation of skin cells. In addition, many polypeptides are immunologically active, making them important therapeutic targets in a whole range of disease states not only within skin, but also in other tissues of the body. Antibodies to the polypeptides of the present invention and small molecule inhibitors related to the polypeptides of the present invention may also be used for modulating immune responses and for treatment of diseases according to the present invention.

In one aspect, the present invention provides methods for using one or more of the inventive polypeptides or polynucleotides to treat disorders in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human.

In this aspect, the polypeptide or polynucleotide is generally present within a pharmaceutical or immunogenic composition. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above

sequences (or variants thereof), and a physiologically acceptable carrier. Immunogenic compositions may comprise one or more of the above polypeptides and a non-specific immune response amplifier, such as an adjuvant or a liposome, into which the polypeptide is incorporated.

- 5 Alternatively, a pharmaceutical or immunogenic composition of the present invention may contain DNA encoding one or more polypeptides as described above, such that the polypeptide is generated *in situ*. In such compositions, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, and bacterial and viral expression systems.
- 10 Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminator signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system
- 5 (*e.g.*, vaccinia or other poxvirus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic, or defective, replication competent virus. Techniques for incorporating DNA into such expression systems are well known in the art. The DNA may also be "naked," as described, for example, in Ulmer *et al.*, *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA
- 10 may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

- Routes and frequency of administration, as well as dosage, vary from individual to individual. In general, the pharmaceutical and immunogenic compositions may be administered by injection (*e.g.*, intradermal, intramuscular, intravenous, or
- 5 subcutaneous), intranasally (*e.g.*, by aspiration) or orally. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg per kg of host, and preferably from about 100 pg to about 1 µg per kg of host. Suitable dose

sizes will vary with the size of the patient, but will typically range from about 0.1 ml to about 5 ml.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax, or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactic galactide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of adjuvants may be employed in the immunogenic compositions of the invention to non-specifically enhance the immune response. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a non-specific stimulator of immune responses, such as lipid A, *Bordetella pertussis*, or *Mycobacterium tuberculosis*. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Freund's Complete Adjuvant (Difco Laboratories, Detroit, Michigan), and Merck Adjuvant (Merck and Company, Inc., Rahway, New Jersey). Other suitable adjuvants include alum, biodegradable microspheres, monophosphoryl lipid A, and Quil A.

The polynucleotides of the present invention may also be used as markers for tissue, as chromosome markers or tags, in the identification of genetic disorders, and for the design of oligonucleotides for examination of expression patterns using techniques well known in the art, such as the microarray technology available from Affymetrix (Santa Clara, CA). Partial polynucleotide sequences disclosed herein may be employed to obtain full length genes by, for example, screening of DNA expression libraries using hybridization probes or PCR primers based on the inventive sequences.

The polypeptides provided by the present invention may additionally be used in assays to determine biological activity, to raise antibodies, to isolate corresponding ligands or receptors, in assays to quantitatively determine levels of protein or cognate corresponding ligand or receptor, as anti-inflammatory agents, and in compositions for skin, connective tissue and/or nerve tissue growth or regeneration. The present invention further provides methods for modulating expression of the inventive polypeptides, for example by inhibiting translation of the relevant polynucleotide. Translation of the relevant polynucleotide may be inhibited, for example, by introducing anti-sense expression vectors; by introducing antisense oligodeoxyribonucleotides or antisense phosphorothioate oligodeoxyribonucleotides; by introducing antisense oligoribonucleotides or antisense phosphorothioate oligoribonucleotides; or by other means which are well known in the art. Cell permeation and activity of antisense oligonucleotides can be enhanced by appropriate chemical modifications, such as the use of phenoxazine-substituted C-5 propynyl uracil oligonucleotides (Flanagan *et al.*, (1999) *Nat. Biotechnol.* 17 (1): 48-52) or 2'-O-(2-methoxy) ethyl (2'-MOE)-oligonucleotides (Zhang *et al.*, (2000) *Nat. Biotechnol.* 18: 862-867). The use of techniques involving antisense polynucleotides is well known in the art and is described, for example, in Robinson-Benion *et al.* (1995), Antisense techniques, *Methods in Enzymol.* 254 (23): 363-375 and Kawasaki *et al.* (1996), *Artific. Organs* 20 (8): 836-848.

The following Examples are offered by way of illustration and not by way of limitation.

Example 1

ISOLATION OF cDNA SEQUENCES FROM SKIN CELL EXPRESSION LIBRARIES

The cDNA sequences of the present invention were obtained by high-throughput sequencing of cDNA expression libraries constructed from specialized rodent or human skin cells as shown in Table 1.

Table 1

<u>Library</u>	<u>Skin cell type</u>	<u>Source</u>
DEPA	dermal papilla	rat

	SKTC	keratinocytes	human
	HNFF	neonatal foreskin fibroblast	human
	MEMS	embryonic skin	mouse
	KSCL	keratinocyte stem cell	mouse
5	TRAM	transit amplifying cells	mouse
	MFSE	epidermis	mouse
	HLEA	small epithelial airway cells	human
	HLEB	small epithelial airway cells	human
	HNKA	NK cells	human

10

These cDNA libraries were prepared as described below.

cDNA Library from Dermal Papilla (DEPA)

15 Dermal papilla cells from rat hair vibrissae (whiskers) were grown in culture and the total RNA extracted from these cells using established protocols. Total RNA, isolated using TRIzol Reagent (BRL Life Technologies, Gaithersburg, Maryland), was used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, California), according to the manufacturer's specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda
20 ZAP cDNA library synthesis kit (Stratagene).

cDNA Library from Keratinocytes (SKTC)

Keratinocytes obtained from human neonatal foreskins (Mitra, R and Nikoloff, B in *Handbook of Keratinocyte Methods*, pp. 17-24, 1994) were grown in serum-free
25 KSFM (BRL Life Technologies) and harvested along with differentiated cells (10^8 cells). Keratinocytes were allowed to differentiate by addition of fetal calf serum at a final concentration of 10% to the culture medium and cells were harvested after 48 hours. Total RNA was isolated from the two cell populations using TRIzol Reagent (BRL Life Technologies) and used to obtain mRNA using a Poly(A) Quik mRNA isolation kit

(Stratagene). cDNAs expressed in differentiated keratinocytes were enriched by using a PCR-Select cDNA Subtraction Kit (Clontech, Palo Alto, California). Briefly, mRNA was obtained from either undifferentiated keratinocytes ("driver mRNA") or differentiated keratinocytes ("tester mRNA") and used to synthesize cDNA. The two
5 populations of cDNA were separately digested with *RsaI* to obtain shorter, blunt-ended molecules. Two tester populations were created by ligating different adaptors at the cDNA ends and two successive rounds of hybridization were performed with an excess of driver cDNA. The adaptors allowed for PCR amplification of only the differentially expressed sequences which were then ligated into T-tailed pBluescript (Hadjeb, N and
10 Berkowitz, GA, *BioTechniques* 20:20-22 1996), allowing for a blue/white selection of cells containing vector with inserts. White cells were isolated and used to obtain plasmid DNA for sequencing.

cDNA library from human neonatal fibroblasts (HNFF)

15 Human neonatal fibroblast cells were grown in culture from explants of human neonatal foreskin and the total RNA extracted from these cells using established protocols. Total RNA, isolated using TRIzol Reagent (BRL Life Technologies, Gaithersburg, Maryland), was used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, California), according to the manufacturer's
20 specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit (Stratagene).

cDNA library from mouse embryonic skin (MEMS)

Embryonic skin was micro-dissected from day 13 post coitum Balb/c mice.
25 Embryonic skin was washed in phosphate buffered saline and mRNA directly isolated from the tissue using the Quick Prep Micro mRNA purification kit (Pharmacia, Sweden). The mRNA was then used to prepare cDNA libraries as described above for the DEPA library.

30 cDNA library from mouse stem cells (KSCL) and transit amplifying (TRAM) cells

Pelts obtained from 1-2 day post-partum neonatal Balb/c mice were washed and incubated in trypsin (BRL Life Technologies) to separate the epidermis from the dermis. Epidermal tissue was disrupted to disperse cells, which were then resuspended in growth medium and centrifuged over Percoll density gradients prepared according to the manufacturer's protocol (Pharmacia, Sweden). Pelleted cells were labeled using Rhodamine 123 (Bertoncello I, Hodgson GS and Bradley TR, *Exp Hematol.* 13:999-1006, 1985), and analyzed by flow cytometry (Epics Elite Coulter Cytometry, Hialeah, Florida). Single cell suspensions of rhodamine-labeled murine keratinocytes were then labeled with a cross reactive anti-rat CD29 biotin monoclonal antibody (Pharmingen, San Diego, California; clone Ha2/5). Cells were washed and incubated with anti-mouse CD45 phycoerythrin conjugated monoclonal antibody (Pharmingen; clone 30F11.1, 10ug/ml) followed by labeling with streptavidin spectral red (Southern Biotechnology, Birmingham, Alabama). Sort gates were defined using listmode data to identify four populations: CD29 bright rhodamine dull CD45 negative cells; CD29 bright rhodamine bright CD45 negative cells; CD29 dull rhodamine bright CD45 negative cells; and CD29 dull rhodamine dull CD45 negative cells. Cells were sorted, pelleted and snap frozen prior to storage at -80°C. This protocol was followed multiple times to obtain sufficient cell numbers of each population to prepare cDNA libraries. Skin stem cells and transit amplifying cells are known to express CD29, the integrin $\beta 1$ chain. CD45, a leukocyte specific antigen, was used as a marker for cells to be excluded in the isolation of skin stem cells and transit amplifying cells. Keratinocyte stem cells expel the rhodamine dye more efficiently than transit amplifying cells. The CD29 bright, rhodamine dull, CD45 negative population (putative keratinocyte stem cells; referred to as K_SCL), and the CD29 bright, rhodamine bright, CD45 negative population (keratinocyte transit amplifying cells; referred to as TRAM) were sorted and mRNA was directly isolated from each cell population using the Quick Prep Micro mRNA purification kit (Pharmacia, Sweden). The mRNA was then used to prepare cDNA libraries as described above for the DEPA library.

cDNA Library from Epithelial Cells (MFSE)

Skin epidermis was removed from flaky skin *fsn* ^{-/-} mice (The Jackson Laboratory, Bar Harbour, ME), the cells dissociated and the resulting single cell suspension placed in culture. After four passages, the cells were harvested. Total RNA,
5 isolated using TRIzol Reagent (BRL Life Technologies, Gaithersburg, MD), was used to obtain mRNA using a Poly(A)Quik mRNA isolation kit (Stratagene, La Jolla, CA), according to the manufacturer's specifications. A cDNA expression library (referred to as the MFSE library) was then prepared from the mRNA by Reverse Transcriptase synthesis using a Lambda ZAP Express cDNA library synthesis kit (Stratagene, La Jolla,
10 CA).

cDNA Libraries from Human Small Airway Epithelial Cells (HLEA and HLEB)

Human small airway epithelium cells SAEC (Cell line number CC-2547, Clonetics Normal Human Cell Systems, Cambrex Corporation, East Rutherford NJ)
15 transformed with human papilloma virus E6E7 that was infected with the bacterium *Yersinia enterocolitica* (ATCC No. 51871, American Type Culture Collection, Manassas VA) and the long form of the Respiratory Syncytial Virus (RSV, ATCC No. VR26), were used as source of RNA to construct the libraries called HLEA and HLEB. Cells from the twelfth passage of SAEC cells were infected with *Y. enterocolitica* for 2 hours at an
20 initial seed of 12.5 bacteria per cell. The cells were disinfected with gentamycin (100 µg/ml) for 2 hours and harvested 4 hours after infection. The cells were then infected with RSV at a moiety of infection of 0.7 for 1 hour and incubated for 6 and 24 hours. Cells were harvested and the RNA extracted following standard protocols.

Total RNA, isolated using TRIzol Reagent (BRL Life Technologies,
25 Gaithersburg, Maryland), was used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, CA), according to the manufacturer's specifications. Two cDNA expression libraries were then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit (Stratagene).

cDNA Library from Epithelial Cells (HNKA)

The subtracted cDNA library (HNKA) from human natural killer (NK) cells was constructed as follows. A NK library was first constructed using pooled RNA extracted from primary NK cells from multiple donors, stimulated for 4 or 20 hours with IL-2 (10 ng/ml), IL-12 (1 ng/ml), IL-15 (50 ng/ml), interferon alpha (IFN- α ; 1,000 U/ml) 5 immobilized anti-CD16 or immobilized anti-NAIL antibody, or from unstimulated cells. RNA was extracted following standard procedures. cDNA was prepared using a TimeSaver kit (Pharmacia, Uppsala, Sweden) following the manufacturer's protocol. The cDNA was ligated to *Bgl*III adaptors and size-selected using cDNA sizing columns 10 (Gibco BRL, Gaithersburg MD). The size-selected NK cDNA was ligated into a pDc 409 vector and transformed into *E. coli* DH105 cells. Single-stranded DNA was prepared from the plasmid library using a helper phage (Stratagene)

A second cDNA library (referred to as FF cDNA library) was constructed using fetal foreskin tissue. RNA was extracted and cDNA prepared following standard 15 protocols. The cDNA was ligated into the plasmid pBluescript following standard protocols. 10 μ g of the FF cDNA library was linearized with the restriction endonuclease *Not*I and used as template to synthesize biotin-labeled cRNA using SP6 polymerase.

The subtracted NK cell library (HNKA) was constructed as follows. The 20 biotinylated FF cRNA was mixed with the NK library, ethanol precipitated and resuspended in 5 μ l buffer (50 mM HEPES pH 7.4, 10 mM EDTA, 1.5 M NaCl, 0.2% SDS). After addition of 5 μ l formamide and heating to 95° for 1 min, the material was left to hybridize for 24 hours at 42°C. 90 μ l of 10 mM HEPES pH 7.3, 1 mM EDTA and 15 μ l streptavidin was added followed by an incubation for 20 min at 50°C. This 25 step was repeated again after extraction with phenol/chloroform.

To the final extracted aqueous phase, the following were added: NaCl to 0.2 M, 1 μ l glycogen and 2 volumes of ethanol. After an overnight precipitation at -20°C, the DNA was pelleted and resuspended in 10 μ l water. A second round of subtraction was performed as above and the DNA transformed into *E. coli* DH105.

cDNA sequences were obtained by high-throughput sequencing of the cDNA libraries described above using a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer.

5

Example 2

CHARACTERIZATION OF ISOLATED cDNA SEQUENCES

The isolated cDNA sequences were compared to sequences in the EMBL DNA database using the computer algorithms FASTA and/or BLASTN. The corresponding protein sequences (DNA translated to protein in each of 6 reading frames) were compared to sequences in the SwissProt database using the computer algorithms FASTX and/or BLASTX. Comparisons of DNA sequences provided in SEQ ID NO: 1-119 to sequences in the EMBL DNA database (using FASTA) and amino acid sequences provided in SEQ ID NO: 120-197 to sequences in the SwissProt database (using FASTX) were made as of March 21, 1998. Comparisons of DNA sequences provided in SEQ ID NO: 198-274 to sequences in the EMBL DNA database (using BLASTN) and amino acid sequences provided in SEQ ID NO: 275-348 to sequences in the SwissProt database (using BLASTP) were made as of October 7, 1998. Comparisons of DNA sequences provided in SEQ ID NO: 349-372 to sequences in the EMBL DNA database (using BLASTN) and amino acid sequences provided in SEQ ID NO: 373-398 to sequences in the SwissProt database (using BLASTP) were made as of January 23, 1999. Comparisons of polynucleotide sequences provided in SEQ ID NO: 418-455 and 466-487 to sequences in the EMBL DNA database (using BLASTN) and polypeptide sequences provided in SEQ ID NO: 456-463 and 488-509 to sequences in the SwissProt database (using BLASTP) were made as of April 23, 2000. Comparisons of polynucleotide sequences provided in SEQ ID NO: 510 and 511 to sequences in the EMBL DNA database (using BLASTN) and polypeptide sequences provided in SEQ ID NO: 512 and 513 to sequences in the SwissProt database (using BLASTP) were made as of July 11, 2000. Comparisons of polynucleotide sequences provided in SEQ ID NO: 514-623 to

sequences in the EMBL66 - HTGs + ENSEMBL (May 1, 2001) DNA database (using BLASTN) and polypeptide sequences provided in SEQ ID NO: 624-725 to sequences in the SP_TR_NRDB + ENSEMBL (April 30, 2001) database (using BLASTP) were made as of May 16, 2001.

5

Isolated cDNA sequences and their corresponding polypeptide sequences were computer analyzed for the presence of signal sequences identifying secreted molecules. Isolated cDNA sequences that have a signal sequence at a putative start site within the sequence are provided in SEQ ID NO: 1-44, 198-238, 349-358, 399, 418-434, 440-449 and 466-471, 516, 519, 520, 523-527, 531, 532, 535-537, 548, 555, 574-580, 585-587, 589, 593, 595, 596, 598-601, 605-607, 609, 612, 613, 615, 616 and 622. The cDNA sequences of SEQ ID NO: 1-6, 198-199, 349-352, 354, 356-358, 419-428, 430-433, 440-444, 446-448, 466, 468-470, 519, 520, 523, 524, 529, 531, 532, 535-537, 579, 585, 587, 598, 605, 609, 613 and 622 were determined to have less than 75% identity (determined as described above), to sequences in the EMBL database using the computer algorithms FASTA or BLASTN, as described above. The polypeptide sequences of SEQ ID NO: 120-125, 275-276, 373-380, 382, 456, 457, 460-462, 488-493, 633, 637, 642, 683, 685, 691, 693, 703, 706, 710, 714, 717, 718, 720, 721 and 725 were determined to have less than 75% identity (determined as described above) to sequences in the SwissProt database using the computer algorithms FASTX or BLASTP, as described above.

Further sequencing of some of the isolated partial cDNA sequences resulted in the isolation of the full-length cDNA sequences provided in SEQ ID NOS: 7-14, 200-231, 372, 418-422, 441-448, 514, 516, 557-561, 567, 568, 619 and 621. The polypeptide sequences encoded by the cDNA sequences of SEQ ID NO: 7-14, 200-231, 372, 514, 516, 557-561, 567, 568, 619 and 621 are provided in SEQ ID NOS: 126-133, 277-308, 396, 624, 626, 666-669, 674 and 724 respectively. The cDNA sequences of SEQ ID NO: 418-422 encode the same amino acid sequences as the cDNA sequences of SEQ ID NO: 7 and 11-14, namely SEQ ID NO: 126 and 130-133, respectively. Comparison of the full-

length cDNA sequences with those in the EMBL database using the computer algorithm FASTA or BLASTN, as described above, revealed less than 75% identity (determined as described above) to known sequences, except for the polynucleotides in SEQ ID NOS: 516, 560 and 619. Comparison of the amino acid sequences provided in SEQ ID NOS: 126-133, 277-308, 666, 668, 669 and 724 with those in the SwissProt database using the computer algorithms FASTX or BLASTP, as described above, revealed less than 75% identity (determined as described above) to known sequences.

Comparison of the polypeptide sequences corresponding to the cDNA sequences of SEQ ID NOS: 15-23 with those in the EMBL database using the computer algorithm FASTA database showed less than 75% identity (determined as described above) to known sequences. These polypeptide sequences are provided in SEQ ID NOS: 134-142.

Further sequencing of some of the isolated partial cDNA sequences resulted in the isolation of full-length cDNA sequences provided in SEQ ID NOS: 24-44, 232-238, 423-434, 449, 466, 468-470, 475, 476 and 484. The polypeptide sequences encoded by the cDNA sequences of SEQ ID NO: 24-44, 232-238, 429, 466, 468-470, 475, 476 and 484 are provided in SEQ ID NOS: 143-163, 309-315, 456, 488, 490-492, 497, 498 and 506, respectively. The cDNA sequences of SEQ ID NO: 423-428, 430-434 and 449 encode the same polypeptide sequences as the cDNA sequences of SEQ ID NO: 27-29, 34, 35, 37, 40-44 and 238, namely SEQ ID NO: 146-148, 153, 154, 156, 159-163 and 315, respectively. These polypeptide sequences were determined to have less than 75% identity, determined as described above to known sequences in the SwissProt database using the computer algorithm FASTX.

Isolated cDNA sequences having less than 75% identity to known expressed sequence tags (ESTs) or to other DNA sequences in the public database, or whose corresponding polypeptide sequence showed less than 75% identity to known protein sequences, were computer analyzed for the presence of transmembrane domains coding for putative membrane-bound molecules. Isolated cDNA sequences that have one or more transmembrane domain(s) within the sequence are provided in SEQ ID NOS: 45-63, 239-253, 359-364, 400-402, 435, 436, 450-452, 455, 470-472, 542, 553-555, 573,

576, 581, 592, 593, 595 and 606. The cDNA sequences of SEQ ID NOS: 45-48, 239-249, 359-361, 363, 450, 451, 455, 472, 473, 553-555, 573, 576 and 592 were found to have less than 75% identity (determined as described above) to sequences in the EMBL database, using the FASTA or BLASTN computer algorithms. The polypeptide sequences encoded by the cDNA sequences of SEQ ID NO: 45-48, 239-249, 359-361, 363, 450, 451, 472, 473, 553-555, 573 and 606 (provided in SEQ ID NOS: 164-167, 316-326, 383, 385-388, 407-408, 460, 461, 494, 495, 662, 663, 664, 679, 682 and 711 respectively) were found to have less than 75% identity, determined as described above, to sequences in the SwissProt database using the FASTX or BLASTP database. The cDNA sequence of SEQ ID NO: 455 encodes the same polypeptide sequence as the cDNA sequence of SEQ ID NO: 359, namely SEQ ID NO: 383.

Comparison of the polypeptide sequences corresponding to the cDNA sequences of SEQ ID NOS: 49-63, 250-253, 436 and 452 with those in the SwissProt database showed less than 75% identity (determined as described above) to known sequences. These polypeptide sequences are provided in SEQ ID NOS: 168-182, 327-330, 457 and 462, respectively.

Using automated search programs to screen against sequences coding for molecules reported to be of therapeutic and/or diagnostic use, some of the cDNA sequences isolated as described above in Example 1 were determined to encode polypeptides that are family members of known protein families. A family member is here defined to have at least 25% identity in the translated polypeptide to a known protein or member of a protein family. These cDNA sequences are provided in SEQ ID NOS: 64-76, 254-264, 365-369, 403, 437-439, 453, 454, 475-487, 510, 511, 514-527, 529-531, 533-536, 538-546, 548, 549, 553-559, 562, 564, 565, 567, 569-575, 577-589, 591-602, 604-612, 616-618, 621 and 622. The polypeptide sequences encoded by the cDNA sequences of SEQ ID NO: 64-76, 254-264, 365-369, 403, 438, 439, 453, 475-487, 510 and 511, 514-527, 529-531, 533-536, 538-546, 548, 549, 553-559, 562, 564, 565, 567, 569-575, 577-589, 591-602, 604-612, 616-618, 621 and 622 are provided in SEQ ID NOS: 183-195, 331-341, 389-393, 409, 458, 459, 463, 497-509, 624-637, 639-641, 643-

646, 648-656, 658, 659, 662-668, 670, 672-681, 683-707, 709-717 and 721-725, respectively. The cDNA sequences of SEQ ID NO: 437 and 454 encode the same amino acid sequences as the cDNA sequences of SEQ ID NO: 68 and 262, namely SEQ ID NO: 187 and 339, respectively. The cDNA sequences of SEQ ID NOS: 64-68, 254-264, 365-369, 437-439, 453, 454, 475-478, 480-482, 484, 485, 487, 511, 514, 515, 517-520, 522, 523, 525, 529-531, 535, 536, 538, 541, 544-546, 549, 553-559, 564, 565, 567, 569-573, 579, 587, 588, 592, 597, 598, 602, 604, 605, 608-611, 617, 621 and 622 show less than 75% identity (determined as described above) to sequences in the EMBL database using the FASTA or BLASTN computer algorithms. Similarly, the amino acid sequences of SEQ ID NOS: 183-195, 331-341, 389-393, 458, 459, 463, 497, 498, 503-505, 507-509, 512, 513, 628, 632, 633, 637, 640, 655, 662-666, 668, 672, 673, 676, 679, 683, 685, 688, 691, 693, 694, 702, 703, 706, 707, 710, 711, 713, 714, 717, 721, 722 and 725 show less than 75% identity to sequences in the SwissProt database.

The isolated cDNA sequences encode proteins that influence the growth, differentiation and activation of several cell types, and that may usefully be developed as agents for the treatment and diagnosis of skin wounds, cancers, growth and developmental defects, and inflammatory disease. The utility for certain of the proteins of the present invention, based on similarity to known proteins, is provided in Table 2 below, together with the location of signal peptides and transmembrane domains for certain of the inventive sequences:

Table 2
FUNCTIONS OF NOVEL PROTEINS

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
64, 372	183, 396	Slit, a secreted molecule required for central nervous system development
65	184	Immunoglobulin receptor family. About 40% of leucocyte membrane polypeptides contain immunoglobulin superfamily domains

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
66, 403 510	185, 409 512	RIP protein kinase, a serine/threonine kinase that contains a death domain to mediate apoptosis
67	186	Extracellular protein with epidermal growth factor domain capable of stimulating fibroblast proliferation
68, 437	187	Transforming growth factor alpha, a protein which binds epidermal growth factor receptor and stimulates growth and mobility of keratinocytes
69	188	DRS protein which has a secretion signal component and whose expression is suppressed in cells transformed by oncogenes
70	189	A33 receptor with immunoglobulin-like domains and is expressed in greater than 95% of colon tumors
71	190	Interleukin-12 alpha subunit, component of a cytokine that is important in the immune defense against intracellular pathogens. IL-12 also stimulates proliferation and differentiation of TH1 subset of lymphocytes
72	191	Tumor Necrosis Factor receptor family of proteins that are involved in the proliferation, differentiation and death of many cell types including B and T lymphocytes.
73	192	Epidermal growth factor family proteins which stimulate growth and mobility of keratinocytes and epithelial cells. EGF is involved in wound healing. It also inhibits gastric acid secretion.
74	193	Fibronectin Type III receptor family. The fibronectin III domains are found on the extracellular regions of cytokine receptors
75	194	Serine/threonine kinases (STK2_HUMAN) which participate in cell cycle progression and signal transduction
76	195	Immunoglobulin receptor family
254	331	Receptor with immunoglobulin-like domains and homology to A33 receptor which is expressed in greater than 95% of colon tumors
255	332	Epidermal growth factor family proteins which stimulate growth and mobility of keratinocytes and epithelial cells. EGF is involved in wound healing. It also inhibits gastric acid secretion.
256	333	Serine/threonine kinases (STK2_HUMAN) which participate in cell cycle progression and signal transduction

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
257	334	Contains protein kinase and ankyrin domains. Possible role in cellular growth and differentiation.
258	335	Notch family proteins which are receptors involved in cellular differentiation.
259	336	Extracellular protein with epidermal growth factor domain capable of stimulating fibroblast proliferation.
260, 453	337, 463	Fibronectin Type III receptor family. The fibronectin III domains are found on the extracellular regions of cytokine receptors.
261	338	Immunoglobulin receptor family
262	339	ADP/ATP transporter family member containing a calcium binding site.
263	340	Mouse CXC chemokine family members are regulators of epithelial, lymphoid, myeloid, stromal and neuronal cell migration and cancers, agents for the healing of cancers, neuro-degenerative diseases, wound healing, inflammatory autoimmune diseases like psoriasis, asthma, Crohns disease and as agents for the prevention of HIV-1 of leukocytes
264	341	Nucleotide-sugar transporter family member.
365	389	Transforming growth factor betas (TGF-betas) are secreted covalently linked to latent TGF-beta-binding proteins (LTBPs). LTBPs are deposited in the extracellular matrix and play a role in cell growth or differentiation.
366	390	Integrins are Type I membrane proteins that function as laminin and collagen receptors and play a role in cell adhesion.
367	391	Integrins are Type I membrane proteins that function as laminin and collagen receptors and play a role in cell adhesion.
368	392	Cell wall protein precursor. Are involved in cellular growth or differentiation.
369	393	HT protein is a secreted glycoprotein with an EGF-like domain. It functions as a modulator of cell growth, death or differentiation.
467	489	Myb proto-oncogene (c-Myb), involved in transcription regulation and activation of transcription

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
471	493	Chondroitin sulfotransferase, a member of the HNK-1 sulfotransferase family. These molecules are involved in the pathogenesis of arteriosclerosis, and proliferation of arterial smooth muscle cells during development of arteriosclerosis.
472	494	36 kDa nucleolar protein HNP36, a novel growth factor responsive gene expressed in the pituitary and parathyroid glands
475	497	Zinc protease is a matrix metalloproteinase whose activity is directed against components of the extracellular matrix and play an important role in the growth, metastasis and angiogenesis of tumors.
476	498	Diapophytoene dehydrogenase crtn-like molecule. This molecule is similar to the diapophytoene dehydrogenase crt molecule in a major photosynthesis gene cluster from the bacterium <i>Heliobacillus mobilis</i>
477	499	Protocadherin 3 family member, involved in cell to cell interactions.
478	500	Integrins are Type I membrane proteins that function as laminin and collagen receptors and play a role in cell adhesion.
479	501	Integrin family member. Integrins are Type I membrane proteins that function as laminin and collagen receptors and play a role in cell adhesion.
480	502	Similar to secreted HT Protein, a secreted glycoprotein with an EGF-like domain. It functions as a modulator of cell growth, death or differentiation.
481	503	Agrin family member: Agrin is produced by motoneurons and induces the aggregation of nicotinic acetylcholine receptors.
482	504	Macrophage Scavenger Receptors bind to a variety of polyanionic ligands and display complex binding characteristics. They have been implicated in various macrophage-associated processes, including atherosclerosis.
483	505	Similar to GARP, a member of the family of leucine-rich repeat-containing proteins involved in platelet-endothelium interactions.
484	506	Epidermal growth factor family proteins which stimulate growth and mobility of keratinocytes and epithelial cells. EGF is involved in wound healing. It also inhibits gastric

P/N SEQ ID NO:	A/A SEQ. ID NO:	SIMILARITY TO KNOWN PROTEINS; FUNCTION
		acid secretion.
485	507	Colony stimulating growth factor family.
486	508	Cytokine receptors
487	509	IL17 Receptor to Interleukin 17 (IL17), a T cell derived cytokine that may play a role in initiation or maintenance of the inflammatory response.
438	458	MEGF6, a protein containing multiple EGF-like-domains.
439	459	Protein kinase family member involved in signal transduction.
454		Peroxisomal calcium-dependent solute carrier, a new member of the mitochondrial transporter superfamily.
511	513	Serine/threonine kinase NEK1 is a NIMA-related protein kinase that phosphorylates serines and threonines, but also possesses tyrosine kinase activity. NEK1 has been implicated in the control of meiosis and belongs to the NIMA kinase subfamily.
514	624 626	Homologue isolated from rat dermal papilla of integrin alpha-11/beta-1 that is involved in muscle development and maintaining integrity of adult muscle and other adult tissues. Integrin alpha-11/beta-1 is a receptor for collagen and belongs to the integrin alpha chain family.
516	625	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 21; nucleotides 42 to 104).
517	626	Homologue isolated from a rat dermal papilla library of OASIS (old astrocyte specifically-induced substance) and that plays a role in regulation of the response of astrocytes to inflammation and trauma of the central nervous system (CNS) during gliosis. The OASIS gene encodes a putative transcription factor belonging to the cyclic AMP responsive element binding protein/activating transcription factor (CREB/ATF) gene family (Honma et al., Brain Res. Mol. Brain Res. 69:93-103, 1999).

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
519	628	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 24; nucleotides 50 to 121).
520	630	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 35; nucleotides 67 to 171).
523	633	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 17; nucleotides 3 to 53).
524	634	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 20; nucleotides 13 to 72).
525, 534	635, 644	Homologue isolated from a rat dermal papilla library of leucyl-specific aminopeptidase, PILS-AP and that plays role in many physiological processes as a substrate-specific peptidase. PILS is a new member of the M1 family of Zn-dependent aminopeptidases that comprises members of closely related enzymes which are known to be involved in a variety of physiologically important processes.
526	636	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 26; nucleotides 114 to 191).
527	637	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 26; nucleotides 23 to 100).
529	639	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 17; nucleotides 37 to 87).
530	640	This is a homologue isolated from a rat dermal papilla library of a maturase that is involved in RNA splicing.
531	641	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 17; nucleotides 180 to 230).
532	642	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 32; nucleotides 245 to 340).
535	645	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 25; nucleotides 188 to 333).

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
536	646	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 21; nucleotides 185 to 247).
537	647	This is a secreted molecule isolated from rat dermal papillae with a signal peptide at the N-terminus (amino acid residues 1 to 24; nucleotides 129 to 200).
541	651	This is a homologue isolated from a rat dermal papilla library of a hepatoma-derived growth factor (HDGF) that is involved in stimulation of cell proliferation.
542	652	This is a receptor-like molecule isolated from rat dermal papillae with two transmembrane domains (amino acid residues 20 to 40 and 58 to 78).
545	655	This is a homologue isolated from a rat dermal papilla library of Link protein (LP) and that is involved in bone formation. LP plays an essential role in endochondral bone formation by stabilizing the supramolecular assemblies of aggrecan and hyaluronan (Deak et al., Cytogenet. Cell Genet. 87:75-79, 1999).
548	658	This is a homologue isolated from a rat dermal papilla library of thrombospondin (TSP). It is a secreted protein with a signal peptide in amino acid residues 1 to 18 (nucleotides 210 to 263). TSP is an extracellular matrix glycoprotein whose expression has been associated with a variety of cellular processes including growth and embryogenesis (Laherty et al., J. Biol. Chem. 267:3,274-3,281, 1992).
553	662	This is a receptor-like molecule isolated from rat dermal papillae with a transmembrane domain (amino acid residues 434 to 454).
554	663	This is a receptor-like molecule isolated from rat dermal papillae with a transmembrane domain (amino acid residues 546 to 566).
555	664	This is a homologue isolated from a rat dermal papilla library of B7-like mouse GL50 (mGL50). It is a receptor-like molecule with a signal peptide in residues 1 to 24 (nucleotides 149 to 220) and a transmembrane domain in amino acid residues 262 to 282. GL50 is a specific ligand for the ICOS receptor and this interaction functions in lymphocyte costimulation (Ling et al., J. Immunol. 164:1,653-1,657, 2000).

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
557, 558, 561-572	666, 667, 670-678	These molecules are differentially expressed in stem cells but not in mature keratinocytes and are involved in developmental processes. They may be employed for diagnosis of tumors with an immature phenotype.
559	668	This is a homologue isolated from a mouse stem cell library of ABSENT IN MELANOMA 1 protein AIM1 and that can be used for diagnosis of tumours with an immature phenotype. AIM1 is a novel gene whose expression is associated with the experimental reversal of tumorigenicity of human malignant melanoma and belongs to the betagamma-crystallin superfamily (Ray et al., Proc. Natl. Acad. Sci. USA 94:3,229-3,234, 1997)
560	669	Homologue isolated from a mouse stem cell library of endothelin-converting enzyme 2 (ECE-2) and that can be used for diagnosis of tumours with an immature phenotype. Endothelins (ET) are a family of potent vasoactive peptides that are produced from biologically inactive intermediates, termed big endothelins, via a proteolytic processing at Trp21-Val/Ile22. ECE-2, that produces mature ET-1 from big ET-1 both in vitro and in transfected cells. ECE-2 acts as an intracellular enzyme responsible for the conversion of endogenously synthesized big ET-1 at the trans-Golgi network, where the vesicular fluid is acidified (Emoto and Yanagisawa, J. Biol. Chem. 270:15,262-15,268, 1995).
573	679	Mouse homologue of EGF-like molecule containing mucin-like hormone receptor 2 (EMR2). The isolated molecule contains three transmembrane regions: amino acid residues 20 to 40, 66 to 86 and 92 to 112. The epidermal growth factor (EGF)-TM7 proteins [EMR1 and EMR2, F4/80, and CD97] constitute a recently defined class B GPCR subfamily and are predominantly expressed on leukocytes. These molecules possess N-terminal EGF-like domains coupled to a seven-span transmembrane (7TM) moiety via a mucin-like spacer domain (Lin et al., Genomics 67:188-200, 2000).
574	680	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 17; nucleotides 238 to 288).
575	681	Mouse homologue of a glucocorticoid-inducible protein GIS5 with a signal peptide at the N-terminus (amino acid residues 1 to 17; nucleotides 56-106).

P/N SEQ ID NO:	A/A SEQ ID NO:	SIMILARITY TO KNOWN PROTEINS; FUNCTION
		residues 1 to 17; nucleotides 56-106).
576	682	This is a murine surface receptor-like molecule with a signal peptide at the N-terminus (amino acid residues 1 to 17; nucleotides 1179 to 199) and a transmembrane domain (amino acid residues 179 to 199).
577	683	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 16; nucleotides 55 to 102).
578	684	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 22; nucleotides 12 to 77).
579	685	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 17; nucleotides 82 to 132).
580	686	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 20; nucleotides 20 to 79).
581	687	This is a murine receptor-like molecule with transmembrane domains at amino acid residues 50 to 70; 84 to 104; 116 to 136 and 179 to 198.
585	691	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 20; nucleotides 260 to 319).
586	695	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 22; nucleotides 295 to 360).
587	693	This is a mouse homologue of serotransferrin, also known as siderophilin or beta-1-metal binding globulin) and that is involved in iron transport. This homologue is a secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 19; nucleotides 43 to 99). Transferrins are iron binding transport proteins which can bind two atoms of ferric iron in association with the binding of an anion, usually bicarbonate. It is responsible for the transport of iron from sites of absorption and heme degradation to those of storage and utilization. Serum transferrin may also have a further role in stimulating cell proliferation. Transferrin belongs to the transferrin family.

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
589	695	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 25; nucleotides 1 to 75).
592	697	This is a murine receptor-like molecule with a transmembrane domain in amino acid residues 52 to 72.
593	698	Mouse homologue of channel inducing factor (CHIF) that plays a role in ion transport. The mouse homologue has a signal peptide at the N-terminus of the predicted polypeptide (amino acid residues 1 to 20; nucleotides 102 to 161) and a transmembrane domain (amino acid residues 38 to 58). CHIF evokes a potassium channel activity (Attali et al., Proc. Natl. Acad. Sci. USA 92:6092-6096, 1995).
595	700	Homologue of hyaluronan receptor LYVE-1 that plays a role in hyaluronan uptake. This mouse homologue has the characteristic signal peptide and transmembrane domain of a receptor. A signal peptide was identified in the isolated molecule in amino acid residues 1 to 18 (nucleotides 62 to 115) and the transmembrane domain in amino acid residues 233 to 253. The extracellular matrix glycosaminoglycan hyaluronan (HA) is an abundant component of skin and mesenchymal tissues where it facilitates cell migration during wound healing, inflammation, and embryonic morphogenesis. Both during normal tissue homeostasis and particularly after tissue injury, HA is mobilized from these sites through lymphatic vessels to the lymph nodes where it is degraded before entering the circulation for rapid uptake by the liver. LYVE-1 is a receptor for HA on the lymph vessel wall and plays a role in the transport of HA from tissue to lymph (Banerji et al., J. Cell Biol. 144:789-801, 1999).
596	701	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 21; nucleotides 7 to 69).
598	703	Homologue of tumor-associated glycoprotein E4 (TAA1 or TAGE4) that belongs to the immunoglobulin superfamily. This molecule has a signal peptide at the N-terminus (amino acid residues 1 to 24; nucleotides 71 to 142) and is therefore a secreted protein.

P/N SEQ ID NO:	A/A SEQ. ID NO.	SIMILARITY TO KNOWN PROTEINS; FUNCTION
599	704	Homologue of the LUNX protein, also known as nasopharyngeal carcinoma-related protein, tracheal epithelium enriched protein or plunc, that is expressed in epithelial cells in the airways. It has a signal peptide at the N-terminus (amino acid residues 1 to 19; nucleotides 39 to 95). Expression of LUNX is restricted to the trachea, upper airway, nasopharyngeal epithelium and salivary gland (Bingle and Bingle, Biochim. Biophys. Acta 1493:363-367, 2000).
600	705	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 23; nucleotides 136 to 204).
601	706	Homologue of prenylcysteine lyase (EC 4.4.1.18) and that is involved in degradation of prenylated proteins. It has a signal peptide at the N-terminus (amino acid residues 1 to 28; nucleotides 22 to 105). Prenylcysteine lyase is a specific enzyme involved in the final step of prenylcysteine metabolism in mammalian cells. The enzyme does not require NADPH as cofactor for prenylcysteine degradation, thus distinguishing it from cytochrome P450- and flavin-containing monooxygenases that catalyze S-oxidation of thioethers (Zhang et al., J. Biol. Chem. 274:35802-35808, 1999).
605	710	Homologue of endoplasmin, endoplasmic reticulum protein 99 (ERp99), 94 kDa glucose-regulated protein (GRP94) and polymorphic tumor rejection antigen 1 (gp96). The isolated molecule has a signal peptide at the N-terminus (amino acid residue 1 to 21; nucleotides 1867 to 206). ERp99 is an abundant, conserved transmembrane glycoprotein of the endoplasmic reticulum membrane and homologous to the 90-kDa heat shock protein (hsp90) and the 94-kDa glucose regulated protein (GRP94) (Mazzarella and Green, J. Biol. Chem. 262:8875-8883, 1987).
606	711	Homologue of PILRalpha, formerly known as inhibitory receptor PIRIalpha and that is involved in signal transduction in various cellular processes. This molecule contains a signal peptide at the N-terminal end (amino acid residues 1-21 and nucleotides 47 to 139) and a transmembrane domain at amino acid residues 191 to 211. SHP-1-mediated dephosphorylation of protein tyrosine

P/N SEQ ID NO:	A/A SEQ. ID NO:	SIMILARITY TO KNOWN PROTEINS; FUNCTION
		residues is central to the regulation of several cell signaling pathways. PILRalpha, a novel immunoreceptor tyrosine-based inhibitory motif-bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is paired with the truncated counterpart PILRbeta (Mousseau et al., J. Biol. Chem. 275:4467-4474, 2000).
607	712	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 18; nucleotides 38 to 91).
609	714	Homologue of retinal short-chain dehydrogenase/reductase retSDR2 that plays a role on retinal metabolism. It has a signal peptide at the N-terminus at amino acid residues 1 – 29 (nucleotides 302 to 388). Retinol dehydrogenases (RDH) catalyze the reduction of all-trans-retinal to all-trans-retinol within the photoreceptor outer segment in the regeneration of bleached visual pigments (Haeseleer et al., J. Biol. Chem. 273:21790-21799, 1998)
612	717	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 22; nucleotides 6 to 71).
613	718	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 25; nucleotides 210 to 284).
615	720	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 16; nucleotides 70 to 117).
616	721	This is a murine secreted molecule with a signal peptide at the N-terminus (amino acid residues 1 to 18; nucleotides 1 to 54).

The locations of open reading frames (ORFs) within certain of the inventive cDNA sequences are shown in Table 3, below.

5

Table 3
LOCATION OF OPEN READING FRAMES

SEQ ID NO Polynucleotide	ORF	SEQ ID NO Polypeptide
514	1-2,067	624
515	2-730	625
516	42-1,772	626
517	1-681	627
518	170-416	628
519	50-770	629
520	67-708	630
521	110-613	631
522	41-457	632
523	3-230	633
524	13-573	634
525	64-2,856	635
526	114-599	636
527	23-520	637
528	953-1,138	638
529	37-687	639
530	145-366	640
531	180-1,508	643
532	245-442	642
533	125-595	643
534	64-2,856	644
535	188-727	645
536	185-1,081	646
537	129-308	647
538	32-853	648
539	2-268	649
540	3-875	650
541	284-892	651
542	37-276	652
543	127-1,794	653
544	1-735	654
545	142-939	655
546	51-1,082	656
547	143-328	657
548	210-3,728	658
549	26-1,354	659
551	1,236-1,892	660
552	853-1,178	661

SEQ ID NO Polynucleotide	ORF	SEQ ID NO Polypeptide
553	54-1,356	662
554	637-2,244	663
555	149-1,072	664
556	18-449	665
557	275-1,171	666
558	453-1,133	667
559	104-2,449	668
560	463-687	669
562	1-1,107	670
563	2-883	671
564	188-2,902	672
565	3-524	673
567	2,584-3,996	674
569	1-960	675
570	315-599	676
571	1-414	677
572	806-1,912	678
573	120-752-	679
574	2381,359	680
575	56-1,456	681
576	13-645	682
577	55-1,323	683
578	12-698	684
579	82-810	685
580	20-586	686
581	65-808	687
582	369-761	688
583	1-769	689
584	164-1,321	690
585	260-1,489	691
586	295-1,131	692
587	43-2,136	693
588	1-1,203	694
589	1-525	695
591	1-584	696
592	1-522	697
593	102-368	698
594	1-517	699

SEQ ID NO Polynucleotide	ORF	SEQ ID NO Polypeptide
595	62-1,018	700
596	7-282	701
597	1-736	702
598	71-1,297	703
599	39-875	704
600	136-930	705
601	22-1,539	706
602	69-521	707
603	104-448	708
604	1-399	709
605	3,068-5,476	710
606	47-721	711
607	38-439	712
608	1-1,656	713
609	302-1,327	714
610	845-1,447	715
611	975-1,375	716
612	6-272	717
613	210-464	718
614	462-869	719
615	70-459	720
616	1-1,107	721
617	1-349	722
618	93-528	723
621	380-1,033	724
622	43-2,115	725

The cDNA sequences of SEQ ID NO: 514, 515, 516, 557, 558, 559, 560, 561,
5 567, 568, 619 and 621 are extended sequences of SEQ ID NO: 479, 480, 353, 91, 108,
82, 92, 81, 105, 90, 362 and 360, respectively. SEQ ID NO: 516, 520, 521, 523, 525,
526, 529, 534-536, 541-543, 546, 548, 549, 557, 574, 575, 577-581, 584-587, 589, 593,
595, 596, 598-601, 605, 607, 609, 610, 614, 616 and 622 represent full-length cDNA
sequences.

The polynucleotide sequences of SEQ ID NOS: 77-117, 265-267, 404-405 and 557-611 are differentially expressed in either keratinocyte stem cells (KSCL) or in transit amplified cells (TRAM) on the basis of the number of times these sequences exclusively appear in either one of the above two libraries; more than 9 times in one and none in the other (Audic S. and Claverie J-M, *Genome Research*, 7:986-995, 1997). The sequences of SEQ ID NOS: 77-89, 265-267 and 365-369 were determined to have less than 75% identity to sequences in the EMBL database using the computer algorithm FASTA or BLASTN, as described above. The polypeptide sequences encoded by the cDNA sequences of SEQ ID NO: 77-117, 265-267, 404-405 and 557-611 are provided in SEQ ID NOS: 666-718. The amino acid sequences of SEQ ID NOS: 666, 668, 669, 671-673, 675, 676, 679, 682, 683, 685, 688, 690, 691, 693, 694, 702, 703, 706-708, 710, 711, 713 and 714 show less than 75% identity to sequences in the SwissProt database.

The polypeptides encoded by these polynucleotide sequences have utility as markers for identification and isolation of these cell types, and antibodies against these proteins may be usefully employed in the isolation and enrichment of these cells from complex mixtures of cells. Isolated polynucleotides and their corresponding proteins exclusive to the stem cell population can be used as drug targets to cause alterations in regulation of growth and differentiation of skin cells, or in gene targeting to transport specific therapeutic molecules to skin stem cells.

20

Example 3

ISOLATION AND CHARACTERIZATION OF THE HUMAN HOMOLOG OF muTR1

The human homolog of muTR1 (SEQ ID NO: 68), obtained as described above in Example 1, was isolated by screening 50,000 pfu's of an oligo dT primed HeLa cell cDNA library. Plaque lifts, hybridization, and screening were performed using standard molecular biology techniques (Sambrook, J, Fritsch, EF and Maniatis, T, eds., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor: New York, 1989). The determined cDNA sequence of the isolated human homolog (huTR1) is provided in SEQ ID NO: 118, with the corresponding

25

polypeptide sequence being provided in SEQ ID NO: 196. The library was screened using an [α 32 P]-dCTP labeled double stranded cDNA probe corresponding to nucleotides 1 to 459 of the coding region within SEQ ID NO: 118.

5 **The polypeptide sequence of huTR1 has regions similar to Transforming Growth Factor-alpha, indicating that this protein functions like an epidermal growth factor (EGF). EGF family members exist in a functional form as small peptides. Alignment of the functional peptides of the EGF family with SEQ ID NO: 196 revealed that an internal segment of SEQ ID NO: 196 (amino acids 54-104) shows greater than 40% identity to the active peptides of EGF, TGF-alpha and Epregrulin. The active
10 peptides of the EGF family are sufficient for activity and contain several conserved residues critical for the maintenance of this activity. These residues are retained in huTR1. This EGF-like protein will serve to stimulate keratinocyte growth and motility, and to inhibit the growth of epithelial-derived cancer cells. This novel gene and its encoded protein may thus be used as agents for the healing of wounds and regulators of
15 epithelial-derived cancers.

Analysis of RNA transcripts by Northern Blotting

Northern analysis to determine the size and distribution of mRNA for huTR1 was performed by probing human tissue mRNA blots (Clontech) with a probe comprising
20 nucleotides 93-673 of SEQ ID NO: 118, radioactively labeled with [α 32 P]-dCTP. Prehybridization, hybridization, washing and probe labeling were performed as described in Sambrook, *et al.*, *Ibid.* mRNA for huTR1 was 3.5-4kb in size and was observed to be most abundant in heart and placenta, with expression at lower levels being observed in spleen, thymus, prostate and ovary (Fig. 1).

25 The high abundance of mRNA for huTR1 in the heart and placenta indicates a role for huTR1 in the formation or maintenance of blood vessels, as heart and placental tissues have an increased abundance of blood vessels, and therefore endothelial cells, compared to other tissues in the body. This, in turn, demonstrates a role for huTR1 in angiogenesis and vascularization of tumors. This is supported by the ability of

Transforming Growth Factor-alpha and EGF to induce *de novo* development of blood vessels (Schreiber, *et al.*, *Science* 232:1250-1253, 1986) and stimulate DNA synthesis in endothelial cells (Schreiber, *et al.*, *Science* 232:1250-1253, 1986), and their over-expression in a variety of human tumors.

5

Purification of muTR1 and huTR1

Polynucleotides 177-329 of muTR1 (SEQ ID NO: 268), encoding amino acids 53-103 of muTR1 (SEQ ID NO: 342), and polynucleotides 208-360 of huTR1 (SEQ ID NO: 269), encoding amino acids 54-104 of huTR1 (SEQ ID NO: 343), were cloned into
0 the bacterial expression vector pProEX HT (BRL Life Technologies), which contains a bacterial leader sequence and N-terminal 6xHistidine tag. These constructs were transformed into competent XL1-Blue *E. coli* as described in Sambrook *et al.*, *Ibid*.

Starter cultures of these recombinant XL1-Blue *E. coli* were grown overnight at 37°C in Terrific broth containing 100 µg/ml ampicillin. This culture was spun down and
15 used to inoculate 500 ml culture of Terrific broth containing 100 µg/ml ampicillin. Cultures were grown until the OD₅₉₅ of the cells was between 0.4 and 0.8, whereupon IPTG was added to 1 mM. Cells were induced overnight and bacteria were harvested by centrifugation.

Both the polypeptide of muTR1 (SEQ ID NO: 342; referred to as muTR1a) and
20 that of huTR1 (SEQ ID NO: 343; referred to as huTR1a) were expressed in insoluble inclusion bodies. In order to purify the polypeptides muTR1a and huTR1a, bacterial cell pellets were re-suspended in lysis buffer (20 mM Tris-HCl pH 8.0, 10 mM beta mercaptoethanol, 1 mM PMSF). To the lysed cells, 1% NP40 was added and the mix incubated on ice for 10 minutes. Lysates were further disrupted by sonication on ice at
25 95W for 4 x 15 seconds and then centrifuged for 15 minutes at 14,000 rpm to pellet the inclusion bodies.

The resulting pellet was re-suspended in lysis buffer containing 0.5% w/v CHAPS and sonicated on ice for 5-10 seconds. This mix was stored on ice for 1 hour, centrifuged at 14,000 rpm for 15 minutes at 4 °C and the supernatant discarded. The pellet was once

more re-suspended in lysis buffer containing 0.5% w/v CHAPS, sonicated, centrifuged and the supernatant removed as before. The pellet was re-suspended in solubilizing buffer (6 M Guanidine HCl, 0.5 M NaCl, 20 mM Tris HCl, pH 8.0), sonicated at 95 W for 4 x 15 seconds and then centrifuged for 20 minutes at 14,000 rpm and 4 °C to remove
5 debris. The supernatant was stored at 4 °C until use.

Polypeptides muTR1a and huTR1a were purified by virtue of the N-terminal 6x Histidine tag contained within the bacterial leader sequence, using a Nickel-Chelating Sepharose column (Amersham Pharmacia, Uppsala, Sweden) and following the manufacturer's recommended protocol. In order to refold the proteins once purified, the
10 protein solution was added to 5x its volume of refolding buffer (1 mM EDTA, 1.25 mM reduced glutathione, 0.25 mM oxidised glutathione, 20 mM Tris-HCl, pH 8.0) over a period of 1 hour at 4 °C. The refolding buffer was stirred rapidly during this time, and stirring continued at 4 °C overnight. The refolded proteins were then concentrated by ultrafiltration using standard protocols.

15

Biological Activities of Polypeptides muTR1a and huTR1a

muTR1 and huTR1 are novel members of the EGF family, which includes EGF, TGF α , epiregulin and others. These growth factors are known to act as ligands for the EGF receptor. The pathway of EGF receptor activation is well documented. Upon
20 binding of a ligand to the EGF receptor, a cascade of events follows, including the phosphorylation of proteins known as MAP kinases. The phosphorylation of MAP kinase can thus be used as a marker of EGF receptor activation. Monoclonal antibodies exist which recognize the phosphorylated forms of 2 MAP kinase proteins – ERK1 and ERK2.

25 In order to examine whether purified polypeptides of muTR1a and huTR1a act as a ligand for the EGF receptor, cells from the human epidermal carcinoma cell line A431 (American Type Culture Collection, No. CRL-1555, Manassas, Virginia) were seeded into 6 well plates, serum starved for 24 hours, and then stimulated with purified muTR1a or huTR1a for 5 minutes in serum free conditions. As a positive control, cells were

stimulated in the same way with 10 to 100 ng/ml TGF-alpha or EGF. As a negative control, cells were stimulated with PBS containing varying amounts of LPS. Cells were immediately lysed and protein concentration of the lysates estimated by Bradford assay. 15 µg of protein from each sample was loaded onto 12% SDS-PAGE gels. The proteins
5 were then transferred to PVDF membrane using standard techniques.

For Western blotting, membranes were incubated in blocking buffer (10mM Tris-HCl, pH 7.6, 100 mM NaCl, 0.1% Tween-20, 5% non-fat milk) for 1 hour at room temperature. Rabbit anti-Active MAP kinase pAb (Promega, Madison, Wisconsin) was added to 50 ng/ml in blocking buffer and incubated overnight at 4 °C. Membranes were
10 washed for 30 mins in blocking buffer minus non-fat milk before being incubated with anti rabbit IgG-HRP antibody, at a 1:3500 dilution in blocking buffer, for 1 hour at room temperature. Membranes were washed for 30 minutes in blocking buffer minus non-fat milk, then once for 5 minutes in blocking buffer minus non-fat milk and 0.1% Tween-20. Membranes were then exposed to ECL reagents for 2 min, and then autoradiographed for
15 5 to 30 min.

As shown in Fig. 2, both muTR1a and huTR1a were found to induce the phosphorylation of ERK1 and ERK2 over background levels, indicating that muTR1 and huTR1 act as ligands for a cell surface receptor that activates the MAP kinase signaling pathway, possibly the EGF receptor. As shown in Fig. 11, huTR1a was also
20 demonstrated to induce the phosphorylation of ERK1 and ERK2 in CV1/EBNA kidney epithelial cells in culture, as compared with the negative control. These assays were conducted as described above. This indicates that huTR1a acts as a ligand for a cell surface receptor that activates the MAP kinase signaling pathway, possibly the EGF receptor in HeLa and CV1/EBNA cells.

25 The ability of muTR1a to stimulate the growth of neonatal foreskin (NF) keratinocytes was determined as follows. NF keratinocytes derived from surgical discards were cultured in KSFM (BRL Life Technologies) supplemented with bovine pituitary extract (BPE) and epidermal growth factor (EGF). The assay was performed in 96 well flat-bottomed plates in 0.1 ml unsupplemented KSFM. MuTR1a, human

transforming growth factor alpha (huTGF α) or PBS-BSA was titrated into the plates and 1×10^3 NF keratinocytes were added to each well. The plates were incubated for 5 days in an atmosphere of 5% CO₂ at 37°C. The degree of cell growth was determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in
5 Fig. 3, both muTR1a and the positive control human TGF α stimulated the growth of NF keratinocytes, whereas the negative control, PBS-BSA, did not.

The ability of muTR1a and huTR1a to stimulate the growth of a transformed human keratinocyte cell line, HaCaT, was determined as follows. The assay was performed in 96 well flat-bottomed plates in 0.1 ml DMEM (BRL Life Technologies)
0 supplemented with 0.2% FCS. MuTR1a, huTR1a and PBS-BSA were titrated into the plates and 1×10^3 HaCaT cells were added to each well. The plates were incubated for 5 days in an atmosphere containing 10% CO₂ at 37°C. The degree of cell growth was determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in Fig. 4, both muTR1a and huTR1a stimulated the growth of HaCaT
5 cells, whereas the negative control PBS-BSA did not.

The ability of muTR1a and huTR1a to inhibit the growth of A431 cells was determined as follows. Polypeptides muTR1a (SEQ ID NO: 342) and huTR1a (SEQ ID NO: 343) and PBS-BSA were titrated as described previously (*J. Cell. Biol.* 93:1-4, 1982), and cell death was determined using the MTT dye reduction as described
10 previously (*J. Imm. Meth.* 93:157-165, 1986). Both muTR1a and huTR1a were found to inhibit the growth of A431 cells, whereas the negative control PBS-BSA did not (Fig. 5).

These results indicate that muTR1 and huTR1 stimulate keratinocyte growth and motility, inhibit the growth of epithelial-derived cancer cells, and play a role in angiogenesis and vascularization of tumors. This novel gene and its encoded protein may
15 thus be developed as agents for the healing of wounds, angiogenesis and regulators of epithelial-derived cancers.

Upregulation of huTR1 and mRNA expression

HeLa cells (human cervical adenocarcinoma) were seeded in 10 cm dishes at a concentration of 1×10^6 cells per dish. After incubation overnight, media was removed and replaced with media containing 100 ng/ml of muTR1, huTR1, huTGF α , or PBS as a negative control. After 18 hours, media was removed and the cells lysed in 2 ml of TRIzol reagent (Gibco BRL Life Technologies, Gaithersburg, Maryland). Total RNA was isolated according to the manufacturer's instructions. To identify mRNA levels of huTR1 from the cDNA samples, 1 μ l of cDNA was used in a standard PCR reaction. After cycling for 30 cycles, 5 μ l of each PCR reaction was removed and separated on a 1.5% agarose gel. Bands were visualized by ethidium bromide staining. As can be seen from Fig. 12, both mouse and human TR1 up-regulate the mRNA levels of huTR1 as compared with cells stimulated with the negative control of PBS. Furthermore, TGF α can also up-regulate the mRNA levels of huTR1.

These results indicate that TR1 is able to sustain its own mRNA expression and subsequent protein expression, and thus is expected to be able to contribute to the progression of diseases such as psoriasis where high levels of cytokine expression are involved in the pathology of the disease. Furthermore, since TGF α can up-regulate the expression of huTR1, the up-regulation of TR1 mRNA may be critical to the mode of action of TGF α .

Serum response element reporter gene assay

The serum response element (SRE) is a promoter element required for the regulation of many cellular immediate-early genes by growth. Studies have demonstrated that the activity of the SRE can be regulated by the MAP kinase signaling pathway. Two cell lines, PC12 (rat pheochromocytoma – neural tumor) and HaCaT (human transformed keratinocytes), containing eight SRE upstream of an SV40 promotor and luciferase reporter gene were developed in-house. 5×10^3 cells were aliquoted per well of 96 well plate and grown for 24 hours in their respective media. HaCaT SRE cells were grown in 5% fetal bovine serum (FBS) in D-MEM supplemented with 2mM L-glutamine (Sigma,

St. Louis, Missouri), 1mM sodium pyruvate (BRL Life Technologies), 0.77mM L-asparagine (Sigma), 0.2mM arginine (Sigma), 160mM penicillin G (Sigma), 70mM dihydrostreptomycin (Roche Molecular Biochemicals, Basel, Switzerland), and 0.5 mg/ml geneticin (BRL Life Technologies). PC12 SRE cells were grown in 5% fetal
5 bovine serum in Ham F12 media supplemented with 0.4 mg/ml geneticin (BRL Life Technologies). Media was then changed to 0.1% FBS and incubated for a further 24 hours. Cells were then stimulated with a titration of TR1 from 1 µg/ml. A single dose of basic fibroblast growth factor at 100 ng/ml (R&D Systems, Minneapolis, Minnesota) or epidermal growth factor at 10 ng/ml (BRL Life Technologies) was used as a positive
10 control. Cells were incubated in the presence of muTR1 or positive control for 6 hours, washed twice in PBS and lysed with 40 µl of lysis buffer (Promega). 10 µl was transferred to a 96 well plate and 10 µl of luciferase substrate (Promega) added by direct injection into each well by a Victor² fluorimeter (Wallac), the plate was shaken and the luminescence for each well read at 3x1 sec Intervals. Fold induction of SRE was
15 calculated using the following equation: Fold induction of SRE = Mean relative luminescence of agonist/Mean relative luminescence of negative control.

As shown in Fig. 13, muTR1 activated the SRE in both PC-12 (Fig. 13A) and HaCaT (Fig. 13B) cells. This indicates that HaCaT and PC-12 cells are able to respond to muTR1 protein and elicit a response. In the case of HaCaT cells, this is a growth
20 response. In the case of PC-12 cells, this may be a growth, a growth inhibition, differentiation, or migration response. Thus, TR1 may be important in the development of neural cells or their differentiation into specific neural subsets. TR1 may also be important in the development and progression of neural tumors.

25 *Inhibition by the EGF receptor assay*

The HaCaT growth assay was conducted as previously described, with the following modifications. Concurrently with the addition of EGF and TR1 to the media, anti-EGF Receptor (EGFR) antibody (Promega, Madison, Wisconsin) or the negative

control antibody, mouse IgG (PharMingen, San Diego, California), were added at a concentration of 62.5 ng/ml.

As seen in Fig. 14, an antibody which blocks the function of the EGFR inhibited the mitogenicity of TR1 on HaCaT cells. This indicates that the EGFR is crucial for transmission of the TR1 mitogenic signal on HaCaT cells. TR1 may bind directly to the EGF receptor. TR1 may also bind to any other members of the EGFR family (for example, ErbB-2, -3, and/or -4) that are capable of heterodimerizing with the EGFR.

Splice variants of huTR1

A variant of huTR1 was isolated from the same library as huTR1, following the same protocols. The sequence referred to as huTR1-1 (also known as TR1 δ) is a splice variant of huTR1 and consists of the ORF of huTR1 minus amino acids 15 to 44 and 87 to 137. These deletions have the effect of deleting part of the signal sequence and following amino terminal linker sequence, residues following the second cysteine residue of the EGF motif and the following transmembrane domain. However, cysteine residue 147 (huTR1 ORF numbering) may replace the deleted cysteine and thus the disulphide bridges are likely not affected. Therefore, huTR1-1 is an intracellular form of huTR1. It functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and TGF α . The determined nucleotide sequence of huTR1-1, is given in SEQ ID NO: 412, with the corresponding amino acid sequence being provided in SEQ ID NO: 415.

Four additional splice variants of huTr1 were isolated by PCR on first strand cDNA made from RNA isolated from HeLa cells by standard protocols. These splice variants of huTR1 are referred to as TR1-2 (also known as TR1 β), TR1-3 (also known as TR1 γ), TR1 ϵ and TR1 ϕ .

TR1-2 consists of the ORF of huTR1 minus amino acids 95 to 137. This deletion has the effect of deleting the transmembrane domain. Therefore TR1-2 is a secreted form of huTR1 and binds with equal or greater affinity to the TR1 receptor as huTR1, since the EGF domain remains intact. It functions as an agonist or an antagonist to huTR1 or other

EGF family members, including EGF and TGF α . The determined cDNA sequence of TR1-2 is given in SEQ ID NO: 410 and the corresponding amino acid sequence in SEQ ID NO: 413.

5 TR1-3 consists of the ORF of huTR1 minus amino acids 36 to 44 and amino acids 86 to 136. These deletions have the effect of deleting part of the amino terminal linker sequence, residues following the second cysteine of the EGF motif and the following transmembrane domain. However, cysteine residue 147 (huTR1 ORF numbering) may replace the deleted cysteine and thus the disulphide bridges are likely not affected. Therefore, TR1-3 is also a secreted form of huTR1 and functions as an agonist or an
10 antagonist to huTR1 or other EGF family members, including EGF and TGF α . The determined cDNA sequence of TR1-3 is given in SEQ ID NO: 411 and the corresponding amino acid sequence is SEQ ID NO: 414.

TR1 ϵ consists of the ORF of huTR1 minus amino acids 86 to 136. This deletion has the effect of deleting residues following the second cysteine of the EGF motif and the
15 transmembrane domain. However, cysteine residue 147 (huTR1 ORF numbering) may replace the deleted cysteine and thus the disulphide bridges are likely not affected. Therefore, TR1 ϵ is also a secreted form of huTR1 and functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and TGF α . The determined cDNA sequence of TR1 ϵ is given in SEQ ID NO: 371 and the corresponding
20 polypeptide sequence in SEQ ID NO: 395.

TR1 ϕ consists of the ORF of huTR1 minus amino acids 36 to 44 and amino acids 95 to 136. These deletions have the effect of deleting part of the amino terminal linker sequence and the transmembrane domain. Therefore TR1 ϕ is a secreted form of huTR1 and binds with equal or greater affinity to the TR1 receptor as huTR1, since the EGF domain remains intact. It functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and TGF α . The determined nucleotide sequence of TR1 ϕ is given in SEQ ID NO: 416 and the corresponding polypeptide sequence in SEQ ID NO: 417.

Example 4

IDENTIFICATION, ISOLATION AND CHARACTERIZATION OF DP3

A partial cDNA fragment, referred to as DP3, was identified by differential display RT-PCR (modified from Liang P and Pardee AB, *Science* 257:967-971, 1992) using mRNA from cultured rat dermal papilla and footpad fibroblast cells, isolated by standard cell biology techniques. This double stranded cDNA was labeled with [α^{32} P]-dCTP and used to identify a full length DP3 clone by screening 400,000 pfu's of an oligo dT-primed rat dermal papilla cDNA library. The determined full-length cDNA sequence for DP3 is provided in SEQ ID NO: 119, with the corresponding amino acid sequence being provided in SEQ ID NO: 197. Plaque lifts, hybridization and screening were performed using standard molecular biology techniques.

Example 5

ISOLATION AND CHARACTERIZATION OF KS1

25 Analysis of RNA transcripts by Northern Blotting

Northern analysis to determine the size and distribution of mRNA for muKS1 (SEQ ID NO: 263) was performed by probing murine tissue mRNA blots with a probe consisting of nucleotides 268-499 of muKS1, radioactively labeled with [α^{32} P]-dCTP. Prehybridization, hybridization, washing, and probe labeling were performed as

described in Sambrook, *et al.*, *Ibid.* mRNA for muKS1 was 1.6 kb in size and was observed to be most abundant in brain, lung, or any muscle, and heart. Expression could also be detected in lower intestine, skin, bone marrow, and kidney. No detectable signal was found in testis, spleen, liver, thymus, stomach.

5

Human homologue of muKS1

MuKS1 (SEQ ID NO: 263) was used to search the EMBL database (Release 50, plus updates to June, 1998) to identify human EST homologues. The top three homologies were to the following ESTs: accession numbers AA643952, HS1301003 and
10 AA865643. These showed 92.63% identity over 285 nucleotides, 93.64% over 283 nucleotides and 94.035% over 285 nucleotides, respectively. Frame shifts were identified in AA643952 and HS1301003 when translated. Combination of all three ESTs identified huKS1 (SEQ ID NO: 270) and translated polypeptide SEQ ID NO: 344. Alignment of muKS1 and huKS1 polypeptides indicated 95% identity over 96 amino acids.

15

Identification of KSCL009274 cDNA sequence

A directionally cloned cDNA library was constructed from immature murine keratinocytes and submitted for high-throughput sequencing. Sequence data from a clone designated KDCL009274 showed 35% identity over 72 amino acids with rat macrophage
20 inflammatory protein-2B (MIP-2B) and 32% identity over 72 amino acids with its murine homologue. The insert of 1633bp (SEQ ID NO: 464; Fig. 15A) contained an open reading frame of 300bp with a 5' untranslated region of 202bp and a 3' untranslated region of 1161bp. A poly-adenylation signal of AATAAA is present 19 base-pairs upstream of the poly-A tail. The mature polypeptide (SEQ ID NO: 465) is 77 amino
25 acids in length containing 4 conserved cysteines with no ELR motif. The putative signal peptide cleavage site between GLY 22 and Ser 23 was predicted by the hydrophobicity profile. This putative chemokine was identical to KS1. The full length sequence was screened against the EMBL database using the BLAST program and showed some identity at the nucleotide level with human EST clones AA643952, AA865643, and

HS1301003, respectively. A recently described human CXC chemokine, BRAK, has some identity with KS1 at the protein level. The alignment of KS1 (referred to in Fig. 15B as KLF-1), BRAK, and other murine α -chemokines is shown in Fig. 15B. The phylogenetic relationship between KS1 and other α -chemokine family members was determined using the Phylip program. KS1 and BRAK demonstrate a high degree of divergence from the other α -chemokines, supporting the relatively low homology shown in the multiple alignment.

Bacterial expression and purification of muKS1 and huKS1

Polynucleotides 269-502 of muKS1 (SEQ ID NO: 271), encoding amino acids 23-99 of polypeptide muKS1 (SEQ ID NO: 345), and polynucleotides 55-288 of huKS1 (SEQ ID NO: 272), encoding amino acids 19-95 of polypeptide huKS1 (SEQ ID NO: 346), were cloned into the bacterial expression vector pET-16b (Novagen, Madison, Wisconsin), which contains a bacterial leader sequence and N-terminal 6xHistidine tag. These constructs were transformed into competent XL1-Blue *E. coli* as described in Sambrook et al., *Ibid*.

Starter cultures of recombinant BL 21 (DE3) *E. coli* (Novagen) containing SEQ ID NO: 271 (muKS1a) and SEQ ID NO: 272 (huKS1a) were grown in NZY broth containing 100 μ g/ml ampicillin (Gibco-BRL Life Technologies) at 37°C. Cultures were spun down and used to inoculate 800 ml of NZY broth and 100 μ g/ml ampicillin. Cultures were grown until the OD₅₉₅ of the cells was between 0.4 and 0.8. Bacterial expression was induced for 3 hours with 1 mM IPTG. Bacterial expression produced an induced band of approximately 15kDa for muKS1a and huKS1a.

MuKS1a and huKS1a were expressed in insoluble inclusion bodies. In order to purify the polypeptides, bacterial cell pellets were re-suspended in lysis buffer (20 mM Tris-HCl pH 8.0, 10 mM β MerCaptoethanol, 1 mM PMSF). To the lysed cells, 1% NP-40 was added and the mix incubated on ice for 10 minutes. Lysates were further disrupted by sonication on ice at 95 W for 4 x 15 seconds and then centrifuged for 10 minutes at 18,000 rpm to pellet the inclusion bodies.

The pellet containing the inclusion bodies was re-suspended in lysis buffer containing 0.5% w/v CHAPS and sonicated for 5-10 seconds. This mix was stored on ice for 1 hour, centrifuged at 14000 rpm for 15 minutes at 4°C and the supernatant discarded. The pellet was once more re-suspended in lysis buffer containing 0.5% w/v CHAPS, sonicated, centrifuged, and the supernatant removed as before. The pellet was re-suspended in solubilizing buffer (6 M guanidine HCl, 0.5 M NaCl, 20 mM Tris-HCl pH 8.0), sonicated at 95W for 4 x 15 seconds and centrifuged for 10 minutes at 18000 rpm and 4°C to remove debris. The supernatant was stored at 4°C. MuKS1a and huKS1a were purified by virtue of the N-terminal 6x histidine tag contained within the bacterial leader sequence, using a Nickel-Chelating sepharose column (Amersham Pharmacia, Uppsala, Sweden) and following the manufacturer's protocol. Proteins were purified twice over the column to reduce endotoxin contamination. In order to re-fold the proteins once purified, the protein solution was dialysed in a 4 M-2 M urea gradient in 20 mM tris-HCl pH 7.5 + 10% glycerol overnight at 4°C. The protein was then further dialysed 2x against 2 litres of 20 mM Tris-HCl pH 7.5 + 10% (w/v) glycerol. Preparations obtained were greater than 95% pure as determined by SDS-PAGE. Endotoxin contamination of purified proteins were determined using a limulus amebocyte lysate assay kit (BIO Whittaker, Walkersville, MD). Endotoxin levels were <0.1 ng/μg of protein. Internal amino acid sequencing was performed on tryptic peptides of KS1.

An Fc fusion protein was produced by expression in HEK 293 T cells. 35μg of KLF-1pIGFc DNA to transfect 6×10^6 cells per flask, 200 mls of Fc containing supernatant was produced. The Fc fusion protein was isolated by chromatography using an Affiprep protein A resin (0.3 ml column, Biorad). After loading, the column was washed with 15 mls of PBS, followed by a 5 ml wash of 50 mM Na citrate pH 5.0. The protein was then eluted with 6 column volumes of 50 mM Na citrate pH 2.5, collecting 0.3 ml fractions in tubes containing 60μl of 2M Tris-HCl pH 8.0. Fractions were analyzed by SDS-PAGE.

Peptide sequencing of muKS1 and huKS1

Bacterially expressed muKS1 and huKS1 were separated on polyacrylamide gels and induced bands of 15 kDa were identified. The predicted size of muKS1 is 9.4 kDa. To obtain the amino acid sequence of the 15 kDa bands, 20 µg recombinant muKS1 and huKS1 was resolved by SDS-PAGE and electroblotted onto Immobilon PVDF membrane
5 (Millipore, Bedford, Massachusetts). Internal amino acid sequencing was performed on tryptic peptides of muKS1 and huKS1 by the Protein Sequencing Unit at the University of Auckland, New Zealand.

The determined amino acid sequences for muKS1 and huKS1 are given in SEQ ID NOS: 397 and 398, respectively. These amino acid sequences confirmed that the
10 determined sequences are identical to those established on the basis of the cDNA sequences. The size discrepancy has previously been reported for other chemokines (Richmond A, Balentien E, Thomas HG, Flaggs G, Barton DE, Spiess J, Bordoni R, Francke U, Derynck R, "Molecular characterization and chromosomal mapping of melanoma growth stimulatory activity, a growth factor structurally related to beta-thromboglobulin," *EMBO J.* 7:2025-2033, 1988; Liao F, Rabin RL, Yannelli JR,
15 Koniaris LG, Vanguri P, Farber JM, "Human Nig chemokine: biochemical and functional characterization," *J. Exp. Med.* 182:1301-1314, 1995). The isoelectric focusing point of these proteins was predicted to be 10.26 using DNASIS (HITACHI Software Engineering, San Francisco, California). Recombinant Fc tagged KS1 expressed and
20 purified using protein A affinity column chromatography revealed a homogenous protein with a molecular mass of 42kDa.

Oxidative burst assay

Oxidative burst assays were used to determine responding cell types. 1×10^7 PBMC cells were resuspended in 5 ml HBSS, 20mM HEPES, 0.5% BSA and incubated
25 for 30 minutes at 37°C with 5 µl 5 mM dichloro-dihydrofluorescein diacetate (H₂DCFDA, Molecular Probes, Eugene, Oregon). 2×10^5 H₂DCFDA-labeled cells were loaded in each well of a flat-bottomed 96 well plate. 10 µl of each agonist was added simultaneously into the well of the flat-bottomed plate to give final concentrations of 100 ng/ml (fMLP was used at 10 µM). The plate was then read on a Victor² 1420

multilabel counter (Wallac, Turku, Finland) with a 485 nm excitation wavelength and 535 nm emission wavelength. Relative fluorescence was measured at 5 minute intervals over 60 minutes.

A pronounced respiratory burst was identified in PBMC with a 2.5 fold difference
5 between control treated cells (TR1) and cells treated with 100 ng/ml muKS1 (Fig. 8). Human stromal derived factor-1 α (SDF1 α) (100 ng/ml) and 10 μ M formyl-Met-Leu-Phe (fMLP) were used as positive controls.

Chemotaxis assay

0 Cell migration in response to muKS1 was tested using a 48 well Boyden's chamber (Neuro Probe Inc., Cabin John, Maryland) as described in the manufacturer's protocol. In brief, agonists were diluted in HBSS, 20mM HEPES, 0.5% BSA and added to the bottom wells of the chemotactic chamber. THP-1 cells were re-suspended in the same buffer at 3×10^5 cells per 50 μ l. Top and bottom wells were separated by a PVP-free polycarbonate filter with a 5 μ m pore size for monocytes or 3 μ m pore size for lymphocytes. Cells were added to the top well and the chamber incubated for 2 hours for monocytes and 4 hours for lymphocytes in a 5% CO₂ humidified incubator at 37°C. After incubation, the filter was fixed and cells scraped from the upper surface. The filter
5 was then stained with Diff-Quick (Dade International Inc., Miami, Florida) and the number of migrating cells counted in five randomly selected high power fields. The results are expressed as a migration index (the number of test migrated cells divided by the number of control migrated cells).
10

Using this assay, muKS1 was tested against T cells and THP-1 cells. MuKS1 induced a titrateable chemotactic effect on THP-1 cells from 0.01 ng/ml to 100 ng/ml
15 (Fig. 9). Human SDF1 α was used as a positive control and gave an equivalent migration. MuKS1 was also tested against IL-2 activated T cells. However, no migration was evidence for muKS1 even at high concentrations, whereas SDF-1 α provided an obvious titrateable chemotactic stimulus. Therefore, muKS1 appears to be chemotactic for THP-1 cells but not for IL-2 activated T cells at the concentrations tested.

Flow cytometric binding studies

Binding of KLF-1 to THP-1 and Jurkat cells was tested in the following manner. THP-1 or Jurkat cells (5×10^6) were resuspended in 3 mls of wash buffer (2% FBS and 0.2% sodium azide in PBS) and pelleted at 4°C, 200 x g for 5 minutes. Cells were then blocked with 0.5% mouse and goat sera for 30 minutes on ice. Cells were washed, pelleted, resuspended in 50 µl of KLF-1Fc at 10 µg/ml and incubated for 30 minutes on ice. After incubation, the cells were prepared as before and resuspended in 50 µl of goat anti-human IgG biotin (Southern Biotechnology Associates, AL) at 10 µg/ml and incubated for 30 minutes on ice. Finally, cells were washed, pelleted and resuspended in 50 µl of streptavidin-RPE (Southern Biotechnology Associates, AL) at 10 µg/ml and incubated for a further 30 minutes on ice in the dark. Cells were washed and resuspended in 250 µl of wash buffer and stained with 1 µl of 10 µg/ml propidium iodide (Sigma) to exclude any dead cells. Purified Fc fragment (10 µg/ml) was used as a negative control in place of KLF-1Fc to determine non-specific binding. Ten thousand gated events were analyzed on log scale using PE filter arrangement with peak transmittance at 575 nm and bandwidth of 10 nm on an Elite cell sorter (Coulter Cytometry).

The respiratory burst and migration assays indicated that KS1 is active on monocytes and not T cells; therefore, the KS1 Fc fusion protein was tested in a binding study with THP-1 and Jurkat T cells. KS1 Fc showed a marked positive shift on THP-1 cells compared with the Fc fragment alone. In contrast, KS1 demonstrated no positive binding with Jurkat cells in an identical experiment.

Full length sequence of muKS1 clone

The nucleotide sequence of muKS1 was extended by determining the base sequence of additional ESTs. Combination of all the ESTs identified the full-length muKS1 (SEQ ID NO: 370) and the corresponding translated polypeptide sequence in SEQ ID NO: 394.

Analysis of human RNA transcripts by Northern blotting

Northern blot analysis to determine the size and distribution of mRNA for the human homologue of muKS1 was performed by probing human tissue blots (Clontech, Palo Alto, California) with a radioactively labeled probe consisting of nucleotides 1 to 288 of huKS1 (SEQ ID NO: 270). Prehybridization, hybridization, washing, and probe labeling were performed as described in Sambrook, *et al.*, *Ibid.* mRNA for huKS1 was 1.6 kb in size and was observed to be most abundance in kidney, liver, colon, small intestine, and spleen. Expression could also be detected in pancreas, skeletal muscle, placenta, brain, heart, prostate, and thymus. No detectable signal was found in lung, ovary, and testis.

Analysis of human RNA transcripts in tumor tissue by Northern blotting

Northern blot analysis to determine distribution of huKS1 in cancer tissue was performed as described previously by probing tumor panel blots (Invitrogen, Carlsbad, California). These blots make a direct comparison between normal and tumor tissue. MRNA was observed in normal uterine and cervical tissue but not in the respective tumor tissue. In contrast, expression was up-regulated in breast tumor and down-regulated in normal breast tissue. No detectable signal was found in either ovary or ovarian tumors.

Injection of bacterially recombinant muKS1 into C3H/HeJ mice

Eighteen C3H/HeJ mice were divided into 3 groups and injected intraperitoneally with muKS1, GV14B, or phosphate buffered saline (PBS). GV14B is a bacterially expressed recombinant protein used as a negative control. Group 1 mice were injected with 50 µg of muKS1 in 1 ml of PBS; Group 2 mice were injected with 50 µg of GV14B in 1 ml of PBS; and Group 3 mice with 1 ml of PBS. After 18 hours, the cells in the peritoneal cavity of the mice were isolated by intraperitoneal lavage with 2 x 4 ml washes with harvest solution (0.02% EDTA in PBS). Viable cells were counted from individual

mice from each group. Mice injected with 50 µg of muKS1 had on average a 3-fold increase in cell numbers (Fig. 10).

20 µg of bacterial recombinant muKS1 was injected subcutaneously into the left hind foot of three C3H/HeJ mice. The same volume of PBS was injected into the same site on the right-hand side of the same animal. After 18 hours, mice were examined for inflammation. All mice showed a red swelling in the foot pad injected with bacterially recombinant KS1. From histology, sites injected with muKS1 had an inflammatory response of a mixed phenotype with mononuclear and polymorphonuclear cells present.

10 Injection of bacterially expressed muKS1a into nude mice

To determine whether T cells are required for the inflammatory response, the experiment was repeated using nude mice. Two nude mice were anaesthetised intraperitoneally with 75 µl of 1/10 dilution of Hypnorm (Janssen Pharmaceuticals, Buckinghamshire, England) in phosphate buffered saline. 20ug of bacterially expressed muKS1a (SEQ ID NO: 345) was injected subcutaneously in the left hind foot, ear and left-hand side of the back. The same volume of phosphate buffered saline was injected in the same sites but on the right-hand side of the same animal. Mice were left for 18 hours and then examined for inflammation. Both mice showed a red swelling in the ear and foot sites injected with the bacterially expressed protein. No obvious inflammation could be identified in either back site. Mice were culled and biopsies taken from the ear, back and foot sites and fixed in 3.7% formol saline. Biopsies were embedded, sectioned and stained with Haemotoxylin and eosin. Sites injected with muKS1a had a marked increase in polymorphonuclear granulocytes, whereas sites injected with phosphate buffered saline had a low background infiltrate of polymorphonuclear granulocytes.

25

Discussion

Chemokines are a large superfamily of highly basic secreted proteins with a broad number of functions (Baggiolini, *et al.*, *Annu. Rev. Immunol.*, 15:675-705, 1997; Ward, *et al.*, *Immunity*, 9:1-11, 1998; Horuk, *Nature*, 393:524-525, 1998). The polypeptide

sequences of muKS1 and huKS1 have similarity to CXC chemokines, suggesting that this protein will act like other CXC chemokines. The *in vivo* data from nude mice supports this hypothesis. This chemokine-like protein may therefore be expected to stimulate leukocyte, epithelial, stromal, and neuronal cell migration; promote angiogenesis and
5 vascular development; promote neuronal patterning, hemopoietic stem cell mobilization, keratinocyte and epithelial stem cell patterning and development, activation and proliferation of leukocytes; and promotion of migration in wound healing events. It has recently been shown that receptors to chemokines act as co-receptors for HIV-1 infection of CD4+ cells (Cairns, *et al.*, *Nature Medicine*, 4:563-568, 1998) and that high
10 circulating levels of chemokines can render a degree of immunity to those exposed to the HIV virus (Zagury, *et al.*, *Proc. Natl. Acad. Sci. USA* 95:3857-3861, 1998). This novel gene and its encoded protein may thus be usefully employed as regulators of epithelial, lymphoid, myeloid, stromal, and neuronal cells migration and cancers; as agents for the treatment of cancers, neuro-degenerative diseases, inflammatory autoimmune diseases
15 such as psoriasis, asthma and Crohn's disease for use in wound healing; and as agents for the prevention of HIV-1 binding and infection of leukocytes.

We have also shown that muKS1 promotes a quantifiable increase in cell numbers in the peritoneal cavity of C3H/HeJ mice injected with muKS1. Furthermore, we have shown that muKS1 induces an oxidative burst in human peripheral blood mononuclear
20 cells and migration in the human monocyte leukemia cell line, THP-1, suggesting that monocyte/macrophages are one of the responsive cell types for KS1. In addition to this, we demonstrated that huKS1 was expressed at high levels in a number of non-lymphoid tissues, such as the colon and small intestine, and in breast tumors. It was also expressed in normal uterine and cervical tissue, but was completely down-regulated in their
25 respective tumors. It has recently been shown that non-ELR chemokines have demonstrated angiostatic properties. IP-10 and Mig, two non-ELR chemokines, have previously been shown to be up-regulated during regression of tumors (Tannenbaum CS, Tubbs R, Armstrong D, Finke JH, Bukowski RM, Hamilton TA, "The CXC Chemokines IP-10 and Mig are necessary for IL-12-mediated regression of the mouse RENCA

tumor," *J. Immunol.* 161: 927-932, 1998), with levels of expression inversely correlating with tumor size (Kanegane C, Sgadari C, Kanegane H, Teruya-Feldstine J, Yao O, Gupta G, Farber JM, Liao F, Liu L, Tosato G, "Contribution of the CXC Chemokines IP-10 and Mig to the antitumor effects of IL-12," *J. Leuko. Biol.* 64: 384-392, 1998).
5 Furthermore, neutralizing antibodies to IP-10 and Mig would reduce the anti-tumor effect, indicating the contribution these molecules make to the anti-tumor effects. Therefore, it is expected that in the case of cervical and uterine tumors, KS1 would have similar properties.

The data demonstrates that KS1 is involved in cell migration showing that one of
10 the responsive cell types is monocyte/macrophage. The human expression data in conjunction with the *in vitro* and *in vivo* biology demonstrates that this molecule may be a useful regulator in cell migration, and as an agent for the treatment of inflammatory diseases, such as Crohn's disease, ulcerative colitis, and rheumatoid arthritis; and cancers, such as cervical adenocarcinoma, uterine leiomyoma, and breast invasive ductal
15 carcinoma.

Example 6

CHARACTERIZATION OF KS2

KS2 contains a transmembrane domain and may function as either a membrane-
20 bound ligand or a receptor. Northern analysis indicated that the mRNA for KS2 was expressed in the mouse keratinocyte cell line, Pam212, consistent with the cDNA being identified in mouse keratinocytes.

Mammalian Expression

25 To express KS2, the extracellular domain was fused to the amino terminus of the constant domain of immunoglobulinG (Fc) that had a C-terminal 6xHistidine tag. This was performed by cloning polynucleotides 20-664 of KS2 (SEQ ID NO: 273), encoding amino acids 1-215 of polypeptide KS2 (SEQ ID NO: 347), into the mammalian expression vector pcDNA3 (Invitrogen, NV Leek, Netherlands), to the amino terminus of

the constant domain of immunoglobulinG (Fc) that had a C-terminal 6xHistidine tag. This construct was transformed into competent XL1-Blue *E. coli* as described in Sambrook et al., *Ibid*. The Fc fusion construct of KS2a was expressed by transfecting Cos-1 cells in 5 x T175 flasks with 180 µg of KS1a using DEAE-dextran. The
5 supernatant was harvested after seven days and passed over a Ni-NTA column. Bound KS2a was eluted from the column and dialysed against PBS.

The ability of the Fc fusion polypeptide of KS2a to inhibit the IL-2 induced growth of concanavalin A stimulated murine splenocytes was determined as follows. A single cell suspension was prepared from the spleens of BALB/c mice and washed into
10 DMEM (GIBCO-BRL) supplemented with 2 mM L-glutamine, 1 mM sodium pyruvate, 0.77 mM L-asparagine, 0.2 mM L-arginine, 160 mM penicillin G, 70 mM dihydrostreptomycin sulfate, 5×10^{-2} mM beta mercaptoethanol and 5% FCS (cDMEM). Splenocytes (4×10^6 /ml) were stimulated with 2 µg/ml concanavalin A for 24 hrs at 37°C in 10% CO₂. The cells were harvested from the culture, washed 3 times in cDMEM and
15 resuspended in cDMEM supplemented with 10 ng/ml rhuIL-2 at 1×10^5 cells/ml. The assay was performed in 96 well round bottomed plates in 0.2 ml cDMEM. The Fc fusion polypeptide of KS2a, PBS, LPS and BSA were titrated into the plates and 1×10^4 activated T cells (0.1 ml) were added to each well. The plates were incubated for 2 days in an atmosphere containing 10% CO₂ at 37°C. The degree of proliferation was
20 determined by pulsing the cells with 0.25 uCi/ml tritiated thymidine for the final 4 hrs of culture after which the cells were harvested onto glass fiber filtermats and the degree of thymidine incorporation determined by standard liquid scintillation techniques. As shown in Fig. 6, the Fc fusion polypeptide of KS2a was found to inhibit the IL-2 induced growth of concanavalin A stimulated murine splenocytes, whereas the negative controls PBS,
25 BSA and LPS did not.

This data demonstrates that KS2 is expressed in skin keratinocytes and inhibits the growth of cytokine induced splenocytes. This indicates a rôle for KS2 in the regulation of skin inflammation and malignancy.

Example 7

Characterization of KS3

KS3 encodes a polypeptide of 40 amino acids (SEQ ID NO: 129). KS3 contains a signal sequence of 23 amino acids that would result in a mature polypeptide of 17 amino acids (SEQ ID NO: 348; referred to as KS3a).

KS3a was prepared synthetically (Chiron Technologies, Victoria, Australia) and observed to enhance transferrin-induced growth of the rat intestinal epithelial cells IEC-18 cells. The assay was performed in 96 well flat-bottomed plates in 0.1 ml DMEM (GIBCO-BRL Life Technologies) supplemented with 0.2% FCS. KS3a (SEQ ID NO: 348), apo-Transferrin, media and PBS-BSA were titrated either alone, with 750 ng/ml Apo-transferrin or with 750 ng/ml BSA, into the plates and 1×10^3 IEC-18 cells were added to each well. The plates were incubated for 5 days at 37°C in an atmosphere containing 10% CO_2 . The degree of cell growth was determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in Fig. 7, KS3a plus Apo-transferrin was found to enhance transferrin-induced growth of IEC-18 cells, whereas KS3a alone or PBS-BSA did not, indicating that KS3a and Apo-transferrin act synergistically to induce the growth of IEC-18 cells.

This data indicates that KS3 is epithelial derived and stimulates the growth of epithelial cells of the intestine. This suggests a role for KS3 in wound healing, protection from radiation- or drug-induced intestinal disease, and integrity of the epithelium of the intestine.

SEQ ID NOS: 1-725 are set out in the attached Sequence Listing. The codes for polynucleotide and polypeptide sequences used in the attached Sequence Listing confirm to WIPO Standard ST.25 (1988), Appendix 2.

All references cited herein, including patent references and non-patent references, are hereby incorporated by reference in their entireties.

Although the present invention has been described in terms of specific embodiments, changes and modifications can be carried out without departing from the

scope of the invention which is intended to be limited only by the scope of the appended claims.

We claim:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) sequences recited in SEQ ID NOS: 466-487, 510, 511 and 514-623; (b) complements of the sequences recited in SEQ ID NOS: 466-487, 510, 511 and 514-623; (c) reverse complements of the sequences recited in SEQ ID NOS: 466-487, 510, 511 and 514-623; (d) reverse sequences of the sequences recited in SEQ ID NOS: 466-487, 510, 511 and 514-623; (e) sequences having at least a 99% probability of being the same as a sequence selected from any of the sequences in (a)-(d), above, as measured by the computer algorithm BLASTP using the running parameters described above; (f) nucleotide sequences having at least 75% identity to any of the sequences in (a)-(d), above, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (g) nucleotide sequences having at least 90% identity to any of the sequences in (a)-(d), above, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (h) nucleotide sequences having at least 95% identity to any of the sequences in (a)-(d), above, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (g) open reading frames of SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455, 464, 466-487, 510, 511 and 514-623.
2. An expression vector comprising an isolated polynucleotide of claim 1.
3. A host cell transformed with an expression vector of claim 2.
4. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 488-509, 512, 513 and 624-725; (b) sequences having at least a 99% probability of being the same as a sequence of SEQ ID NOS: 488-509, 512, 513 and 624-725, as measured by the computer algorithm BLASTP using the running parameters described above; (c) sequences having

at least 75% identity to a sequence provided in SEQ ID NOS: 488-509, 512, 513 and 624-725, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (d) sequences having at least 90% identity to a sequence provided in SEQ ID NOS: 488-509, 512, 513 and 624-725, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (e) sequences having at least 95% identity to a sequence provided in SEQ ID NOS: 488-509, 512, 513 and 624-725, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (f) sequences encoded by a sequence provided in SEQ ID NOS: 488-509, 512, 513 and 624-725.

5. An isolated polynucleotide encoding a polypeptide of claim 4.

6. An expression vector comprising an isolated polynucleotide of claim 5.

7. A host cell transformed with an expression vector of claim 6.

8. An isolated polypeptide comprising at least a functional portion of a polypeptide having an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 196, 488-509, 512, 513 and 624-725; (b) sequences having at least a 99% probability of being the same as a sequence of SEQ ID NOS: 196, 488-509, 512, 513 and 624-725, as measured by the computer algorithm BLASTP using the running parameters described above; (c) sequences having at least 75% identity to a sequence provided in SEQ ID NOS: 196, 488-509, 512, 513 and 624-725, as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above; (d) sequences having at least 90% identity to a sequence provided in SEQ ID NOS: 196, 488-509, 512, 513 and 624-725, as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above; (e) sequences having at least 95% identity to a sequence provided in SEQ ID

NOS: 196, 488-509, 512, 513 and 624-725, as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above; and (f) sequences encoded by a sequence provided in SEQ ID NOS: 466-487, 510, 511 and 514-623.

9. A method for stimulating keratinocyte growth and motility in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

10. The method of claim 9, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398; (b) sequences having at least about 50% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least about 75% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (d) sequences having at least about 90% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (e) sequences comprising amino acids 54-104 of SEQ ID NO: 196.

11. A method for inhibiting the growth of cancer cells in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

12. The method of claim 11, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 342, 343, 397 and 398; (b) sequences having at least 75% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least 90%

identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (e) sequences comprising amino acids 54-104 of SEQ ID NO: 196.

13. A method for modulating angiogenesis in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

14. The method of claim 13, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 342, 343, 397 and 398; (b) sequences having at least 75% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 397 and 398 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least 90% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 397 and 398 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 397 and 398 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (e) sequences comprising amino acids 54-104 of SEQ ID NO: 196..

15. A method for inhibiting angiogenesis and vascularization of tumors in a patient, comprising administering to a patient a composition comprising a polypeptide of claim 4.

16. The method of claim 15, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 342, 343, 397 and 398; (b) sequences having at least 75% identity to a sequence of SEQ ID NOS:

187, 196, 340, 342-346, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least 90% identity to a sequence of SEQ ID NOS: 187, 196, 340, 342-346, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 187, 196, 340, 342-346, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (e) sequences comprising amino acids 54-104 of SEQ ID NO: 196.

17. A method for modulating skin inflammation in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

18. The method of claim 17, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 338 and 347; and (b) sequences having at least 75% identity to a sequence of SEQ ID NOS: 338 and 347 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least 90% identity to a sequence of SEQ ID NOS: 338 and 347 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 338 and 347 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

19. A method for stimulating the growth of epithelial cells in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

20. The method of claim 19, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 129 and 348; (b) sequences having at least 75% identity to a sequence of SEQ ID NOS: 129 and 348 as measured by the computer algorithm BLASTP using the running parameters and identity

test defined above; (c) sequences having at least 90% identity to a sequence of SEQ ID NOS: 129 and 348 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 129 and 348 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

21. A method for inhibiting the binding of HIV-1 to leukocytes in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

22. The method of claim 21, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 340, 344, 345, 346 and 465; (b) sequences having at least 75% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least 90% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

23. A method for treating an inflammatory disease in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

24. The method of claim 23, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 340, 344, 345, 346 and 465; (b) sequences having at least 75% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least 90%

identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

25. A method for treating cancer in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

26. The method of claim 25, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 340, 344, 345, 346 and 465; (b) sequences having at least 75% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least 90% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

27. A method for treating a neurological disease in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

28. The method of claim 27, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 340, 342-346, 397 and 398; (b) sequences having at least 75% identity to a sequence of SEQ ID NOS: 187, 196, 340, 342-346, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (c) sequences having at least 90% identity to a sequence of SEQ ID NOS: 187, 196, 340, 342-346, 397

and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; (d) sequences having at least 95% identity to a sequence of SEQ ID NOS: 187, 196, 340, 342-346, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above; and (e) sequences comprising amino acids 54-104 of SEQ ID NO: 196.

SEQUENCE LISTING

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Watson, James D.
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 Onrust, Rene
 Murison, James G.
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<210> 7

<211> 861

<212> DNA

<213> Rat

<400> 7

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<210> 8

<211> 398

<212> DNA

<213> Mouse

<400> 8

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<210> 9

<211> 1060

<212> DNA

<213> mouse

<220>

<400> 9

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<210> 10

<211> 353

<212> DNA

<213> mouse

<400> 10

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<210> 11

<211> 969

<212> DNA

<213> mouse

<400> 11

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<210> 12
 <211> 1411
 <212> DNA
 <213> mouse

<400> 12

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<210> 13
 <211> 888
 <212> DNA
 <213> mouse

<400> 13

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aacttaaat tgcttggggg aggggagcag ttctagtcc atgaggcaca aatggaggtc      180
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<210> 14
 <211> 547
 <212> DNA
 <213> mouse

<400> 14

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<210> 15

<211> 318

<212> DNA

<213> Rat

<400> 15

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<210> 16

<211> 856

<212> DNA

<213> Rat

<400> 16

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<210> 17

<211> 349

<212> DNA

<213> Rat

<400> 17

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<210> 18
 <211> 1057
 <212> DNA
 <213> Rat

<220>

<400> 18						
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<210> 19
 <211> 750
 <212> DNA
 <213> Rat

<400> 19						
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<210> 20
 <211> 849
 <212> DNA
 <213> Rat

<400> 20
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<210> 21
<211> 312
<212> DNA
<213> Human

<400> 21
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<210> 22
<211> 1023
<212> DNA
<213> mouse

<400> 22
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<210> 23
<211> 997

<212> DNA
<213> mouse

<400> 23

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<210> 24
<211> 529
<212> DNA
<213> Rat

<400> 24

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<210> 25
<211> 1230
<212> DNA
<213> Rat

<400> 25

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<210> 26
 <211> 393
 <212> DNA
 <213> Rat

<400> 26						
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<210> 27
 <211> 778
 <212> DNA
 <213> Rat

<400> 27						
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aacaactcct	attgaatcca	ctacaggaag	ggggggcgcg	gatcactgtc	tgcaactaa	720
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<210> 28
 <211> 1123
 <212> DNA
 <213> Rat

<400> 28						
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<210> 29
 <211> 849
 <212> DNA
 <213> Rat

<400> 29						
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gaccagcc						849

<210> 30
 <211> 1015
 <212> DNA
 <213> Rat

<220>						
<400> 30						
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<210> 31
 <211> 452
 <212> DNA
 <213> Human

<400> 31
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<210> 32
 <211> 434
 <212> DNA
 <213> mouse

<400> 32
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<210> 33
 <211> 903
 <212> DNA
 <213> mouse

<400> 33
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<210> 34
 <211> 1359

<212> DNA
<213> mouse

<220>
<221> unsure
<222> (644) ... (644)

<400> 34

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<210> 35
<211> 797
<212> DNA
<213> mouse

<400> 35

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<210> 36
<211> 896
<212> DNA
<213> mouse

<400> 36

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tggtaggag	cctggctagg	tatctttgag	agatggatgc	agctggctac	tcaggcaggt	480
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gtgaggctgg	ccctcagcac	acacaggaga	gcagcttaag	tgggacctaa	aaaggaccca	780
atgttacttg	gtttaatgaa	ggccccctca	accccaacag	cccctcctgc	tcaggggacac	840
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<210> 37

<211> 501

<212> DNA

<213> mouse

<400> 37

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cagcatcgtt	cttatatgcg	actaacagaa	aaggaagatg	aatcattacc	aatagatata	180
gttcttcaga	cacttctggc	ctttgcagtt	acctgttatg	gcatagttca	tatcgcaggg	240
gagttcaaag	acatggatgc	cacttcagaa	ttaaagaata	agacatttga	taccttaagg	300
aatcacccat	ctttttatgt	gtttaacat	cgtggtcgag	tgctgttccg	gccttcagat	360
gcaacaaatt	cttcaaacct	agatgcattg	tcctctaata	catcgttgaa	gttacgaaag	420
tttgactcac	tgcccggtta	agctttttac	aaattaaata	acaggacaga	cacagaattg	480
agtattggag	tttgggggtg	a				501

<210> 38

<211> 766

<212> DNA

<213> mouse

<400> 38

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cgggcggcat	cccccgccg	ccgcacgcac	aggccggcgc	cctccttgcc	tccctgctcc	180
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ggcgtgtg	gcctcgcgcg	tggacgggtc	caagtgttag	tggtcccgga	aggggcccga	300
gatccgctac	agcgacgtga	agaagctgga	aatgaagcca	aagtaccac	actgcgagga	360
gaagatgggt	atcgtcacca	ccaaagagca	tgtccaaggt	accggggcca	ggagcactgc	420
ctgcacccta	agctgcagag	caccaaagcg	ttcatcaagt	ggtacaatgc	ctggaacgag	480
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ataagacaaa	ttatatattg	ctatgaagct	cttcttacca	gggtcagttt	ttacatttta	660
tagctgtgtg	tgaagggctt	ccagatgtga	gatccagctc	gcctgcgcac	cagacttcat	720
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<210> 39

<211> 480

<212> DNA

<213> mouse

<400> 39

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tggctttcct	ttttagtttt	tttacttttt	agtttagttt	gttcttttcc	ttccccaata	180
aatcattctc	acatgcttcc	atgtttgttt	ctgagaggtg	ggggctcaaa	tgtatagaaa	240
gtaggcccca	gtccataagg	aggtgtgaac	acacccctt	actgcttatt	acccatttga	300
caggaacgcc	caggagggga	gggggagggg	aagaggtag	ttctgcacag	tcggacattt	360
ctgttgcttt	tgcattgtta	atatagacgt	tcctgtcgat	ccttgggaga	tcattggcctt	420
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<210> 40

<211> 962

<212> DNA

<213> mouse

<400> 40

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aaatgatgcc	acagaaatcc	tttattcaca	tgtgggttaa	cctgtcccgg	cacacccag	180
cagcaacagc	accctgaatc	aagccaggaa	tggaggcagg	catttcagta	gcactggact	240
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aatgagtgg	ttgcagtga	agccaggcat	cctgtagtgt	ccatccccct	ccccatccca	900
gtcatttctt	taaaagcacc	tgatgctgca	ttctgttaca	gtttaaaaaa	aaaaaaaaaa	960
aa						962

<210> 41

<211> 794

<212> DNA

<213> mouse

<400> 41

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ggtggggaac	acagcgccgg	ggctcggaga	ccatggcggg	cgctgcgggtg	aagtacttaa	180
gtcaggagga	ggctcaggcc	gtggaccaag	agctttttta	cgagtatcag	ttcagcgtgg	240
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ccacgtctat	gtccaagagt	cccccgactg	tcttgggtcat	ctgtggcccc	ggaataaacg	360
gaggggatgg	gctggtctgt	gcgcgacacc	tcaaaacttt	tggttaccag	ccaactatct	420
attaccccaa	aagacctaac	aagcccctct	tcactgggct	agtgactcag	tgtcagaaaa	480
tggacattcc	tttcttggt	gaaatgcccc	cagaggatgg	gatgtagaga	agggaaaccc	540
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ctttactggc	cgatatcatt	accttggggg	tcgctttgta	ccacctgtc	tagagaagaa	660
gtaccagctg	aacctgccat	cttacctga	cacagagtgt	gtctaccgtc	tacagtaagg	720
gaggtgggta	ggcaggattc	tcaataaaga	cttgggtact	tctgtcttga	aaaaaaaaaa	780
aaaaaaaact	cgag					794

<210> 42
 <211> 1152
 <212> DNA
 <213> mouse

<400> 42
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 tctgtgacta tagggaggtt agcacttttt ctaattggaa ttcttctctg tctgtgggcc 180
 ccacccctca cccgctcttg gacctggacca gatacatgca gcctctttct ccagcacagc 240
 ctttccctga gcctgaggtt agggcagagt ttagaggggt ggctaagtgt atgttttcat 300
 gtatgcattc atgcctgtga gtgtgtggct tgctgtcgtg tcctctggga tcccaagcca 360
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 gttggggggt ggacccaggg tgggttgatt gtctctttgt aaggaagtat gtgtcggggg 480
 tgacacgagg ctaagcccga gaaaccccg gacacagcac tgcataagaa actggtttcc 540
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 gtccctagac ttcagcaact ccgctgcgtg gcctgagccc agcgggaggg atggggagag 720
 aatttttttg agtccgtgcc tbtggtgggc agtccctgag cttcagctga agcagtgtt 780
 tttggtgcc ctcacctgc actacttgac cttgaggctc tgagtatctc ctgtgcacag 840
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<210> 43
 <211> 446
 <212> DNA
 <213> mouse

<400> 43
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 ccaggctcctc tggagaaata accagtgtc ttaaccacta agccatctca acagcccaaa 240
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 ctaatataga ttatttatga attcaggtgg cttaatggtat tatgcatgaa ttagtagtaa 360
 aacaagaact agggccagca agtggcctaa ggtgtcctgc taacctctc agccacctga 420
 gttcagctc caggaaccac acagtg 446

<210> 44
 <211> 391
 <212> DNA
 <213> mouse

<400> 44
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 agttgctgat gcctcctgat ggctcacgg acacagactt ccagtcatgc gaggacagcc 360
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<210> 45

<211> 516

<212> DNA

<213> Rat

<400> 45

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cagcgaggtc	cctgacaggg	cacctgacag	ccggcaggaa	gagggcctgg	acttcttcca	480
gcagctccag	gctgacattc	tggcttgcta	ctcaga			516

<210> 46

<211> 306

<212> DNA

<213> mouse

<400> 46

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gctgctggga	ccagtcttag	cctcttgttg	caagtggtag	gaatgtgaat	ctttgcgacc	120
agggggatca	gaaatggggt	ctcccatttc	tgggtgtctg	ccagtccttc	caggtgggct	180
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<210> 47

<211> 439

<212> DNA

<213> mouse

<400> 47

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gcacataatta	ctgagccatt	gcaagcaatg	ggaggggtcc	acaatgacac	acacacacac	180
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tgtattttgg	ccaaacttgg	aaaatagggt	tccttctctg	ttttgcttcc	agccttttat	300
ttgcaagtga	tcttccatgc	agtatgaaac	atgcagacag	cactggagtg	tggcaagagt	360
gagcttgccc	cacaagtctc	tcggggatgt	tgtactcttg	tgtgtgttta	cagtatcatg	420
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<210> 48

<211> 159

<212> DNA

<213> mouse

<220>

<221> unsure

<222> (3)...(3)

<400> 48

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<210> 49
 <211> 465
 <212> DNA
 <213> Rat

<400> 49
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 ttcagcttgc tgcgtgcaagc ccttctcctg ctgcctcgtc taccacatgc accggggcagc 360
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 accagacaat tgactcgtca gactcacctg cagacccctc tgcaa 465

<210> 50
 <211> 337
 <212> DNA
 <213> Rat

<220>

<400> 50
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 acatggtgag ctagagcgna gtcnactct cccatt 337

<210> 51
 <211> 371
 <212> DNA
 <213> Rat

<220>
 <221> unsure
 <222> (80) ... (80)

<221> unsure
 <222> (312) ... (312)

<221> unsure
 <222> (319) ... (319)

<221> unsure
 <222> (353) ... (354)

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 aagcctgcct cgctgccagc cttgccctag cgctaaatgg tgtctttacc aacatcataa 300
 gactgatagt gngcaaggnc acgcccacaa tgcttctacc gagtgttccc cgnnccgggat 360
 tgccattct t 371

<210> 52
 <211> 228
 <212> DNA
 <213> Rat

<400> 52
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 gagagtcac actgacaaca gagatggacc agtacagaat tacctgct 228

<210> 53
 <211> 361
 <212> DNA
 <213> Human

<400> 53
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 g 361

<210> 54
 <211> 403
 <212> DNA
 <213> Human

<220>

<400> 54
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 aagtcctgta cacgggaaga cactgggaca tacacttgta tgg 403

<210> 55
 <211> 413
 <212> DNA
 <213> Human

<400> 55
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<210> 56

<211> 452
 <212> DNA
 <213> Human

<400> 56
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<210> 57
 <211> 190
 <212> DNA
 <213> Rat

<220>

<400> 57
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<210> 58
 <211> 413
 <212> DNA
 <213> mouse

<400> 58
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<210> 59
 <211> 325
 <212> DNA
 <213> mouse

<220>
 <221> unsure
 <222> (213)...(213)

<221> unsure
 <222> (223)...(223)

<221> unsure
 <222> (227)...(227)

<221> unsure

<222> (243)...(243)

<400> 59

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tcttgggtga ccaacatctt cctgtctttg agnaaccagg ggnacgnatg ggagccaccc      240
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<210> 60

<211> 372

<212> DNA

<213> mouse

<400> 60

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ggcatttggt gcgtctttcc tcctgtggcc ttcagcactg ataagaatct attattggta      180
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ttactccttc cggggcaggc caggacacaa gccatccatc cttatgctcc atggattctc      300
cgcacacaaa ggacatgtgg ctacgcgtgg ccaagttcct tcccgaaga acctgcactt      360
tggtgtgtg ga                                     372

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<210> 61

<211> 363

<212> DNA

<213> mouse

<220>

<221> unsure

<222> (15)...(15)

<400> 61

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ccaagagctt tccaccaaa aagccccctc aagcactgac catgtctatt atggaccaca      180
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<210> 62

<211> 399

<212> DNA

<213> mouse

<400> 62

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<210> 63

<211> 399
 <212> DNA
 <213> mouse

<220>

<400> 63

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<210> 64
 <211> 2481
 <212> DNA
 <213> Rat

<400> 64

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```

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<210> 65
<211> 3008
<212> DNA
<213> mouse

```

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<220>
<221> misc_feature
<222> (1)...(435)
<223> n = A,T,C or G

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aaaaaaaa						3008

<210> 66

<211> 1888

<212> DNA

<213> mouse

<220>

<221> unsure

<222> (1690)...(1690)

<221> unsure

<222> (1755)...(1755)

<221> unsure

<222> (1864)...(1864)

<400> 66

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<210>	67
<211>	1260
<212>	DNA
<213>	Rat

<210>	68
<211>	1729
<212>	DNA
<213>	mouse

25

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<210> 69

<211> 355

<212> DNA

<213> Rat

<400> 69

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<210> 70

<211> 1421

<212> DNA

<213> Human

<400> 70

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<210> 71

<211> 378
 <212> DNA
 <213> Human

<400> 71
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<210> 72
 <211> 267
 <212> DNA
 <213> mouse

<400> 72
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 actcgtgct gcagcctgta tgctccaggc aaggaggact gtccaaaaga aagggtgcata 180
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<210> 73
 <211> 1633
 <212> DNA
 <213> Mouse

<220>
 <221> misc_feature
 <222> (1)...(1633)
 <223> n = A,T,C or G

<400> 73
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 tgagcgccgc tgtcccagg accggttttg caagggctgt gaacacaagt gtgcctgcag 240
 gaatgggggc ctgtgtcatg ctaccaatgg cagctgctcc tgccccctgg gctgmatggg 300
 gccacactgt gagcacgcct gccctgctgg gcgctatggt gctgcctgcc tcttgagatg 360
 ttcctgtcag aacaatggca gctgtgagcc cacctccggc gcttgccctc gtggccctgg 420
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<210> 74
 <211> 1252
 <212> DNA
 <213> mouse

<400> 74						
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ctgcattact	gtgggcaaca	ctaccacaca	cgtgatgaag	aacctccttc	cagaaacgac	120
ataccggatc	agaattcagg	ctatcaatga	aattggagtt	ggaccattta	gtcagttcat	180
taaagcaaaa	actcggccat	taccgccttc	gcctcctagg	cttgagtgtg	ctgcgtcttg	240
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catggtgtac	acactacagc	tgggaagacag	gaacaagagg	tttatctcaa	tctaccgagg	360
accagccac	acctacaagg	tccagagact	gacagagttt	acctgctact	ccttcaggat	420
ccaggcaatg	agcgaggcag	gggaggggccc	ttactcagaa	acctacacct	tcagcacaac	480
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gtttggctgc	acctatttga	gatgcaaaac	taggaagagg	ttaactgga	ttttttttta	1140
aacaataata	aataaaggaa	taagaagag	aagggaagcg	cgggcaagct	ccagacaccg	1200
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<210> 75
 <211> 2411
 <212> DNA
 <213> mouse

<400> 75						
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acaacttcaa	gtctgacatc	tggctctctg	gctgtctgct	atatgagatg	gctgcactgc	120
agagtccttt	ctacggcgac	aagatgaact	tgtattctct	gtgtaagaag	atagagcagt	180
gtgactaccc	gcctctcccg	tcagatcact	attcggagga	gctacgacag	ctagttaata	240
tatgcatcaa	cccagatcca	gagaagcgac	ccgacatcgc	ctatgtttat	gatgtggcaa	300
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aagataactt	aaaagtgttt	ttgtgcagat	catacctccc	cgcttatgtc	tgggtgttaa	420
gattactgtc	tcagagctaa	tgcgctttga	atccttaacc	agttttcata	tgagcttcat	480
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agaatgcaag	cccaacaaga	gtttttcgtt	tgagaattgt	ttcgagtttc	tgctgataga	600
ctgtgtttat	agatagtcag	tgcccgatgg	tgaagcacac	acacataggc	acatgtccag	660
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aaactttttg	agaaagattt	aaaattttta	gtttatacat	tcaaaatgca	actatttaatt	900

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tggtgctgtg	aatgtcgata	ttgtttggca	gggttataat	tttagagtat	gctctagagt	1500
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caaaaaaaaaa	a					2411

<210> 76
 <211> 1335
 <212> DNA
 <213> mouse

<400> 76						
acccaaacag	ccggggacca	tgctgtcgct	ccgtcctctg	cttccacacc	tgggactggt	60
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tggtggggat	gtaacctata	cagtgcagg	ccccgtgaac	gattcagtc	gtgccgtgat	240
cctgaaagca	gtgaaggagg	acgacagccc	agtgggcacc	tggaaggtaa	catatgagaa	300
gtgcaacgac	agcagtgctc	actataactt	gacatcccaa	agccagtcgg	tcttcagac	360
aaactggaca	gttcctactt	ccgaggatgt	gactaaagtc	aacctgcagg	tcctcatcgt	420
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cacagccaat	accacagccg	tgaccacagc	caagaccaca	gccaaaagcc	tgcccatccg	660
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ctcatttcag	gccagtgctt	aaacataccc	gaatgaaggt	tttatgtcct	cagtcgcgag	840
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cctggatctt	tcaggggaca	aattccgctt	cttgtaaata	cttagtccat	ccatcctgct	960
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gtgacttatg	tgactgtagg	aaaaagagaa	atgagtgtat	atcctgtggc	tactagcaga	1200
tttccactgt	gccagaccac	gtcggtaggt	tttgaaggaa	gtatatgaaa	actgtgcctc	1260
agaagccaat	gacaggacac	atgacttttt	ttttctaagt	caaataaaca	atatattgaa	1320
caaggaaaaa	aaaaa					1335

<210> 77
 <211> 440
 <212> DNA
 <213> mouse

<220>
 <221> misc_feature
 <222> (1)...(440)
 <223> n = A,T,C or G

<400> 77
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 tcaggccct caacctccac atcagaacag gcagagcctg tgggtgtcagc tgttgatcca 180
 aaggcaaccc ttgggtgggt tgggttgta aagtagtgat gctaatttct aagcaacaag 240
 ctctgagctg cagccccag gccctccagg gcagtccagg gcagtgccag ggttcagggt 300
 agttctaggg gtctagtatc tggatcaaca agtcccagag ttgggcccag tggctgctga 360
 cttgttcaat gaccaagaat atacgacctt acctttttta ttgggttggg caaccacagc 420
 tccgagtaag tcatcaaggc 440

<210> 78
 <211> 204
 <212> DNA
 <213> mouse

<400> 78
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 ctctctatcc ttctccgtct ttagggcctc ctccagtggt tgttttctaa caacgcaggc 120
 atgagaaggc actcactgtg tgcctcctca ggcctggcct ctccctggtga ttgtcttctt 180
 cctctgtgtc ctcttcatcc caat 204

<210> 79
 <211> 300
 <212> DNA
 <213> mouse

<220>
 <
 <400> 79
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 cagcaccctat atagcaagag agcatacaag aagcacctgt gactgcactc tgaagaatcc 120
 aacaccttct tctggcctcc atggcacaca gaaaccccca acacatgtc atccactctc 180
 aaagagacat acataaaaaa aaatatttag gtcctgggtc cctcagagac tagtcttca 240
 aggtcctaaa tacaacgna gcggaccgca aagggtgagg gagtggnoct gaagaagcta 300

<210> 80
 <211> 214
 <212> DNA
 <213> mouse

<400> 80
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 aggtgaggaa acccaggaag cagggtcatg accccgcaga ggtcggggct cctggtgcag 120
 aggatcagat cttgtgtgac ttctgtcttg gggccagcag agtaagggca gtgaaatcct 180
 gtctgacctg catggtgaaa tactgtaagg agca 214

<210> 81
 <211> 152
 <212> DNA
 <213> mouse

<220>

<400> 81
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 cagtcatttt taagcacacg gaccttttgt gagacagtcg tgatcttaac tgggtgtca 120
 ctgatggagc tgaacggtat cccctaaaag ta 152

<210> 82
 <211> 181
 <212> DNA
 <213> mouse

<220>

<400> 82
 tctcagtgat gatgagaagc tccggaggag gcaggagaaa gcaggggccc gccctccct 60
 ggggtctccac ccacccacgc ccgctaaggc cacctgttct cccatggaga tgatgaagaa 120
 gctcatagct ggacaaggcc cggaacctca gccagtaac cgacctactt cccgcctggg 180
 a 181

<210> 83
 <211> 332
 <212> DNA
 <213> mouse

<220>

<400> 83
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 cagatgacat tcacgtctac ttctctctgt gttgggggta tgggtctgca cacctgccc 180
 ggcctaggct gggggatttt gaagtatctt agattatgga gtagaccag agtttgcaag 240
 tatctgcttt aaagtgcac ataaacatag cctctgacc atcttcaca gtgggaccct 300
 gatctggcct ctccctggaa gaagagagaa ag 332

<210> 84
 <211> 213
 <212> DNA
 <213> mouse

<400> 84
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 acattgttgg cgcacacgca acgtgctgga cacaagcatg ctctcatccc cagatgtggt 180
 gcgcattgct ctgtccctgc agcccttctt gca 213

<210> 85
 <211> 273

<212> DNA
<213> mouse

<220>
<221> misc_feature
<222> (1)...(273)
<223> n = A,T,C or G

<400> 85
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cantcccccg tccatcctga agcgggctcc tcgggagcgt ccaggtcang tggcctttaa 180
cggcatcanc gtctactatt tcccacgggtg ccaaggattc accagtgtgc ccaagccgtg 240
gtggctgtac cctgggnatg gcttctcggc aca 273

<210> 86
<211> 218
<212> DNA
<213> mouse

<400> 86
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cccagcctat gtggagccta tgactgtggt ttgtcacc 218

<210> 87
<211> 335
<212> DNA
<213> mouse

<400> 87
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gctgggtgga cagagtgtga ccagaaactc cctgtggggt ctgataaagg attctcccat 180
aggcaagggt cagagaacct gggcctcctg ttctcaggga ggccctgtcta tccccagcct 240
ctgagctggt tcgtcctagt tggtagtcta agtggcatag ccctcttgag gcctctgatg 300
tggaaggggc acagaattgc aattattctt gcatg 335

<210> 88
<211> 410
<212> DNA
<213> mouse

<400> 88
aaaccccgcc aggaacacaaa taccgggtgta tcggctttac tgaatgcatt tattcccaaa 60
gggaaactga aaagcaacct agggacactg taagcagaaa gctgaggett ttaaaaaccc 120
accttggcaa tgtaacttgg gaggttccca cacacccagg gctgtgcata gtgaaattct 180
gtctcctgag acgctgagaa acccttctct gcagctataa tgggcctggc cgcccagtg 240
ggagctgtag cttccacaga cgtagccctc aggaacttca ggagggatgc cacagtctat 300
ttctgaaaac aaaaccgtgt caacttcttt actttacaaa tgcaagtttt cagaatccac 360
catctctctg caccataacc ccatgcctca cccccagac cctgtgttag 410

<210> 89
<211> 279
<212> DNA
<213> mouse

<220>

<400> 89

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cacacacaca	cacacacaca	cacacacaca	cacccaagg	cttagagacc	attgcagaag	120
agaagagttt	atgggaaatc	ttggagaaaa	cattggatgg	tttgagagaa	tggtaggag	180
atcagactag	ctagtccagg	aagcagtgaa	ggggggcggg	gttagaagat	gaggtcagaa	240
gacaggggtg	agggcattgt	ccgacagaac	cattgctgt			279

<210> 90

<211> 398

<212> DNA

<213> mouse

<400> 90

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ctgaagaaca	tctgttgcca	gaacggccac	accaaacaga	tggagtgtcc	cagcacttag	300
cttcttaaat	aacatcggaa	ccattcagcc	agcgagtctg	tgtttgcttt	ttgttaaat	360
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<210> 91

<211> 279

<212> DNA

<213> mouse

<400> 91

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gttcgaggaa	gcccggtcgg	accatagtgg	ccacggcggg	gaggtaggcg	tggacagggc	180
tgaccagtcc	aagttaagga	cgttcgggtc	catgttaacc	ctgccttgta	cgtccagcat	240
cgtaagaaaa	aacacttgag	aaccgaaga	ggagatgga			279

<210> 92

<211> 401

<212> DNA

<213> mouse

<400> 92

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cacgctctgc	aatgaatcat	gtggcaccga	gtctacgcca	aggccccga	gaaactttat	180
tccatagatg	ggcagatggg	tcccaaagtt	acactacaga	actacaaatc	gactcttaaa	240
attaaaacgg	gactttacaa	gcattctaga	agactcaaac	ttgaagcaat	ttttggaaaa	300
taaatgtaca	gagaaaagat	cttgaagcta	ctgaacagag	aaccctcatt	aaccgagcaa	360
atacatccta	tggagcttcc	gaggagtaca	cagacagacc	g		401

<210> 93

<211> 339

<212> DNA

<213> mouse

<400> 93

```

ccactgacct tcccagaagg tgacagccgg cggcggatgt tgtcaaggag ccgagatagt      60
ccagcagtg ctcggtaacc agaagacggg ctgtctcccc ccaaagacg gcgacattcg      120
atgagaagtc accacagtga tctcacattt tgcgagatta tcctgatgga gatggagtcc      180
catgatgcag cctggccttt cctagagcct gtgaaccctc gcttggtgag tggataaccga      240
cgtgtcatca agaaccctat ggatttttcc accatgcgag aacgcctgct ccgtggaggg      300
tacctagct cagaagagtt tgcagctgat gctctgctg      339

```

<210> 94
 <211> 55
 <212> DNA
 <213> mouse

```

<400> 94
gggggtgtggg caacttggat aacctcagct gcttccatct ggctgacatc tttgg      55

```

<210> 95
 <211> 186
 <212> DNA
 <213> mouse

```

<400> 95
ggactctggc ttcctggggc tgccggccgac ctcggtggtat cccgctctga ggcggcggcg      60
gcgggggcccc agaaacaaga agcgcggctg gaggaggctc gccgaggagc cgctgggggtt      120
agagggtcgac cagttcctgg aagacgtccg gctacaggag cgcacgaccg gtggcttgtt      180
ggcaga      186

```

<210> 96
 <211> 244
 <212> DNA
 <213> mouse

```

<400> 96
ggtgaccaa aqcccttctg ccccttccc agagactctg acttgaccct ctttccaatt      60
ccctctcccc aaggccatgg attatgaagc ccctctgtaa gatggtgagc caggggccct      120
aagagggcat gaggcacacc ctgatcactg tctcaggcct ttgtgggcac tgactcgacc      180
ctggcccacc tcacgcccc aggccagtgt gcaactggtg gctcttgagg gctcttacgc      240
cctt      244

```

<210> 97
 <211> 116
 <212> DNA
 <213> mouse

<220>
 <221> unsure
 <222> (11)...(11)

<221> unsure
 <222> (13)...(13)

<221> unsure
 <222> (41)...(41)

```

<400> 97
acccggtctg ngnactgccc gccttctggg gcttccctta naggatacag tcttttacc      60
atctaggact cctgccaccc tgactgctga cttacagcta tgagggtccc gcttct      116

```

<210> 98
 <211> 307
 <212> DNA
 <213> mouse

<400> 98
 ccccgggcca tctgtcgcca taccggggccc gtgcaagctt ttgcagggtt tagaagatgg 60
 cgaattcatg acacctgtga tccaaggacaa cccctcaggc tgggggtccct gtgcccgttcc 120
 tgagcaattt cgggatatgc cctaccagcc attcagcaaa ggagatcggc tgggaaaggt 180
 tgcagactgg acagggggcca cataccagga caagaggtag acaacaagt attcctctca 240
 gttcgggtggg gggagtcagt atgcatattt ccatgaggag gatgagacaa gctttccagc 300
 tgggtgg 307

<210> 99
 <211> 360
 <212> DNA
 <213> mouse

<220>
 <221> misc_feature
 <222> (1)... (360)
 <223> n = A,T,C or G

<400> 99
 ccttgggtgca ccagctccag cctcaggact tctcctcct ggccctgaca gccagctct 60
 tgtcccagca gaatccagtg acaggaagga gtttctgagg cagggggagga ggcttctcca 120
 tgggaaccag acagccttgc ttcactgtat aagtgccctg atcacacgca gaatgaagtg 180
 ccaggttgct cagaagcaca aagggtgtgg ctactggccc taaccatgga ctacgtgggt 240
 ctaaccaaag actctagaac tctgggggtgg gggagaaaca atgtgttctg tgctccagaa 300
 ccttnggctt cctggcccat atggatgggc ttggcaagga acctacctct tctctaaggt 360

<210> 100
 <211> 257
 <212> DNA
 <213> mouse

<400> 100
 tgccgcgctg agaggggggg cgcgaccacc agcgccacca ccaccaccgc cgccgcccgc 60
 ggggtggggtg ggagggggcgg gagccaccgc taccgcccgc gcctcccggg tggggcgcct 120
 tctccttaga cgccggcgac ccaggacgag ggcttcatca ctgtaaatgg ttgcaagccg 180
 acaaagctgc acctcctgaa aaagacggac agcccatcgc gtgagctgta gaaatttgtg 240
 gacgcatttc tatcggt 257

<210> 101
 <211> 203
 <212> DNA
 <213> mouse

<400> 101
 ccaaagtgcc cattgtgatt caagacgata gccttccac gggggcccct ccacagatcc 60
 gcatcctcaa gagggccacc agcaacgggtg tggtcagcag ccccaactcc accagcaggc 120
 cagcccttcc tgtcaagtcc ctagcacagc gggaggcaga gtatgcagag gctcggagag 180
 ggatcctagg cagtgccagc cct 203

<210> 102
 <211> 300

<212> DNA
<213> mouse

<400> 102
agtacagaga cctcggctgc agcttaaacc tcggacagtg gcaacgcccc tcaatcaagt 60
agccaacccc aactcagcca tctttggggg agccaggccc agagaggaag tggttcagaa 120
ggagcaagaa tgagcttagg ttgggaggga atggggcgtg ggggagctgg agcaagacca 180
cggcctgggtg gcagccggtc gccctacagg cccattccc gcctggcact gtcctcctta 240
cagcggaaac acagagcttg tgagtgcagt tcagctgtta acaagtgggt tctagtacat 300

<210> 103
<211> 370
<212> DNA
<213> mouse

<220>

<400> 103
cagcaactgt ttcaggagct gcacgggtga cgcctgctga ctgatgcgtt ggaactaaca 60
ctgggctgtg cccccaaga aaacctccg gtgatgcttc cagcccaaga gacggagagg 120
gccatggaga tctcaaagt gctctttaat atcacctttg actctgtcaa gagggaggtt 180
gatgaggaag atgctgccot ttaccggtag ctggggactc ttctgcggca ctgcgtgatg 240
gttgaagctg ctggggaccg cacagaggag ttccacggcc acacgggtgaa tctcctgggg 300
aacttgcccc tcaagtgttt ggatgtgctt ctggccctgg agctccacga aggatcctta 360
gagtcagtgg 370

<210> 104
<211> 423
<212> DNA
<213> mouse

<400> 104
tttcccagdc tggtaggagca gccgaactggc gagtgtgcca actgtcccggt gcttcccagc 60
tcctaccttg cctgtcttct ctctcctggg aagatgttcc tggtaggggt gacgggaggc 120
atcgccctcag gcaagagctc cgtcatccag gtattccaac agctgggctg tgctgtaatc 180
gacgtggagc tcattgcgag gcacgttgtc cagccagggt atcctgcccc ccggcgata 240
gtagaggcct ttggcactga agtcttgctg gagaatggcg acatcgaccg caaggtcctc 300
ggagacctga tcttcaacca gcctgaccgt cggcagctgc tcaactccat taccaccct 360
gagatccgca aggaaatgat gaaggagacc ttcaagtact tctccgaggt accgatacgt 420
gat 423

<210> 105
<211> 117
<212> DNA
<213> mouse

<400> 105
agcttgggtg tggatcatatt taaactgata aagactcttc ataggagctg agggtagcaa 60
gcccgctcgt gtgactgggg tctcacacag gttcagcact tggagcatag tgagggtg 117

<210> 106
<211> 133
<212> DNA
<213> mouse

<400> 106

```

ttttttttt aaaataccac catttccaat cccaaaagaa catggcactt gtttgtttct 60
tccccttctc attcattcca gactttcaag tgttttcttc aatactgagg ctttctcctg 120
cagctctggg ctg 133

```

```

<210> 107
<211> 217
<212> DNA
<213> mouse

```

```

<220>
<221> unsure
<222> (1)...(1)

<221> unsure
<222> (11)...(11)

```

```

<221> unsure
<222> (18)...(23)

```

```

<221> unsure
<222> (34)...(34)

```

```

<221> unsure
<222> (37)...(38)

```

```

<221> unsure
<222> (40)...(42)

```

```

<221> unsure
<222> (50)...(52)

```

```

<221> unsure
<222> (55)...(58)

```

```

<221> unsure
<222> (152)...(152)

```

```

<221> unsure
<222> (155)...(155)

```

```

<221> unsure
<222> (165)...(165)

```

```

<400> 107
nttttttttg ngcgcacnnn nnnngnnncg ccnggnngn nnagcctacn nncannnngt 60
tttcttctcc aggctgaaga cctgaacgtc aagttggaag gggagccttc catgcggaaa 120
ccaaagcagc ggccgcggcc ggagccctc ancancacca ccaangeggg cactttcatc 180
gcccctcctg tctactccaa catcaccctc taccaga 217

```

```

<210> 108
<211> 346
<212> DNA
<213> mouse

```

```

<220>

```

```

<400> 108

```

```

gggcatagaa ggcacatcga aaagaatact tatttgaatt gaaggaagat gaagaggcct      60
gcaggaaggc tcagaagaca ggagtgtttt acctctttca tgacctggat cctttgctcc      120
aggcgtcagg acatcgatac ctggtgcccc ggcttagccg agcagagtgt gaagggctgc      180
tgggtaagtt cggacaggat tcgcaaagaa ttgaagattc ggtgctggtt ggggtgctccg      240
agcagcagga agcatgtttt gctttggatc taggtctgaa gagtgcctcc tccagccgtg      300
gacaagtatc gctgctccag cagcttgact gctgtaaaga ggatct      346

```

<210> 109
 <211> 242
 <212> DNA
 <213> mouse

```

<400> 109
ccacattgtc cacaactgga aggcacgatg gttcatcctt cggcagaaca cgctcctgta      60
ttacaagcta gaggggtggcc ggcgagtaac ccgcaccaag gggaggattg tccttgatgg      120
ctgcaccatc acctgccccct gcctggagta tgaaaaccgg ccgctcctca ttaaaactgaa      180
gacccgaact tccactgagt acttcctgga agcctgttct cgagaggaga gagactcctg      240
gg      242

```

<210> 110
 <211> 310
 <212> DNA
 <213> mouse

<220>
 <221> misc_feature
 <222> (1)...(310)
 <223> n = A,T,C or G

```

<400> 110
ccccgccggg aatccagggt gtagctgggt gagtcgcctc cggagagtga cgcgcagact      60
cggtcccccc ggcggccgcc ctctgcggg cctcgccgcg gtctcccttg ctccctgaga      120
tcgctgagcg ctgagcagcg gcccgggaga ggaggccttg ggcgacgggg cgcggagagg      180
gagggcgggg gggcantggg ggcgcgcggg atctctatat ggcgacgggt ctgtcgggtc      240
tggctgtccg gctgtcgcgc tcggccggnc ggccgggttc tatggggtct tctgcaaagg      300
ggttgacccg      310

```

<210> 111
 <211> 228
 <212> DNA
 <213> mouse

```

<400> 111
ttctttttta acatttggtg gtttttttct ttactctttt tttcttttcc ttctttttct      60
gccctcaacc ccccaactcc tttggtatga agtactttta acatttata ttcattgtta      120
cactttaaat tttgtaagga aaactctgat atttcattcc tcctgaacca ctaatgttag      180
aatttatctc taagaatcag tcaacatgta tactcttaat agtgaatt      228

```

<210> 112
 <211> 292
 <212> DNA
 <213> mouse

```

<400> 112
gtgggggtccc agacttgcca accaaagggc cattcctggt atatggttct ggcttcagct      60
ctggtggcat ggactatggt atggttgggt gcaaggaggc tgggaccgag tctcgcttca      120
aacagtggac ctcaatgatg gaagggtgc catctgtggc cacacaagaa gccaccatgc      180

```


acaaaaacgg cgctatagtg gccctggta agaccgagg aggttcacca tacaaccagt 240
 ttgatataat ccaggtgac aactgggtg gccatacggg tcctgctggt ga 292

<210> 113
 <211> 255
 <212> DNA
 <213> mouse

<220>

<400> 113
 ttagatgact taggacttta atgttttcca tgcagtcgat tgaaaacact gatacatgaa 60
 caaccagaaa aagacctcag caatgtatag acctggaata tatagtgttg ccctgggttaa 120
 actacaagaa cagccacgtg atcacagttt gaggggtggaa ggcaggggtg tgactgagtt 180
 ttgtttaacg gcctaaccga aaagcaaaga atcaaccatt tcttctactt gtggcaagaa 240
 acgagagtca tgggtg 255

<210> 114
 <211> 197
 <212> DNA
 <213> mouse

<400> 114
 gaccacatg tgaacagccg cgtgtatgtc aactgctct gtgtgtgatt tcttcacgtg 60
 tgcattgtgc ctcttggctt ttccacttat tgcctcgttc gtaagaaacc aaccataagg 120
 tgccaaggag gttttatttc tttttttttt aaagatgaca aatgtacaga tgtagtaga 180
 gatgttaatg tacagat 197

<210> 115
 <211> 205
 <212> DNA
 <213> mouse

<400> 115
 aaaacatttc aaaaaacagc aaaacaaaat tgatacaatc aaaaaaacia cactataacc 60
 aacatagggtg aaaacagcca aacacataat gtacaatctg gtgttccagg acaaacatct 120
 gtcataatata tggatatatac atatatactt tttcactcaa tatattatga caatatatat 180
 ttaaaaatttt gttatagaca aaaaa 205

<210> 116
 <211> 202
 <212> DNA
 <213> mouse

<220>

<400> 116
 cctccctcat cctctacttc ccttttccct cctgcttgat tttctcattc cagaccccta 60
 tgcacacaca cacacacaca cacacacaca caggaacaca cgcacacaca cacacacacg 120
 cacacacaca ctgtccatcc atagttactt atttagtttt ccattccctag agagatctaa 180
 tcatccccta gtcagtcgct aa 202

<210> 117
 <211> 240
 <212> DNA
 <213> mouse

<400> 117

ccgccaggag	aggagataca	cagccagtga	tgtggaccac	cggatggctg	ttgctgctgc	60
cgcttctgct	gtgtgaagga	gcgcaagccc	tggagtgcta	cagctgcgtg	cagaaggcgg	120
acgatggatg	cgctccgcac	aggatgaaga	cagtcaaatg	tgggccggg	gtggacgtct	180
gtaccgaggc	cgtagggagcg	gtagagacca	tcacgggca	attctctgtg	gcggtgcggg	240

<210> 118

<211> 527

<212> DNA

<213> Human

<400> 118

ccgtcagtct	agaaggataa	gagaaagaaa	gttaagcaac	tacaggaaat	ggctttggga	60
gttccaatat	cagtctatct	tttattcaac	gcaatgacag	cactgaccga	agaggcagcc	120
gtgactgtaa	cacctccaat	cacagcccag	caaggtaact	ggacagttaa	caaaacagaa	180
gctcacaaca	tagaaggacc	catagccttg	aagttctcac	acctttgcct	ggaagatcat	240
aacagttact	gcatcaacgg	tgcttgtgca	ttccaccatg	agctagagaa	agccatctgc	300
agggtgttta	ctgggttatac	tggagaaagg	tgtgagcact	tgactttaac	ttcatatgct	360
gtggattctt	atgaaaaata	cattgcaatt	gggattgggtg	ttggattact	attaagtggg	420
tttcttggtt	ttttttactg	ctatataaga	aagagggtgc	taaaattgaa	atcgccttac	480
aatgtctgtt	ctggagaaag	acgaccactg	tgaggccttt	gtgaaga		527

<210> 119

<211> 655

<212> DNA

<213> Rat

<400> 119

atggcgcgcc	ccgcgccctg	gtgggtggctg	cgcccgctgg	cgccgctcgc	cctggcgctg	60
gcgctggtcc	gggtgccctc	agcccgggcc	gggcagatgc	cgcccccgc	agagcgcggg	120
cccccagtac	ggctcttcac	cgaggaggag	ctggcccgtc	acagcgcgga	ggaggaggat	180
caacccatct	acttggcagt	gaaggaggatg	gtgttcgatg	tcacctctgg	gaaggagttt	240
tatggacgtg	gagcccccta	caacgccttg	gccgggaagg	actcgagcag	agggtgtggc	300
aagatgtcgc	tggatcctgc	agacctcact	catgacattt	ctggtctcac	tgccaaggag	360
ctggaagccc	tcgatgacat	cttcagcaag	gtgtacaaag	ccaaataccc	cattgttggc	420
tacacggccc	gcaggatcct	caacgaggat	ggcagcccca	acctggactt	caagcctgaa	480
gaccagcccc	atcttgacat	aaaggacgag	ttctaattgtc	tagctgagaa	gctgggtcta	540
gggagagggtg	aggggacagg	agttaaattgt	cccacggaac	aagcagggga	agcctctgag	600
tgtctgcat	ctgaataaaa	ctgatattta	actgggaaaa	aaaaaaaaaa	aaaaa	655

<210> 120

<211> 176

<212> PRT

<213> Rat

<400> 120

Met	Val	Pro	Cys	Phe	Leu	Leu	Ser	Leu	Leu	Leu	Val	Arg	Pro	Ala
1				5				10					15	
Pro	Val	Val	Ala	Tyr	Ser	Val	Ser	Leu	Pro	Ala	Ser	Phe	Leu	Glu
			20					25				30		
Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	Gly	Ser	Ser	Ala	Ser	Pro	Ser
		35					40				45			
Leu	Leu	Pro	Pro	Arg	Thr	Pro	Ala	Phe	Ser	Pro	Thr	Pro	Gly	Arg
	50					55					60			
Gln	Pro	Thr	Ala	Pro	Val	Gly	Pro	Val	Pro	Pro	Thr	Asn	Leu	Leu
65				70					75				80	

Gly Ile Val Asp Phe Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val
 85 90 95
 Gly Ser Leu Thr Phe Leu Ile Met Phe Ile Val Cys Ala Ala Leu Ile
 100 105 110
 Thr Arg Gln Lys His Lys Ala Thr Ala Tyr Tyr Pro Ser Ser Phe Pro
 115 120 125
 Glu Lys Lys Tyr Val Asp Gln Arg Asp Arg Ala Gly Gly Pro His Ala
 130 135 140
 Phe Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Gln Glu Glu Gly
 145 150 155 160
 Leu Asp Phe Phe Gln Gln Leu Gln Ala Asp Ile Leu Ala Cys Tyr Ser
 165 170 175

<210> 121

<211> 116

<212> PRT

<213> Rat

<400> 121

Met Glu Leu Leu Tyr Trp Cys Leu Leu Cys Leu Leu Leu Pro Leu Thr
 1 5 10 15
 Ser Arg Thr Gln Lys Leu Pro Thr Arg Asp Glu Glu Leu Phe Gln Met
 20 25 30
 Gln Ile Arg Asp Lys Ala Leu Phe His Asp Ser Ser Val Ile Pro Asp
 35 40 45
 Gly Ala Glu Ile Ser Ser Tyr Leu Phe Arg Asp Thr Pro Arg Arg Tyr
 50 55 60
 Phe Phe Met Val Glu Glu Asp Asn Thr Pro Leu Ser Val Thr Val Thr
 65 70 75 80
 Pro Cys Asp Ala Pro Leu Glu Trp Lys Leu Ser Leu Gln Glu Leu Pro
 85 90 95
 Glu Glu Ser Ser Ala Asp Gly Ser Gly Asp Pro Glu Pro Leu Asp Gln
 100 105 110
 Gln Lys Gln Gln
 115

<210> 122

<211> 64

<212> PRT

<213> Human

<400> 122

Met Asn Leu Leu Ile Gly Ser Ile Ile Leu Ser Ser Phe Leu Val Leu
 1 5 10 15
 Ser Asp Gly Asp Thr Thr Ala Ser Pro Ser Ser Met Ser Ser Ser
 20 25 30
 Val Leu Asn His Ile Ser Ser Ser Ser Ser Ser Val Trp His Leu Phe
 35 40 45
 Asp Ile Cys Asp Ser Ser Lys Trp Asn Ala Tyr Cys Gln Val Trp Gly
 50 55 60

<210> 123

<211> 68

<212> PRT

<213> Human

<400> 123

```

Met Leu Thr Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg
 1           5           10           15
Arg Lys Met Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly Val Leu Gly
          20           25           30
Ile Phe Gly Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr
          35           40           45
Gly Pro Thr Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe
 50           55           60
Ser Cys Leu Leu
65

```

```

<210> 124
<211> 110
<212> PRT
<213> mouse

```

```

<400> 124
Met Ile Ser Pro Ala Trp Ser Leu Phe Leu Ile Gly Thr Lys Ile Gly
 1           5           10           15
Leu Phe Phe Gln Val Ala Pro Leu Ser Val Val Ala Lys Ser Cys Pro
          20           25           30
Ser Val Cys Arg Cys Asp Ala Gly Phe Ile Tyr Cys Asn Asp Arg Ser
          35           40           45
Leu Thr Ser Ile Pro Val Gly Ile Pro Glu Asp Ala Thr Thr Leu Tyr
 50           55           60
Leu Gln Asn Asn Gln Ile Asn Asn Val Gly Ile Pro Ser Asp Leu Lys
65           70           75           80
Asn Leu Leu Lys Val Gln Arg Ile Tyr Leu Tyr His Asn Ser Leu Asp
          85           90           95
Glu Phe Pro Thr Asn Leu Pro Lys Tyr Val Lys Glu Leu His
          100          105          110

```

```

<210> 125
<211> 330
<212> PRT
<213> mouse

```

```

<400> 125
Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu Ser Leu Pro Leu Leu
 1           5           10           15
Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala Cys Pro Cys Leu Arg
          20           25           30
Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe
          35           40           45
Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys
 50           55           60
Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser
65           70           75           80
Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His
          85           90           95
Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr
          100          105          110
Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu
          115          120          125
Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu
          130          135          140
Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala

```

145	Ser	Val	Arg	Leu	Cys	Tyr	Gln	Trp	Ala	Leu	Glu	Cys	Glu	Asp	Leu	Ser	160
					165					170						175	
Ser	Pro	Phe	Asp	Thr	Gln	Lys	Ile	Val	Ser	Gly	Gly	His	Thr	Val	Asp		
				180				185						190			
Leu	Pro	Tyr	Glu	Phe	Leu	Leu	Pro	Cys	Met	Cys	Ile	Glu	Ala	Ser	Tyr		
				195			200				205						
Leu	Gln	Glu	Asp	Thr	Val	Arg	Lys	Lys	Cys	Pro	Phe	Gln	Ser	Trp			
	210				215					220							
Pro	Glu	Ala	Tyr	Gly	Ser	Asp	Phe	Trp	Gln	Ser	Ile	Arg	Phe	Thr	Asp		
225					230					235					240		
Tyr	Ser	Gln	His	Asn	Gln	Met	Val	Met	Ala	Leu	Thr	Leu	Arg	Cys	Pro		
				245					250					255			
Leu	Lys	Leu	Glu	Ala	Ser	Leu	Cys	Trp	Arg	Gln	Asp	Pro	Leu	Thr	Pro		
				260				265					270				
Cys	Glu	Thr	Leu	Pro	Asn	Ala	Thr	Ala	Gln	Glu	Ser	Glu	Gly	Trp	Tyr		
		275					280					285					
Ile	Leu	Glu	Asn	Val	Asp	Leu	His	Pro	Gln	Leu	Cys	Phe	Lys	Phe	Ser		
	290				295						300						
Phe	Glu	Asn	Ser	Ser	His	Val	Glu	Cys	Pro	His	Gln	Ser	Gly	Ser	Leu		
305					310					315					320		
Pro	Ser	Trp	Thr	Val	Ser	Met	Asp	Thr	Gln								
				325					330								

```
<210> 126
<211> 37
<212> PRT
<213> Rat
```

[illegible]

```
<210> 127
<211> 42
<212> PRT
<213> mouse
```

Met Gly Ser Pro Ile Ser Gly Val Cys Pro Val Leu Pro Gly Gly Leu															
1 5 10 15															
Phe Val Ala Leu Gly Trp Ile Phe Leu Leu Phe His Arg Asp Ala Phe															
20 25 30															
Ser Leu His Thr Met Ser Ala Gly Phe Pro															
35 40															

```
<210> 128
<211> 253
<212> PRT
<213> mouse
```

<400> 128
Met Met Tyr Trp Ile Val Phe Ala Ile Phe Met Ala Ala Glu Thr Phe

```

      1           5           10           15
Thr Asp Ile Phe Ile Ser Trp Ser Gly Pro Arg Ile Gly Arg Pro Trp
      20           25           30
Gly Trp Glu Gly Pro His His His His Leu Ala Ser Gly Ser His
      35           40           45
Lys Pro Leu Pro Leu Leu Thr His Arg Phe Pro Phe Tyr Tyr Glu Phe
      50           55           60
Lys Met Ala Phe Val Leu Trp Leu Leu Ser Pro Tyr Thr Lys Gly Ala
      65           70           75           80
Ser Leu Leu Tyr Arg Lys Phe Val His Pro Ser Leu Ser Arg His Glu
      85           90           95
Lys Glu Ile Asp Ala Cys Ile Val Gln Ala Lys Glu Arg Ser Tyr Glu
      100           105           110
Thr Met Leu Ser Phe Gly Lys Arg Ser Leu Asn Ile Ala Ala Ser Ala
      115           120           125
Ala Val Gln Ala Ala Thr Lys Ser Gln Gly Ala Leu Ala Gly Arg Leu
      130           135           140
Arg Ser Phe Ser Met Gln Asp Leu Arg Ser Ile Pro Asp Thr Pro Val
      145           150           155           160
Pro Thr Tyr Gln Asp Pro Leu Tyr Leu Glu Asp Gln Val Pro Arg Arg
      165           170           175
Arg Pro Pro Ile Gly Tyr Arg Pro Gly Gly Leu Gln Gly Ser Asp Thr
      180           185           190
Glu Asp Glu Cys Trp Ser Asp Asn Glu Ile Val Pro Gln Pro Pro Val
      195           200           205
Arg Pro Arg Glu Lys Pro Leu Gly Arg Ser Gln Ser Leu Arg Val Val
      210           215           220
Lys Arg Lys Pro Leu Thr Arg Glu Gly Thr Ser Arg Ser Leu Lys Val
      225           230           235           240
Arg Thr Arg Lys Lys Ala Met Pro Ser Asp Met Asp Ser
      245           250

```

<210> 129
 <211> 40
 <212> PRT
 <213> mouse

```

      <400> 129
Met Lys Ala Met Ala Leu Ser Leu Gly Ala Ser Pro Val Leu Ala Phe
      1           5           10           15
Leu Leu Ser Gly Tyr Ser Asp Gly Tyr Gln Val Cys Ser Arg Phe Gly
      20           25           30
Ser Lys Val Pro Gln Phe Leu Asn
      35           40

```

<210> 130
 <211> 87
 <212> PRT
 <213> mouse

```

      <400> 130
Met Ile Ala Val Thr Phe Ala Ile Val Leu Gly Val Ile Ile Tyr Arg
      1           5           10           15
Ile Ser Thr Ala Ala Ala Leu Ala Met Asn Ser Ser Pro Ser Val Arg
      20           25           30
Ser Asn Ile Arg Val Thr Val Thr Ala Val Ile Ile Asn Leu
      35           40           45

```

Val Val Ile Ile Leu Leu Asp Glu Val Tyr Gly Cys Ile Ala Arg Trp
 50 55 60
 Leu Thr Lys Ile Gly Glu Cys His Val Gln Asp Ser Ile Gly Ser Met
 65 70 75 80
 Gly Leu Gly Gln Gly Gln Pro
 85

<210> 131
 <211> 70
 <212> PRT
 <213> mouse

<400> 131
 Met Phe Gly Leu Val His Val Cys Thr Cys Val Cys Val Cys Val Cys
 1 5 10 15
 Val Cys Val Cys Val Cys Ile Cys Ser Cys Gly Tyr Val His Val Pro
 20 25 30
 Cys Gly Cys Val Cys Leu Trp Gly Pro Glu Val Arg Tyr Leu Pro Leu
 35 40 45
 Ser Leu His Pro Gly Gly Phe Cys Phe Val Leu Phe Cys Phe Gly Pro
 50 55 60
 Gly Leu Ser Leu Ile Ser
 65 70

<210> 132
 <211> 63
 <212> PRT
 <213> mouse

<400> 132
 Met Trp Leu Leu Val Ala Leu Thr Leu Ser Val Tyr Ser Leu Val Ala
 1 5 10 15
 Phe Val Thr Gly Met Leu Cys Asp Thr Val Val Ile Lys Met Leu Met
 20 25 30
 Ser Leu His Lys Ser Ser Lys Leu Asn Pro Arg Ala Lys Cys Gly Gly
 35 40 45
 Val Pro Leu Ile Pro Ala Leu Trp Gly Gln Val Gln Val Val Leu
 50 55 60

<210> 133
 <211> 39
 <212> PRT
 <213> mouse

<400> 133
 Met Asp Asn Thr Leu Ser Ile Ile Ile Tyr Leu Leu Phe Ile Phe Ala
 1 5 10 15
 Ile Ser Val Leu Asp Ser Gln Leu Ser Thr Arg Cys Leu Trp Trp Phe
 20 25 30
 Ser Lys Asp Leu Glu Val Thr
 35

<210> 134
 <211> 90
 <212> PRT
 <213> Rat

<400> 134
 Met Pro Thr Met Trp Pro Leu Leu His Val Leu Trp Leu Ala Leu Val
 1 5 10 15
 Cys Gly Ser Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala
 20 25 30
 Ala Ser Lys Thr Leu Leu Glu Lys Thr Gln Phe Ser Asp Lys Pro Val
 35 40 45
 Gln Asp Arg Gly Leu Val Val Thr Asp Ile Lys Ala Glu Asp Val Val
 50 55 60
 Leu Glu His Arg Ser Tyr Cys Ser Ala Arg Ala Arg Glu Arg Asn Phe
 65 70 75 80
 Ala Gly Glu Val Leu Gly Ile Cys His Ser
 85 90

<210> 135
 <211> 193
 <212> PRT
 <213> Rat

<400> 135
 Met Thr Ser Gly Pro Gly Gly Pro Ala Ala Ala Thr Gly Gly Gly Lys
 1 5 10 15
 Asp Thr His Gln Trp Tyr Val Cys Asn Arg Glu Lys Leu Cys Glu Ser
 20 25 30
 Leu Gln Ser Val Phe Val Gln Ser Tyr Leu Asp Gln Gly Thr Gln Ile
 35 40 45
 Phe Leu Asn Asn Ser Ile Glu Lys Ser Gly Trp Leu Phe Ile Gln Leu
 50 55 60
 Tyr His Ser Phe Val Ser Ser Val Phe Thr Leu Phe Met Ser Arg Thr
 65 70 75 80
 Ser Ile Asn Gly Leu Leu Gly Arg Gly Ser Met Phe Val Phe Ser Pro
 85 90 95
 Asp Gln Phe Gln Arg Leu Leu Lys Ile Asn Pro Asp Trp Lys Thr His
 100 105 110
 Arg Leu Leu Asp Leu Gly Ala Gly Asp Gly Glu Val Thr Lys Ile Met
 115 120 125
 Ser Pro His Phe Glu Glu Ile Tyr Ala Thr Glu Leu Ser Glu Thr Met
 130 135 140
 Ile Trp Gln Leu Gln Lys Lys Lys Tyr Arg Val Leu Gly Ile Asn Glu
 145 150 155 160
 Trp Gln Asn Thr Gly Phe Gln Tyr Asp Val Ile Ser Cys Leu Asn Leu
 165 170 175
 Leu Asp Arg Cys Asp Gln Pro Leu Thr Leu Leu Lys Asp Ile Arg Met
 180 185 190
 Ser

<210> 136
 <211> 106
 <212> PRT
 <213> Rat

<400> 136
 Met Ala Ala Pro Met Asp Arg Thr His Gly Gly Arg Ala Ala Arg Ala
 1 5 10 15
 Leu Arg Arg Ala Leu Ala Leu Ala Ser Leu Ala Gly Leu Leu Leu Ser
 20 25 30

Gly Leu Ala Gly Ala Leu Pro Thr Leu Gly Pro Gly Trp Arg Arg Gln
 35 40 45
 Asn Pro Glu Pro Pro Ala Ser Arg Thr Arg Ser Leu Leu Asp Ala
 50 55 60
 Ala Ser Gly Gln Leu Arg Leu Glu Tyr Gly Phe His Pro Asp Ala Val
 65 70 75 80
 Ala Trp Ala Asn Leu Thr Asn Ala Ile Arg Glu Thr Gly Trp Ala Tyr
 85 90 95
 Leu Asp Leu Gly Thr Asn Gly Ser Tyr Lys
 100 105

<210> 137

<211> 286

<212> PRT

<213> Rat

<400> 137

Met Ala Ala Ala Met Pro Leu Gly Leu Ser Leu Leu Leu Leu Val Leu
 1 5 10 15
 Val Gly Gln Gly Cys Cys Gly Arg Val Glu Gly Pro Arg Asp Ser Leu
 20 25 30
 Arg Glu Glu Leu Val Ile Thr Pro Leu Pro Ser Gly Asp Val Ala Ala
 35 40 45
 Thr Phe Gln Phe Arg Thr Arg Trp Asp Ser Asp Leu Gln Arg Glu Gly
 50 55 60
 Val Ser His Tyr Arg Leu Phe Pro Lys Ala Leu Gly Gln Leu Ile Ser
 65 70 75 80
 Lys Tyr Ser Leu Arg Glu Leu His Leu Ser Phe Thr Gln Gly Phe Trp
 85 90 95
 Arg Thr Arg Tyr Trp Gly Pro Pro Phe Leu Gln Ala Pro Ser Gly Ala
 100 105 110
 Glu Leu Trp Val Trp Phe Gln Asp Thr Val Thr Asp Val Asp Lys Ser
 115 120 125
 Trp Lys Glu Leu Ser Asn Val Leu Ser Gly Ile Phe Cys Ala Ser Leu
 130 135 140
 Asn Phe Ile Asp Ser Thr Asn Thr Val Thr Pro Thr Ala Ser Phe Lys
 145 150 155 160
 Pro Leu Gly Leu Ala Asn Asp Thr Asp His Tyr Phe Leu Arg Tyr Ala
 165 170 175
 Val Leu Pro Arg Glu Val Val Cys Thr Glu Asn Leu Thr Pro Trp Lys
 180 185 190
 Lys Leu Leu Pro Cys Ser Ser Lys Ala Gly Leu Ser Val Leu Leu Lys
 195 200 205
 Ala Asp Arg Leu Phe His Thr Ser Tyr His Ser Gln Ala Val His Ile
 210 215 220
 Arg Pro Ile Cys Arg Asn Ala His Cys Thr Ser Ile Ser Trp Glu Leu
 225 230 235 240
 Arg Gln Thr Leu Ser Val Val Phe Asp Ala Phe Ile Thr Gly Gln Gly
 245 250 255
 Lys Lys Glu Ala Cys Pro Leu Ala Ser Gln Ser Leu Val Tyr Val Asp
 260 265 270
 Ile Thr Gly Tyr Ser Gln Asp Asn Glu Thr Leu Glu Val Ser
 275 280 285

<210> 138

<211> 198

<212> PRT

<213> Rat

<400> 138

```

Met Thr Val Phe Arg Lys Val Thr Thr Met Ile Ser Trp Met Leu Leu
 1          5          10          15
Ala Cys Ala Leu Pro Cys Ala Ala Asp Pro Met Leu Gly Ala Phe Ala
 20          25          30
Arg Arg Asp Phe Gln Lys Gly Gly Pro Gln Leu Val Cys Ser Leu Pro
 35          40          45
Gly Pro Gln Gly Pro Pro Gly Pro Pro Gly Ala Pro Gly Ser Ser Gly
 50          55          60
Met Val Gly Arg Met Gly Phe Pro Gly Lys Asp Gly Gln Asp Gly Gln
 65          70          75          80
Asp Gly Asp Arg Gly Asp Ser Gly Glu Glu Gly Pro Pro Gly Arg Thr
 85          90          95
Gly Asn Arg Gly Lys Gln Gly Pro Lys Gly Lys Ala Gly Ala Ile Gly
100          105          110
Arg Ala Gly Pro Arg Gly Pro Lys Gly Val Ser Gly Thr Pro Gly Lys
115          120          125
His Gly Ile Pro Gly Lys Lys Gly Pro Lys Gly Lys Lys Gly Glu Pro
130          135          140
Gly Leu Pro Gly Pro Cys Ser Cys Gly Ser Ser Arg Ala Lys Ser Ala
145          150          155          160
Phe Ser Val Ala Val Thr Lys Ser Tyr Pro Arg Glu Arg Leu Pro Ile
165          170          175
Lys Phe Asp Lys Ile Leu Met Asn Glu Gly Gly His Tyr Asn Ala Ser
180          185          190
Ser Gly Lys Phe Val Cys
195

```

<210> 139

<211> 233

<212> PRT

<213> Rat

<400> 139

```

Met Ala Ser Ala Leu Glu Glu Leu Gln Lys Asp Leu Glu Glu Val Lys
 1          5          10          15
Val Leu Leu Glu Lys Ser Thr Arg Lys Arg Leu Arg Asp Thr Leu Thr
 20          25          30
Asn Glu Lys Ser Lys Ile Glu Thr Glu Leu Arg Asn Lys Met Gln Gln
 35          40          45
Lys Ser Gln Lys Lys Pro Glu Phe Asp Asn Glu Lys Pro Ala Ala Val
 50          55          60
Val Ala Pro Leu Thr Thr Gly Tyr Thr Val Lys Ile Ser Asn Tyr Gly
 65          70          75          80
Trp Asp Gln Ser Asp Lys Phe Val Lys Ile Tyr Ile Thr Leu Thr Gly
 85          90          95
Val His Gln Val Pro Ala Glu Asn Val Gln Val His Phe Thr Glu Arg
100          105          110
Ser Phe Asp Leu Leu Val Lys Asn Leu Asn Gly Lys Asn Tyr Ser Met
115          120          125
Ile Val Asn Asn Leu Leu Lys Pro Ile Ser Val Glu Ser Ser Ser Lys
130          135          140
Lys Val Lys Thr Asp Thr Val Ile Ile Leu Cys Arg Lys Lys Ala Glu
145          150          155          160
Asn Thr Arg Trp Asp Tyr Leu Thr Gln Val Glu Lys Glu Cys Lys Glu

```

165 170 175
 Lys Glu Lys Pro Ser Tyr Asp Thr Glu Ala Asp Pro Ser Glu Gly Leu
 180 185 190
 Met Asn Val Leu Lys Lys Ile Tyr Glu Asp Gly Asp Asp Met Lys
 195 200 205
 Arg Thr Ile Asn Lys Ala Trp Val Glu Ser Arg Glu Lys Gln Ala Arg
 210 215 220
 Glu Asp Thr Glu Phe Leu Gln Pro Gly
 225 230

<210> 140
 <211> 38
 <212> PRT
 <213> Human

<400> 140
 Met Gly Leu Ala Leu Cys Leu Ala Ser Ala Gly Ile Ser Gly Ser Arg
 1 5 10 15
 Ser Ala Phe Leu Gly Val Pro Arg Pro Arg Pro Thr Leu Ile Lys Leu
 20 25 30
 Ile Asp Thr Val Asp Leu
 35

<210> 141
 <211> 322
 <212> PRT
 <213> mouse

<400> 141
 Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Thr Leu Pro Ser
 1 5 10 15
 Leu Gly Ala Gly Gly Glu Ser Pro Glu Ala Pro Pro Gln Ser Trp Thr
 20 25 30
 Gln Leu Trp Leu Phe Arg Phe Leu Leu Asn Val Ala Gly Tyr Ala Ser
 35 40 45
 Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Leu Arg Arg Lys Asn
 50 55 60
 Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65 70 75 80
 Val Phe Gly Asn Glu Pro Lys Ala Pro Asp Glu Val Leu Leu Ala Pro
 85 90 95
 Arg Thr Glu Thr Ala Glu Ser Thr Pro Ser Trp Gln Val Leu Lys Leu
 100 105 110
 Val Phe Cys Ala Ser Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Ile
 115 120 125
 Leu Gln Glu Arg Val Met Thr Gly Ser Tyr Gly Ala Thr Ala Thr Ser
 130 135 140
 Pro Gly Glu His Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
 145 150 155 160
 Val Leu Ala Leu Val Val Ala Gly Leu Tyr Cys Val Leu Arg Lys Gln
 165 170 175
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
 180 185 190
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
 195 200 205
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
 210 215 220

```

Met Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225      230      235      240
Leu Thr Ala Gly Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
      245      250      255
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
      260      265      270
Val Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
      275      280      285
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
      290      295      300
Gly Val Asn Leu Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
305      310      315      320
Gln Gly

```

```

<210> 142
<211> 312
<212> PRT
<213> mouse

```

```

<400> 142
Met Leu Cys Leu Cys Leu Tyr Val Pro Ile Ala Gly Ala Ala Gln Thr
1      5      10      15
Glu Phe Gln Tyr Phe Glu Ser Lys Gly Leu Pro Ala Glu Leu Lys Ser
      20      25      30
Ile Phe Lys Leu Ser Val Phe Ile Pro Ser Gln Glu Phe Ser Thr Tyr
      35      40      45
Arg Gln Trp Lys Gln Lys Ile Val Gln Ala Gly Asp Lys Asp Leu Asp
      50      55      60
Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr Leu Gln Asp His Glu
      65      70      75      80
Lys Lys Leu Arg Leu Val Phe Lys Ser Leu Asp Lys Lys Asn Asp Gly
      85      90      95
Arg Ile Asp Ala Gln Glu Ile Met Gln Ser Leu Arg Asp Leu Gly Val
      100      105      110
Lys Ile Ser Glu Gln Gln Ala Glu Lys Ile Leu Lys Ser Met Asp Lys
      115      120      125
Asn Gly Thr Met Thr Ile Asp Trp Asn Glu Trp Arg Asp Tyr His Leu
      130      135      140
Leu His Pro Val Glu Asn Ile Pro Glu Ile Ile Leu Tyr Trp Lys His
      145      150      155      160
Ser Thr Ile Phe Asp Val Gly Glu Asn Leu Thr Val Pro Asp Glu Phe
      165      170      175
Thr Val Glu Glu Arg Gln Thr Gly Met Trp Trp Arg His Leu Val Ala
      180      185      190
Gly Gly Gly Ala Gly Ala Val Ser Arg Thr Cys Thr Ala Pro Leu Asp
      195      200      205
Arg Leu Lys Val Leu Met Gln Val His Ala Ser Arg Ser Asn Asn Met
      210      215      220
Cys Ile Val Gly Gly Phe Thr Gln Met Ile Arg Glu Gly Gly Ala Lys
      225      230      235      240
Ser Leu Trp Arg Gly Asn Gly Ile Asn Val Leu Lys Ile Ala Pro Glu
      245      250      255
Ser Ala Ile Lys Phe Met Ala Tyr Glu Gln Met Lys Arg Leu Val Gly
      260      265      270
Ser Asp Gln Glu Thr Leu Arg Ile His Glu Arg Leu Val Ala Gly Ser
      275      280      285

```

Leu Ala Gly Ala Ile Ala Gln Ser Ser Ile Tyr Pro Met Glu Val Leu
 290 295 300
 Lys Thr Arg Met Ala Leu Arg Lys
 305 310

<210> 143
 <211> 163
 <212> PRT
 <213> Rat

<400> 143
 Met Pro Leu Val Thr Thr Leu Phe Tyr Ala Cys Phe Tyr His Tyr Thr
 1 5 10 15
 Glu Ser Glu Gly Thr Phe Ser Ser Pro Val Asn Leu Lys Lys Thr Phe
 20 25 30
 Lys Ile Pro Asp Arg Gln Tyr Val Leu Thr Ala Leu Ala Ala Arg Ala
 35 40 45
 Lys Leu Arg Ala Trp Asn Asp Val Asp Ala Leu Phe Thr Thr Lys Asn
 50 55 60
 Trp Leu Gly Tyr Thr Lys Lys Arg Ala Pro Ile Gly Phe His Arg Val
 65 70 75 80
 Val Glu Ile Leu His Lys Asn Ser Ala Pro Val Gln Ile Leu Gln Glu
 85 90 95
 Tyr Val Asn Leu Val Glu Asp Val Asp Thr Lys Leu Asn Leu Ala Thr
 100 105 110
 Lys Phe Lys Cys His Asp Val Val Ile Asp Thr Cys Arg Asp Leu Lys
 115 120 125
 Asp Arg Gln Gln Leu Leu Ala Tyr Arg Ser Lys Val Asp Lys Gly Ser
 130 135 140
 Ala Glu Glu Glu Lys Ile Asp Val Ile Leu Ser Ser Ser Gln Ile Arg
 145 150 155 160
 Trp Lys Asn

<210> 144
 <211> 330
 <212> PRT
 <213> Rat

<400> 144
 Met Ala Gly Trp Ala Gly Ala Glu Leu Ser Val Leu Asn Pro Leu Arg
 1 5 10 15
 Ala Leu Trp Leu Leu Leu Ala Ala Ala Phe Leu Leu Ala Leu Leu Leu
 20 25 30
 Gln Leu Ala Pro Ala Arg Leu Leu Pro Ser Cys Ala Leu Phe Gln Asp
 35 40 45
 Leu Ile Arg Tyr Gly Lys Thr Lys Gln Ser Gly Ser Arg Arg Pro Ala
 50 55 60
 Val Cys Arg Ala Phe Asp Val Pro Lys Arg Tyr Phe Ser His Phe Tyr
 65 70 75 80
 Val Val Ser Val Leu Trp Asn Gly Ser Leu Leu Trp Phe Leu Ser Gln
 85 90 95
 Ser Leu Phe Leu Gly Ala Pro Phe Pro Ser Trp Leu Trp Ala Leu Leu
 100 105 110
 Arg Thr Leu Gly Val Thr Gln Phe Gln Ala Leu Gly Met Glu Ser Lys
 115 120 125
 Ala Ser Arg Ile Gln Ala Gly Glu Leu Ala Leu Ser Thr Phe Leu Val

130 135 140
 Leu Val Phe Leu Trp Val His Ser Leu Arg Arg Leu Phe Glu Cys Phe
 145 150 155 160
 Tyr Val Ser Val Phe Ser Asn Thr Ala Ile His Val Val Gln Tyr Cys
 165 170 175
 Phe Gly Leu Val Tyr Tyr Val Leu Val Gly Leu Thr Val Leu Ser Gln
 180 185 190
 Val Pro Met Asn Asp Lys Asn Val Tyr Ala Leu Gly Lys Asn Leu Leu
 195 200 205
 Leu Gln Ala Arg Trp Phe His Ile Leu Gly Met Met Met Phe Phe Trp
 210 215 220
 Ser Ser Ala His Gln Tyr Lys Cys His Val Ile Leu Ser Asn Leu Arg
 225 230 235 240
 Arg Asn Lys Lys Gly Val Val Ile His Cys Gln His Arg Ile Pro Phe
 245 250 255
 Gly Asp Trp Phe Glu Tyr Val Ser Ser Ala Asn Tyr Leu Ala Glu Leu
 260 265 270
 Met Ile Tyr Ile Ser Met Ala Val Thr Phe Gly Leu His Asn Val Thr
 275 280 285
 Trp Trp Leu Val Val Thr Tyr Val Phe Phe Ser Gln Ala Leu Ser Ala
 290 295 300
 Phe Phe Asn His Arg Phe Tyr Lys Ser Thr Phe Val Ser Tyr Pro Lys
 305 310 315 320
 His Arg Lys Ala Phe Leu Pro Phe Leu Phe
 325 330

<210> 145

<211> 301

<212> PRT

<213> Rat

<400> 145

Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr Gly
 1 5 10 15
 Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser
 20 25 30
 Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu
 35 40 45
 Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr
 50 55 60
 Pro Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val
 65 70 75 80
 Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile
 85 90 95
 Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr
 100 105 110
 Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn
 115 120 125
 Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg
 130 135 140
 Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu
 145 150 155 160
 Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser
 165 170 175
 Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe
 180 185 190
 Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp

```

      195              200              205
Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser
  210              215              220
Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys
  225              230              235
Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu
      245              250              255
Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu
      260              265              270
Gln Arg Cys Leu Leu Gly Leu Pro Val Trp Glu Gly Ser Pro His Leu
      275              280              285
Pro Thr Gly His Trp Leu Arg Glu Leu Trp Ser Leu Leu
  290              295              300

```

<210> 146
 <211> 61
 <212> PRT
 <213> Rat

```

      <400> 146
Met Glu Asn Ile Tyr Tyr Thr Asn Leu Ile Thr Ile Leu Gly Asn Lys
  1              5              10              15
His Ala Asn Gln Met Glu Leu Asn Leu Gln Ala Leu Ile Leu Ser Pro
      20              25              30
Trp Phe Ala Val Cys Ala Pro Pro Gly Phe Ala Arg Asp Gln Ala Val
      35              40              45
Arg Gly Leu Ala Leu Ala Gly Arg Arg Ile Thr Val Val
  50              55              60

```

<210> 147
 <211> 105
 <212> PRT
 <213> Rat

```

      <400> 147
Met Leu Arg Arg Gln Leu Val Trp Trp His Leu Leu Ala Leu Leu Phe
  1              5              10              15
Leu Pro Phe Cys Leu Cys Gln Asp Glu Tyr Met Glu Ser Pro Gln Ala
      20              25              30
Gly Gly Leu Pro Pro Asp Cys Ser Lys Cys Cys His Gly Asp Tyr Gly
      35              40              45
Phe Arg Gly Tyr Gln Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ile
  50              55              60
Pro Gly Asn His Gly Asn Asn Gly Asn Asn Gly Ala Thr Gly His Glu
  65              70              75              80
Gly Ala Lys Gly Glu Lys Gly Asp Lys Gly Asp Leu Gly Pro Arg Gly
      85              90              95
Glu Arg Gly Gln His Gly Pro Lys Gly
      100              105

```

<210> 148
 <211> 210
 <212> PRT
 <213> Rat

```

      <400> 148
Met Leu Gly Ala Thr Ser Leu Ser Trp Pro Trp Val Leu Trp Ala Val

```

```

      1           5           10           15
Ala Gln Arg Asp Ser Val Asp Ala Ile Gly Met Phe Leu Gly Gly Leu
      20           25           30
Val Ala Thr Ile Phe Leu Asp Ile Ile Tyr Ile Ser Ile Phe Tyr Ser
      35           40           45
Ser Val Ala Val Gly Asp Thr Gly Arg Phe Ser Ala Gly Met Ala Ile
      50           55           60
Phe Ser Leu Leu Leu Gln Ala Leu Leu Leu Leu Pro Arg Leu Pro His
      65           70           75           80
Ala Pro Gly Ser Glu Gly Val Ser Ser Arg Ser Ala Arg Ile Ser Ser
      85           90           95
Asp Leu Leu Arg Asn Ile Val Pro Thr Arg Gln Leu Thr Arg Gln Thr
      100          105          110
His Leu Gln Thr Pro Leu Gln Ala Trp Arg Thr Arg Ala Lys Leu Pro
      115          120          125
Pro Gly Gly Thr Glu Ala Val Pro Gly Arg Pro Gly Ala Gln Gln Asp
      130          135          140
Ala Cys His Leu Leu Tyr Trp Thr Tyr Asn Gly Val Ser Ser Ile Pro
      145          150          155          160
Cys His Arg Gly Gly Leu Ser His Val Pro Ser Glu Val Pro Ala Glu
      165          170          175
Lys Ser Pro Val Leu Ile Leu His Ala Ala Pro Pro Phe Lys Thr Pro
      180          185          190
Val Asn Pro Trp Ala Arg Thr Val Val Gly Phe Phe Pro Ser Ser Pro
      195          200          205
Ser Leu
      210

```

<210> 149

<211> 301

<212> PRT

<213> Rat

<400> 149

```

Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr Gly
      1           5           10           15
Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser
      20           25           30
Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu
      35           40           45
Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr
      50           55           60
Pro Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val
      65           70           75           80
Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile
      85           90           95
Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr
      100          105          110
Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn
      115          120          125
Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg
      130          135          140
Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu
      145          150          155          160
Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser
      165          170          175
Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe

```



```

      180      185      190
Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp
      195      200      205
Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser
      210      215      220
Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys
      225      230      235
Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu
      245      250      255
Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu
      260      265      270
Gln Arg Cys Leu Leu Gly Leu Pro Val Trp Glu Gly Ser Pro His Leu
      275      280      285
Pro Thr Gly His Trp Leu Arg Glu Leu Trp Ser Leu Leu
      290      295      300

```

<210> 150
 <211> 80
 <212> PRT
 <213> Human

```

      <400> 150
Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe Cys
  1      5      10      15
Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys Gly Glu
      20      25      30
Phe Gln Asp Thr Lys Val Tyr Cys Thr Arg Glu Ser Asn Pro His Cys
      35      40      45
Gly Ser Asp Gly Gln Thr Tyr Gly Asn Lys Cys Ala Phe Cys Lys Ala
      50      55      60
Ile Val Lys Ser Gly Gly Lys Ile Ser Leu Lys His Pro Gly Lys Cys
      65      70      75      80

```

<210> 151
 <211> 27
 <212> PRT
 <213> mouse

```

      <400> 151
Met Leu Lys Ala Ser Leu His Ile Leu Phe Leu Gly Ile Leu Asn Val
  1      5      10      15
Pro Ile Val Asp Thr Ser Thr Lys Thr Gly Val
      20      25

```

<210> 152
 <211> 86
 <212> PRT
 <213> mouse

```

      <400> 152
Met Leu Gln Gly Pro Ala Pro Ser Cys Phe Trp Val Phe Ser Gly Ile
  1      5      10      15
Cys Val Phe Trp Asp Phe Ile Phe Ile Phe Phe Asn Val Leu Ser
      20      25      30
Leu Gly Asn Arg Glu Ile Ser Ala Lys Asp Phe Ala Asp Gln Pro Ala
      35      40      45
Gly Ala Gln Gly Met Trp Gly Ile Trp Gly His Thr Ile Thr Cys Gly

```

50 55 60
 Leu Ala Pro Gly Ala Lys Pro Cys Ser Leu Lys Arg Glu Gly Pro Asp
 65 70 75 80
 Leu Leu Ser Phe Pro Pro
 85

<210> 153
 <211> 72
 <212> PRT
 <213> mouse

<400> 153
 Met Ser Ala Ile Phe Asn Phe Gln Ser Leu Leu Thr Val Ile Leu Leu
 1 5 10 15
 Leu Ile Cys Thr Cys Ala Tyr Ile Arg Ser Leu Ala Pro Ser Ile Leu
 20 25 30
 Asp Arg Asn Lys Thr Gly Leu Leu Gly Ile Phe Trp Lys Cys Ala Arg
 35 40 45
 Ile Gly Glu Arg Lys Ser Pro Tyr Val Ala Ile Cys Cys Ile Val Met
 50 55 60
 Ala Phe Ser Ile Leu Phe Ile Gln
 65 70

<210> 154
 <211> 169
 <212> PRT
 <213> mouse

<400> 154
 Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly
 1 5 10 15
 Ser Arg Leu Pro Arg Val Ile Ser Gln Ser Val Cys Arg Ala Arg
 20 25 30
 Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly
 35 40 45
 Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln
 50 55 60
 Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu
 65 70 75 80
 Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr
 85 90 95
 Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly
 100 105 110
 Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe
 115 120 125
 Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu
 130 135 140
 Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu
 145 150 155 160
 Gly Glu Met Pro Pro Glu Asp Gly Met
 165

<210> 155
 <211> 61
 <212> PRT
 <213> mouse

<400> 155
 Met Glu Lys Gln Met Asp Ala Ser Val Ser Val Ile Phe Gly Ser Ile
 1 5 10 15
 Val Ile Ser Ala Phe Leu Tyr Leu Ser Leu Ala Gly Pro Trp Ala Val
 20 25 30
 Thr Val Thr Gln Met Arg Thr Ile Ile Thr Met Asp Gln Leu Arg
 35 40 45
 Asp Ala Leu Ile Leu Asp Gln Leu Lys Val Ala Val Ser
 50 55 60

<210> 156
 <211> 131
 <212> PRT
 <213> mouse

<400> 156
 Met Ala Pro Ser Leu Trp Lys Gly Leu Val Gly Val Gly Leu Phe Ala
 1 5 10 15
 Leu Ala His Ala Ala Phe Ser Ala Ala Gln His Arg Ser Tyr Met Arg
 20 25 30
 Leu Thr Glu Lys Glu Asp Glu Ser Leu Pro Ile Asp Ile Val Leu Gln
 35 40 45
 Thr Leu Leu Ala Phe Ala Val Thr Cys Tyr Gly Ile Val His Ile Ala
 50 55 60
 Gly Glu Phe Lys Asp Met Asp Ala Thr Ser Glu Leu Lys Asn Lys Thr
 65 70 75 80
 Phe Asp Thr Leu Arg Asn His Pro Ser Phe Tyr Val Phe Asn His Arg
 85 90 95
 Gly Arg Val Leu Phe Arg Pro Ser Asp Ala Thr Asn Ser Ser Asn Leu
 100 105 110
 Asp Ala Leu Ser Ser Asn Thr Ser Leu Lys Leu Arg Lys Phe Asp Ser
 115 120 125
 Leu Arg Arg
 130

<210> 157
 <211> 133
 <212> PRT
 <213> mouse

<400> 157
 Met Arg Leu Leu Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Cys
 1 5 10 15
 Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro
 20 25 30
 Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
 35 40 45
 Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Glu His Val
 50 55 60
 Gln Gly Thr Gly Ala Arg Ser Thr Ala Cys Thr Leu Ser Cys Arg Ala
 65 70 75 80
 Pro Asn Ala Ser Ser Ser Gly Thr Met Pro Gly Thr Arg Ser Ala Gly
 85 90 95
 Ser Thr Lys Asn Arg Val Asp Asp His Gly Lys Lys Asn Ser Arg Pro
 100 105 110
 Val Glu Arg Leu Gln Gln Arg Thr Leu Gln Ile Lys Ile Lys Ala Leu
 115 120 125

Ser Phe Ser Gln Ala
130

<210> 158
<211> 78
<212> PRT
<213> mouse

<400> 158
Gly Thr Arg Lys Pro Leu Pro Met Glu Ala His Ser Arg Arg Glu Lys
1 5 10 15
Ala Ser Gly Leu Arg Leu Ala Trp His Tyr Glu Cys Ser Gly Val Ser
20 25 30
Val Trp Trp Met Cys Val Leu Gly Trp Leu Ser Phe Leu Val Phe Leu
35 40 45
Leu Phe Ser Leu Val Cys Ser Phe Pro Ser Pro Ile Asn His Ser His
50 55 60
Met Leu Pro Cys Leu Phe Leu Arg Gly Gly Gly Ser Asn Val
65 70 75

<210> 159
<211> 206
<212> PRT
<213> mouse

<400> 159
Met Leu Pro Pro Ala Ile His Leu Ser Leu Ile Pro Leu Leu Cys Ile
1 5 10 15
Leu Met Arg Asn Cys Leu Ala Phe Lys Asn Asp Ala Thr Glu Ile Leu
20 25 30
Tyr Ser His Val Val Lys Pro Val Pro Ala His Pro Ser Ser Asn Ser
35 40 45
Thr Leu Asn Gln Ala Arg Asn Gly Gly Arg His Phe Ser Ser Thr Gly
50 55 60
Leu Asp Arg Asn Ser Arg Val Gln Val Gly Cys Arg Glu Leu Arg Ser
65 70 75 80
Thr Lys Tyr Ile Ser Asp Gly Gln Cys Thr Ser Ile Ser Pro Leu Lys
85 90 95
Glu Leu Val Cys Ala Gly Glu Cys Leu Pro Leu Pro Val Leu Pro Asn
100 105 110
Trp Ile Gly Gly Gly Tyr Gly Thr Lys Tyr Trp Ser Arg Arg Ser Ser
115 120 125
Gln Glu Trp Arg Cys Val Asn Asp Lys Thr Arg Thr Gln Arg Ile Gln
130 135 140
Leu Gln Cys Gln Asp Gly Ser Thr Arg Thr Tyr Lys Ile Thr Val Val
145 150 155 160
Thr Ala Cys Lys Cys Lys Arg Tyr Thr Arg Gln His Asn Glu Ser Ser
165 170 175
His Asn Phe Glu Ser Val Ser Pro Ala Lys Pro Ala Gln His His Arg
180 185 190
Glu Arg Lys Arg Ala Ser Lys Ser Ser Lys His Ser Leu Ser
195 200 205

<210> 160
<211> 169
<212> PRT
<213> mouse

<400> 160
 Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly
 1 5 10 15
 Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg
 20 25 30
 Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly
 35 40 45
 Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln
 50 55 60
 Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu
 65 70 75 80
 Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr
 85 90 95
 Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly
 100 105 110
 Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe
 115 120 125
 Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu
 130 135 140
 Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu
 145 150 155 160
 Gly Glu Met Pro Pro Glu Asp Gly Met
 165

<210> 161
 <211> 114
 <212> PRT
 <213> mouse

<400> 161
 Met Ser Val Thr Ile Gly Arg Leu Ala Leu Phe Leu Ile Gly Ile Leu
 1 5 10 15
 Leu Cys Pro Val Ala Pro Ser Leu Thr Arg Ser Trp Pro Gly Pro Asp
 20 25 30
 Thr Cys Ser Leu Phe Leu Gln His Ser Leu Ser Leu Ser Leu Arg Leu
 35 40 45
 Gly Gln Ser Leu Glu Gly Gly Leu Ser Val Cys Phe His Val Cys Ile
 50 55 60
 His Ala Cys Glu Cys Val Ala Cys Cys Arg Val Leu Trp Asp Pro Lys
 65 70 75 80
 Pro Arg Gly Ser Ser Leu Cys Arg Trp Val Leu Gly Ser Ile Thr Cys
 85 90 95
 Leu Phe Met Tyr Glu Val Gly Gly Trp Thr Gln Gly Gly Leu Ile Val
 100 105 110
 Ser Leu

<210> 162
 <211> 46
 <212> PRT
 <213> mouse

<400> 162
 Met His Tyr Pro Cys Leu Ala Cys Leu Phe Val Asn Val His Trp Cys
 1 5 10 15
 Phe Ala Trp Met Cys Ile Leu Val Lys Met Ser Glu Leu Leu Glu Leu

20 25 30
 Glu Leu Glu Thr Met Val Ser Cys Leu Val Asp Val Gly Asn
 35 40 45

<210> 163
 <211> 122
 <212> PRT
 <213> mouse

<400> 163
 Met Phe Thr Phe Val Val Leu Val Ile Thr Ile Val Ile Cys Leu Cys
 1 5 10 15
 His Val Cys Phe Gly His Phe Lys Tyr Leu Ser Ala His Asn Tyr Lys
 20 25 30
 Ile Glu His Thr Glu Thr Asp Ala Val Ser Ser Arg Ser Asn Gly Arg
 35 40 45
 Pro Pro Thr Ala Gly Ala Val Pro Lys Ser Ala Lys Tyr Ile Ala Gln
 50 55 60
 Val Leu Gln Asp Ser Glu Gly Asp Gly Asp Gly Asp Gly Ala Pro Gly
 65 70 75 80
 Ser Ser Gly Asp Glu Pro Pro Ser Ser Ser Ser Gln Asp Glu Glu Leu
 85 90 95
 Leu Met Pro Pro Asp Gly Leu Thr Asp Thr Asp Phe Gln Ser Cys Glu
 100 105 110
 Asp Ser Leu Ile Glu Asn Glu Ile His Gln
 115 120

<210> 164
 <211> 60
 <212> PRT
 <213> Rat

<400> 164
 Met Ser Phe Val Lys Ile Glu Ala Thr Pro Thr Gln Thr Lys Trp Pro
 1 5 10 15
 Phe Ser Val Val Pro Gln Ser Leu Leu Val Thr Val Tyr Ile Cys Tyr
 20 25 30
 Ile Phe Leu Val Ile Phe Phe Phe Phe Glu Ala Cys Gln Glu Val
 35 40 45
 Leu Cys Ser Phe Phe Asp Phe Ser Arg Arg Arg Gly
 50 55 60

<210> 165
 <211> 57
 <212> PRT
 <213> mouse

<400> 165
 Met Gly Ser Pro Ile Ser Gly Val Cys Pro Val Leu Pro Gly Gly Leu
 1 5 10 15
 Phe Val Ala Leu Gly Trp Ile Phe Leu Leu Phe His Arg Asp Ala Phe
 20 25 30
 Ser Leu His Thr Met Ser Ala Gly Phe Pro Lys Ser Pro Ala Asn Pro
 35 40 45
 His His Pro Pro Leu Arg Leu Ser Pro
 50 55

<210> 166
 <211> 75
 <212> PRT
 <213> mouse

<400> 166
 Lys Thr Arg Arg Thr Leu Thr Gly Gln Leu Gly Leu Phe Ser Val Asp
 1 5 10 15
 Phe Met Val Cys Ile Phe Leu Phe Leu Phe Phe Cys Phe Leu Phe Pro
 20 25 30
 Phe Pro Leu Phe Leu Val Arg Lys His Ile Leu Leu Ser His Cys Lys
 35 40 45
 Gln Trp Glu Gly Ser Thr Met Thr His Thr His Thr His Thr His Ile
 50 55 60
 His Ile His Thr Pro Pro Arg Gln Cys Gln Ser
 65 70 75

<210> 167
 <211> 52
 <212> PRT
 <213> mouse

<400> 167
 Val Arg Ser Leu Glu Gln Leu Gly Leu Phe Ser Val Asp Phe Met Val
 1 5 10 15
 Cys Ile Phe Leu Phe Leu Phe Phe Cys Phe Leu Phe Pro Phe Pro Leu
 20 25 30
 Phe Leu Val Arg Lys His Ile Leu Leu Ser His Cys Lys Gln Trp Glu
 35 40 45
 Gly Ser Thr Met
 50

<210> 168
 <211> 119
 <212> PRT
 <213> Rat

<400> 168
 Met Leu Gly Ala Thr Ser Leu Ser Trp Pro Trp Val Leu Trp Ala Val
 1 5 10 15
 Ala Gln Arg Asp Ser Val Asp Ala Ile Gly Met Phe Leu Gly Gly Leu
 20 25 30
 Val Ala Thr Ile Phe Leu Asp Ile Ile Tyr Ile Ser Ile Phe Tyr Ser
 35 40 45
 Ser Val Ala Val Gly Asp Thr Gly Arg Phe Ser Ala Gly Met Ala Ile
 50 55 60
 Phe Ser Leu Leu Leu Gln Ala Leu Leu Leu Leu Pro Arg Leu Pro His
 65 70 75 80
 Ala Pro Gly Ser Glu Gly Val Ser Ser Arg Ser Ala Arg Ile Ser Ser
 85 90 95
 Asp Leu Leu Arg Asn Ile Val Pro Thr Arg Gln Leu Thr Arg Gln Thr
 100 105 110
 His Leu Gln Thr Pro Leu Gln
 115

<210> 169
 <211> 104

<212> PRT

<213> Rat

<220>

<400> 169

Leu	Val	Pro	Lys	Ser	Ala	Arg	Ala	Ser	Leu	Leu	Cys	Cys	Gly	Pro	Lys
1			5						10					15	
Leu	Ala	Ala	Cys	Gly	Ile	Val	Leu	Ser	Ala	Trp	Gly	Val	Ile	Met	Leu
			20					25					30		
Ile	Met	Leu	Gly	Ile	Phe	Phe	Asn	Val	His	Ser	Ala	Val	Xaa	Ile	Xaa
		35					40					45			
Asp	Val	Pro	Phe	Thr	Glu	Lys	Asp	Phe	Glu	Asn	Gly	Pro	Gln	Asn	Ile
	50					55					60				
Tyr	Asn	Leu	Tyr	Glu	Gln	Val	Ser	Tyr	Asn	Cys	Phe	Ile	Ala	Ala	Gly
65					70					75					80
Leu	Tyr	Leu	Leu	Xaa	Gly	Gly	Phe	Ser	Phe	Cys	Gln	Val	Arg	Leu	Asn
			85						90					95	
Lys	Arg	Lys	Glu	Tyr	Met	Val	Arg								
			100												

<210> 170

<211> 123

<212> PRT

<213> Rat

<220>

<221> UNSURE

<222> (27)...(27)

<221> UNSURE

<222> (104)...(104)

<221> UNSURE

<222> (118)...(118)

<400> 170

Met	Arg	Pro	Gly	Ala	Asp	Trp	Ala	Ala	Val	Cys	Ala	Leu	Trp	Pro	Ser
1			5						10					15	
Trp	Arg	Pro	Ser	Cys	Ser	Leu	Pro	Ser	Ser	Xaa	Arg	Ile	Gln	Pro	Asp
			20					25					30		
Glu	Leu	Trp	Leu	Tyr	Arg	Asn	Pro	Tyr	Val	Lys	Ala	Glu	Tyr	Phe	Pro
		35				40						45			
Thr	Gly	Pro	Met	Phe	Val	Ile	Ala	Phe	Leu	Thr	Pro	Leu	Ser	Leu	Ile
	50				55					60					
Phe	Phe	Ala	Lys	Phe	Leu	Arg	Lys	Ala	Asp	Ala	Asp	Arg	Gln	Arg	Ala
65					70					75					80
Ser	Leu	Pro	Arg	Cys	Gln	Pro	Cys	Pro	Ser	Ala	Lys	Trp	Cys	Leu	Tyr
			85					90					95		
Gln	His	His	Lys	Thr	Asp	Ser	Xaa	Gln	Gly	His	Ala	Gln	Ile	Ala	Ser
			100					105					110		
Thr	Glu	Cys	Ser	Pro	Xaa	Gly	Ile	Ala	His	Ser					
			115				120								

<210> 171

<211> 75

<212> PRT

<213> Rat

<400> 171

```

Ser Ala Gly Val Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile
 1          5          10          15
Ala Phe Gly Pro Ala Leu Ser Leu Tyr Val Phe Thr Ile Ala Thr Asp
 20          25          30
Pro Leu Arg Val Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val
 35          40          45
Ser Leu Leu Leu Ser Ser Val Phe Trp Phe Leu Val Arg Val Ile Thr
 50          55          60
Asp Asn Arg Asp Gly Pro Val Gln Asn Tyr Leu
 65          70          75

```

<210> 172

<211> 79

<212> PRT

<213> Human

<400> 172

```

Lys Thr Ser Tyr His Tyr His Thr Asn Val Glu Glu Leu Thr Ile Pro
 1          5          10          15
Glu Thr Arg Asn Asn Leu Tyr Ile Ser Ile Ser Trp Leu Trp Cys Leu
 20          25          30
Val Leu Val Leu Leu Ser Thr Met Ile Leu Asn Lys His Gly Trp Met
 35          40          45
Lys Ala Asn Ala Tyr Ser Leu Val Pro Ser Ile Ile Tyr Ser Pro Ser
 50          55          60
Tyr Leu Lys Leu Leu Leu Arg Leu Tyr Lys Leu Gln Ile Cys Cys
 65          70          75

```

<210> 173

<211> 134

<212> PRT

<213> Human

<220>

<400> 173

```

Leu Arg Gly Arg Gly Arg Gly Val Cys Ser Gln Glu Ser Phe Gly Gly
 1          5          10          15
Cys Cys Val Ser Gly Leu Ile Ala Met Gly Thr Lys Ala Gln Val Glu
 20          25          30
Arg Lys Leu Leu Cys Leu Phe Ile Leu Ala Ile Leu Leu Cys Ser Leu
 35          40          45
Ala Leu Gly Ser Val Thr Val His Ser Ser Glu Pro Glu Val Arg Ile
 50          55          60
Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser
 65          70          75          80
Ser Pro Arg Val Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu
 85          90          95
Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr
 100          105          110
Phe Leu Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr
 115          120          125
Gly Thr Tyr Thr Cys Met
 130

```

<210> 174
 <211> 137
 <212> PRT
 <213> Human

<400> 174
 Ala Trp Ser Arg Pro Arg Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala
 1 5 10 15
 Leu Gln Ala Thr Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe
 20 25 30
 Leu Ala Met Phe Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly
 35 40 45
 Gly Asp Asp Lys Val Lys Lys Ala Arg Ile Ala Met Gly Gly Gly Ile
 50 55 60
 Ile Phe Ile Val Ala Gly Leu Ala Ala Leu Val Ala Cys Ser Trp Tyr
 65 70 75 80
 Gly His Gln Ile Val Thr Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn
 85 90 95
 Ile Lys Tyr Glu Phe Gly Pro Ala Ile Phe Ile Gly Trp Ala Gly Ser
 100 105 110
 Ala Leu Val Ile Leu Gly Gly Ala Leu Ser Pro Val Pro Val Leu Gly
 115 120 125
 Ile Arg Ala Gly Leu Gly Thr Cys Pro
 130 135

<210> 175
 <211> 43
 <212> PRT
 <213> Human

<400> 175
 Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe Cys
 1 5 10 15
 Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys Gly Glu
 20 25 30
 Ser Arg Thr Pro Arg Pro Thr Ala Leu Gly Asn
 35 40

<210> 176
 <211> 63
 <212> PRT
 <213> Rat

<400> 176
 Pro Asn Thr Arg Pro Arg Arg His Thr Ala Cys Arg Val Ser Ile Ser
 1 5 10 15
 Val Phe Tyr Met Leu His Thr Glu Leu Lys Lys Cys Trp Phe Phe Leu
 20 25 30
 Phe Cys Phe Ser Leu Phe Leu Trp Phe Cys Phe Trp Phe Cys Phe Leu
 35 40 45
 Leu Pro Arg Phe Asp Tyr Leu Pro Met Pro Ser Thr Arg Pro Arg
 50 55 60

<210> 177
 <211> 52
 <212> PRT

<213> mouse

<400> 177

```

Met Leu Gln Gly Pro Ala Pro Ser Cys Phe Trp Val Phe Ser Gly Ile
 1           5           10           15
Cys Val Phe Trp Asp Phe Ile Phe Ile Ile Phe Phe Asn Val Leu Ser
          20           25           30
Leu Gly Asn Arg Glu Ile Ser Ala Lys Asp Phe Ala Asp Gln Pro Ala
          35           40           45
Gly Ala Gln Gly
50

```

<210> 178

<211> 62

<212> PRT

<213> mouse

<400> 178

```

Val Ser Pro Arg Pro Thr Tyr Pro Ser Thr Ala Ser Ser Met Ala Ala
 1           5           10           15
Phe Leu Val Thr Gly Phe Phe Phe Ser Leu Phe Val Val Leu Gly Met
          20           25           30
Glu Pro Arg Ala Leu Phe Arg Pro Asp Lys Ala Leu Pro Leu Ser Cys
          35           40           45
Ala Lys Pro Thr Ser Leu Cys Val Gln Ser Ser Phe Leu Gly
50           55           60

```

<210> 179

<211> 123

<212> PRT

<213> mouse

<400> 179

```

Ala Ser Arg Thr Ala Val Met Ser Leu Cys Arg Cys Gln Gln Gly Ser
 1           5           10           15
Arg Ser Arg Met Asp Leu Asp Val Val Asn Met Phe Val Ile Ala Gly
          20           25           30
Gly Thr Leu Ala Ile Pro Ile Leu Ala Phe Val Ala Ser Phe Leu Leu
          35           40           45
Trp Pro Ser Ala Leu Ile Arg Ile Tyr Tyr Trp Tyr Trp Arg Arg Thr
50           55           60
Leu Gly Met Gln Val Arg Tyr Ala His His Glu Asp Tyr Gln Phe Cys
65           70           75           80
Tyr Ser Phe Arg Gly Arg Pro Gly His Lys Pro Ser Ile Leu Met Leu
          85           90           95
His Gly Phe Ser Ala His Lys Gly His Val Ala Gln Arg Gly Gln Val
          100          105          110
Pro Ser Arg Lys Asn Leu His Phe Gly Cys Val
          115          120

```

<210> 180

<211> 120

<212> PRT

<213> mouse

<220>

<221> UNSURE

<222> (5)...(5)

<400> 180

Ala	Arg	Arg	Arg	Xaa	Arg	Trp	Arg	Arg	Gly	Cys	Cys	Trp	Leu	Ile	Gly
1				5					10					15	
Thr	Gly	Leu	Arg	Ala	Ala	Thr	Trp	Thr	Val	Leu	Cys	Ser	Pro	Asn	Ser
			20					25					30		
Ser	Leu	Val	Val	Ala	Arg	His	Thr	Lys	Ser	Phe	Pro	Pro	Lys	Lys	Pro
		35					40				45				
Leu	Gln	Ala	Leu	Thr	Met	Ser	Ile	Met	Asp	His	Ser	Pro	Thr	Thr	Gly
		50				55					60				
Val	Val	Thr	Val	Ile	Val	Ile	Leu	Ile	Ala	Ile	Ala	Ala	Leu	Gly	Gly
65					70				75					80	
Leu	Ile	Leu	Gly	Cys	Trp	Cys	Tyr	Leu	Arg	Leu	Gln	Arg	Ile	Ser	Gln
			85					90					95		
Ser	Glu	Asp	Glu	Glu	Ser	Ile	Val	Gly	Asp	Gly	Glu	Thr	Lys	Glu	Pro
			100					105					110		
Phe	Tyr	Trp	Cys	Ser	Thr	Leu	Leu								
		115					120								

<210> 181

<211> 60

<212> PRT

<213> mouse

<400> 181

Lys	Gly	Pro	Glu	Val	Ser	Cys	Cys	Ile	Lys	Tyr	Phe	Ile	Phe	Gly	Phe
1				5					10					15	
Asn	Val	Ile	Phe	Trp	Phe	Leu	Gly	Ile	Thr	Phe	Leu	Gly	Ile	Gly	Leu
			20					25					30		
Trp	Ala	Trp	Asn	Glu	Lys	Gly	Val	Leu	Ser	Asn	Ile	Ser	Ser	Ile	Thr
		35					40					45			
Asp	Leu	Gly	Gly	Phe	Asp	Pro	Val	Trp	Leu	Phe	Leu				
	50					55					60				

<210> 182

<211> 72

<212> PRT

<213> mouse

<220>

<400> 182

Lys	Pro	Thr	Val	Gly	Ser	Ala	Glu	Val	Ala	Ile	Ala	Val	Phe	Leu	Val
1				5					10					15	
Ile	Cys	Ile	Ile	Val	Val	Leu	Thr	Ile	Leu	Gly	Tyr	Cys	Phe	Phe	Lys
			20					25					30		
Asn	Gln	Arg	Lys	Glu	Phe	His	Ser	Pro	Leu	His	His	Pro	Pro	Pro	Thr
		35					40					45			
Pro	Ala	Ser	Ser	Thr	Val	Ser	Thr	Thr	Glu	Asp	Thr	Glu	His	Leu	Val
	50					55					60				
Tyr	Asn	His	Thr	Thr	Gln	Pro	Leu								
65						70									

<210> 183

<211> 771

<212> PRT

<213> Rat

<220>

<400> 183

Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu Val Pro Lys Glu Leu
 1 5 10 15
 Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu Ser Asn Asn Arg Ile
 20 25 30
 Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met Thr Gln Leu Leu Thr
 35 40 45
 Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile Pro Pro Arg Thr Phe
 50 55 60
 Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu His Gly Asn Asp Ile
 65 70 75 80
 Ser Val Val Pro Glu Gly Ala Phe Gly Asp Leu Ser Ala Leu Ser His
 85 90 95
 Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp Cys Asn Met Gln Trp
 100 105 110
 Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu Pro Gly Ile Ala Arg
 115 120 125
 Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu Leu Thr Thr Pro
 130 135 140
 Ser Lys Asn Phe Thr Cys Gln Gly Pro Val Asp Val Thr Ile Gln Ala
 145 150 155 160
 Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys Asn Asp Gly Thr Cys
 165 170 175
 Asn Asn Asp Pro Val Asp Phe Tyr Arg Cys Thr Cys Pro Tyr Gly Phe
 180 185 190
 Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala Cys Thr Ser Asn Pro
 195 200 205
 Cys Lys His Gly Gly Thr Cys His Leu Lys Pro Arg Arg Glu Thr Trp
 210 215 220
 Ile Trp Cys Thr Cys Ala Asp Gly Phe Glu Gly Glu Ser Cys Asp Ile
 225 230 235 240
 Asn Ile Asp Asp Cys Glu Asp Asn Asp Cys Glu Asn Asn Ser Thr Cys
 245 250 255
 Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys Pro Pro Glu Tyr Thr
 260 265 270
 Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys Ala Gln Asp Leu Asn
 275 280 285
 Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr Pro Lys Gly Phe Lys
 290 295 300
 Cys Asp Cys Thr Pro Gly Tyr Ile Gly Glu His Cys Asp Ile Asp Phe
 305 310 315 320
 Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly Ala His Cys Thr Asp
 325 330 335
 Ala Val Asn Gly Tyr Thr Cys Val Cys Pro Glu Gly Tyr Ser Gly Leu
 340 345 350
 Phe Cys Glu Phe Ser Pro Pro Met Val Phe Leu Arg Thr Ser Pro Cys
 355 360 365
 Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys Ile Ile Arg Val Asn
 370 375 380
 Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Leu Gly Glu Lys Cys Glu
 385 390 395 400

Lys	Leu	Val	Ser	Val	Ser	Ile	Leu	Val	Asn	Lys	Glu	Ser	Tyr	Leu	Gln
				405					410					415	
Ile	Pro	Ser	Ala	Lys	Val	Arg	Pro	Gln	Thr	Asn	Ile	Thr	Leu	Gln	Ile
			420					425					430		
Ala	Thr	Asp	Glu	Asp	Ser	Gly	Ile	Leu	Leu	Tyr	Lys	Gly	Asp	Lys	Asp
		435					440					445			
His	Ile	Ala	Val	Glu	Ser	Ile	Glu	Gly	Ile	Arg	Ala	Ser	Tyr	Asp	Thr
	450					455				460					
Gly	Ser	His	Pro	Ala	Ser	Ala	Ile	Tyr	Ser	Val	Glu	Thr	Ile	Asn	Asp
465					470					475					480
Gly	Asn	Phe	His	Ile	Val	Glu	Leu	Leu	Thr	Leu	Asp	Ser	Ser	Leu	Ser
				485					490					495	
Leu	Ser	Val	Asp	Gly	Gly	Ser	Pro	Lys	Ile	Ile	Thr	Asn	Leu	Ser	Lys
			500					505					510		
Gln	Ser	Thr	Leu	Asn	Phe	Asp	Ser	Pro	Leu	Tyr	Val	Gly	Gly	Met	Pro
			515				520					525			
Gly	Lys	Asn	Asn	Val	Ala	Ser	Leu	Arg	Gln	Ala	Pro	Gly	Gln	Asn	Gly
	530					535				540					
Thr	Ser	Phe	His	Gly	Cys	Ile	Arg	Asn	Leu	Tyr	Ile	Asn	Ser	Glu	Leu
545				550						555					560
Gln	Asp	Phe	Arg	Lys	Val	Pro	Met	Gln	Thr	Gly	Ile	Leu	Pro	Gly	Cys
				565					570					575	
Glu	Pro	Cys	His	Lys	Lys	Val	Cys	Ala	His	Gly	Thr	Cys	Gln	Pro	Ser
			580					585					590		
Ser	Gln	Ser	Gly	Phe	Thr	Cys	Glu	Cys	Glu	Glu	Gly	Trp	Met	Gly	Pro
		595					600					605			
Leu	Cys	Asp	Gln	Arg	Thr	Asn	Asp	Pro	Cys	Leu	Gly	Asn	Lys	Cys	Val
	610					615					620				
His	Gly	Thr	Cys	Leu	Pro	Ile	Asn	Ala	Phe	Ser	Tyr	Ser	Cys	Lys	Cys
625					630					635					640
Leu	Glu	Gly	His	Gly	Gly	Val	Leu	Cys	Asp	Glu	Glu	Glu	Asp	Leu	Phe
			645						650					655	
Asn	Pro	Leu	Pro	Gly	Asp	Gln	Val	Gln	Ala	Arg	Glu	Val	Gln	Ala	Leu
			660					665					670		
Trp	Ala	Arg	Ala	Ala	Leu	Leu	Trp	Met	Gln	Gln	Trp	Ile	His	Arg	Gly
	675						680					685			
Gln	Leu	Thr	Gln	Arg	Ile	Ser	Cys	Arg	Gly	Glu	Arg	Ile	Arg	Asp	Tyr
	690					695					700				
Tyr	Gln	Ser	Ser	Arg	Val	Arg	Cys	Leu	Ser	Asn	Asp				

```
<210> 184
<211> 340
<212> PRT
<213> mouse
```

<400> 184																
Asp	Gly	Ser	Leu	Trp	Leu	Gln	Ala	Thr	Gln	Pro	Asp	Asp	Ala	Gly	His	
1				5					10					15		
Tyr	Thr	Cys	Val	Pro	Ser	Asn	Gly	Phe	Leu	His	Pro	Pro	Ser	Ala	Ser	
			20					25						30		
Ala	Tyr	Leu	Thr	Val	Leu	Tyr	Pro	Ala	Gln	Val	Thr	Val	Met	Pro	Pro	
		35					40					45				
Glu	Thr	Pro	Leu	Pro	Thr	Gly	Met	Arg	Gly	Val	Ile	Arg	Cys	Pro	Val	
	50					55					60					
Arg	Ala	Asn	Pro	Pro	Leu	Leu	Phe	Val	Thr	Trp	Thr	Lys	Asp	Gly	Gln	
65					70					75				80		
Ala	Leu	Gln	Leu	Asp	Lys	Phe	Pro	Gly	Trp	Ser	Leu	Gly	Pro	Glu	Gly	

```

      85      90      95
Ser Leu Ile Ile Ala Leu Gly Asn Glu Asp Ala Leu Gly Glu Tyr Ser
      100      105      110
Cys Thr Pro Tyr Asn Ser Leu Gly Thr Ala Gly Pro Ser Pro Val Thr
      115      120      125
Arg Val Leu Leu Lys Ala Pro Pro Ala Phe Ile Asp Gln Pro Lys Glu
      130      135      140
Glu Tyr Phe Gln Glu Val Gly Arg Glu Leu Leu Ile Pro Cys Ser Ala
      145      150      155      160
Arg Gly Asp Pro Pro Pro Ile Val Ser Trp Ala Lys Val Gly Arg Gly
      165      170      175
Leu Gln Gly Gln Ala Gln Val Asp Ser Asn Asn Ser Leu Val Leu Arg
      180      185      190
Pro Leu Thr Lys Glu Ala Gln Gly Arg Trp Glu Cys Ser Ala Ser Asn
      195      200      205
Ala Val Ala Arg Val Thr Thr Ser Thr Asn Val Tyr Val Leu Gly Thr
      210      215      220
Ser Pro His Val Val Thr Asn Val Ser Val Val Pro Leu Pro Lys Gly
      225      230      235      240
Ala Asn Val Ser Trp Glu Pro Gly Phe Asp Gly Gly Tyr Leu Gln Arg
      245      250      255
Phe Ser Val Trp Tyr Thr Pro Leu Ala Lys Arg Pro Asp Arg Ala His
      260      265      270
His Asp Trp Val Ser Leu Ala Val Pro Ile Gly Ala Thr His Leu Leu
      275      280      285
Val Pro Gly Leu Gln Ala His Ala Gln Tyr Gln Phe Ser Val Leu Ala
      290      295      300
Gln Asn Lys Leu Gly Ser Gly Pro Phe Ser Glu Ile Val Leu Ser Ile
      305      310      315      320
Pro Glu Gly Leu Pro Thr Thr Pro Ala Ala Pro Gly Leu Pro Ala Thr
      325      330      335
Arg Ser Arg Val
      340

```

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<210> 185
<211> 536
<212> PRT
<213> mouse

```

```

      <400> 185
Lys Val Glu Gly Glu Gly Arg Gly Arg Trp Ala Leu Gly Leu Leu Arg
      1      5      10      15
Thr Phe Asp Ala Gly Glu Phe Ala Gly Trp Glu Lys Val Gly Ser Gly
      20      25      30
Gly Phe Gly Gln Val Tyr Lys Val Arg His Val His Trp Lys Thr Trp
      35      40      45
Leu Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Asp Arg Glu Arg
      50      55      60
Met Glu Leu Leu Glu Glu Ala Lys Lys Met Glu Met Ala Lys Phe Arg
      65      70      75      80
Tyr Ile Leu Pro Val Tyr Gly Ile Cys Gln Glu Pro Val Gly Leu Val
      85      90      95
Met Glu Tyr Met Glu Thr Gly Ser Leu Glu Lys Leu Leu Ala Ser Glu
      100      105      110
Pro Leu Pro Trp Asp Leu Arg Phe Arg Ile Val His Glu Thr Ala Val
      115      120      125
Gly Met Asn Phe Leu His Cys Met Ser Pro Pro Leu Leu His Leu Asp

```

130	135	140
Leu Lys Pro Ala Asn Ile	Leu Leu Asp Ala His Tyr Gln Met Ser Arg	
145	150	155
Phe Leu Asp Phe Gly Leu Ala Lys Cys Asn Gly Met Ser His Ser His		160
	165	170
Asp Leu Ser Met Asp Gly Leu Phe Gly Thr Ile Gly Tyr Leu Pro Pro		175
	180	185
Glu Arg Ile Arg Glu Lys Ser Arg Leu Phe Asp Thr Lys His Asp Val		190
	195	200
Tyr Ser Phe Ala Ile Val Ile Trp Gly Val Leu Thr Gln Asn Asn Pro		205
	210	215
Phe Ala Asp Glu Lys Asn Ile Leu His Ile Met Met Lys Val Val Lys		220
225	230	235
Gly His Arg Pro Glu Leu Pro Pro Ile Cys Arg Pro Arg Pro Arg Ala		240
	245	250
Cys Ala Ser Leu Ile Gly Leu Met Gln Arg Cys Trp His Ala Asp Pro		255
	260	265
Gln Val Arg Pro Thr Phe Gln Glu Ile Thr Ser Glu Thr Glu Asp Leu		270
	275	280
Cys Glu Lys Pro Asp Glu Glu Val Lys Asp Leu Ala His Glu Pro Gly		285
	290	295
Glu Lys Ser Ser Leu Glu Ser Lys Ser Glu Ala Arg Pro Glu Ser Ser		300
305	310	315
Arg Leu Lys Arg Ala Ser Ala Pro Pro Phe Asp Asn Asp Cys Ser Leu		320
	325	330
Ser Glu Leu Leu Ser Gln Leu Asp Ser Gly Ile Phe Pro Arg Leu Leu		335
	340	345
Lys Gly Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Cys Lys Leu Pro		350
	355	360
Ser Ser Ser Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val Asp Ser		365
	370	375
Ala Phe Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg Glu Ala		380
385	390	395
Ser Thr Gly Asp Leu Gly Pro Thr Asp Ile Gln Lys Lys Lys Leu Val		400
	405	410
Asp Ala Ile Ile Ser Gly Asp Thr Ser Arg Leu Met Lys Ile Leu Gln		415
	420	425
Pro Gln Asp Val Asp Leu Val Leu Asp Ser Ser Ala Ser Leu Leu His		430
	435	440
Leu Ala Val Glu Ala Gly Gln Glu Glu Cys Val Lys Trp Leu Leu Leu		445
	450	455
Asn Asn Ala Asn Pro Asn Leu Thr Asn Arg Lys Gly Ser Thr Pro Leu		460
465	470	475
His Met Ala Val Glu Arg Lys Gly Arg Gly Ile Val Glu Leu Leu Leu		480
	485	490
Ala Arg Lys Thr Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr Ala		495
	500	505
Leu His Phe Ala Ala Gln Asn Gly Asp Glu Gly Gln His Lys Ala Ala		510
	515	520
Ala Arg Glu Glu Cys Phe Cys Gln		525
530	535	

<210> 186

<211> 337

<212> PRT

<213> Rat

<220>

<400> 186

```

Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp
 1      5      10      15
Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile
      20      25      30
Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr
      35      40      45
Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly
      50      55      60
Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr
      65      70      75      80
Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp
      85      90      95
Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn
      100     105     110
Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu
      115     120     125
Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu
      130     135     140
Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys
      145     150     155     160
Ser Cys Pro Pro Gly Tyr Val Leu Leu Glu Asp Asn Arg Ser Cys Gln
      165     170     175
Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Pro Leu Gln
      180     185     190
Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Val
      195     200     205
Cys Glu Glu Pro Tyr Leu Leu Ile Gly Asp Asn Arg Cys Met Cys Pro
      210     215     220
Ala Glu Asn Thr Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Phe Arg
      225     230     235     240
Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln
      245     250     255
Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile
      260     265     270
Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro
      275     280     285
Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp
      290     295     300
Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe
      305     310     315     320
Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro
      325     330     335
Phe

```

<210> 187

<211> 152

<212> PRT

<213> mouse

<400> 187

```

Met Ala Leu Gly Val Leu Ile Ala Val Cys Leu Leu Phe Lys Ala Met
 1      5      10      15

```

Lys Ala Ala Leu Ser Glu Glu Ala Glu Val Ile Pro Pro Ser Thr Ala
 20 25 30
 Gln Gln Ser Asn Trp Thr Phe Asn Asn Thr Glu Ala Asp Tyr Ile Glu
 35 40 45
 Glu Pro Val Ala Leu Lys Phe Ser His Pro Cys Leu Glu Asp His Asn
 50 55 60
 Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Lys Gln
 65 70 75 80
 Ala Ile Cys Arg Cys Phe Thr Gly Tyr Thr Gly Gln Arg Cys Glu His
 85 90 95
 Leu Thr Leu Thr Ser Tyr Ala Val Asp Ser Tyr Glu Lys Tyr Ile Ala
 100 105 110
 Ile Gly Ile Gly Val Gly Leu Leu Ile Ser Ala Phe Leu Ala Val Phe
 115 120 125
 Tyr Cys Tyr Ile Arg Lys Arg Cys Ile Asn Leu Lys Ser Pro Tyr Ile
 130 135 140
 Ile Cys Ser Gly Gly Ser Pro Leu
 145 150

<210> 188

<211> 118

<212> PRT

<213> Rat

<220>

<400> 188

Leu Val Pro Gln Phe Gly Thr Arg Ile Arg Tyr Thr Ala Tyr Asp Arg
 1 5 10 15
 Ala Tyr Asn Arg Ala Ser Cys Lys Phe Ile Val Lys Val Gln Val Arg
 20 25 30
 Arg Cys Pro Ile Leu Lys Pro Pro Gln His Gly Tyr Leu Thr Cys Ser
 35 40 45
 Ser Ala Gly Asp Asn Tyr Gly Ala Ile Cys Glu Tyr His Cys Asp Gly
 50 55 60
 Gly Tyr Glu Arg Gln Gly Thr Pro Ser Arg Val Cys Gln Ser Ser Arg
 65 70 75 80
 Gln Trp Ser Gly Ser Pro Pro Val Cys Thr Pro Met Lys Ile Asn Val
 85 90 95
 Asn Val Asn Ser Ala Ala Gly Leu Leu Asp Gln Phe Tyr Glu Lys Gln
 100 105 110
 Arg Leu Leu Ile Val Ser
 115

<210> 189

<211> 299

<212> PRT

<213> Human

<220>

<400> 189

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
 1 5 10 15
 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
 20 25 30
 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu

```

      35      40      45
Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
 50      55      60
Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
65      70      75      80
Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
      85      90      95
Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
      100      105      110
Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
      115      120      125
Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
      130      135      140
Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
      145      150      155      160
Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
      165      170      175
Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
      180      185      190
Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
      195      200      205
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
      210      215      220
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
      225      230      235      240
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
      245      250      255
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
      260      265      270
Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
      275      280      285
Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
      290      295

```

<210> 190
 <211> 91
 <212> PRT
 <213> Human

```

      <400> 190
Gln Pro Thr Val Phe Trp Pro Lys Thr Ser Ala Lys Lys Gly Asn Trp
 1      5      10      15
Val Leu Arg Leu Gly Leu Ser Asn Pro Asp Arg Pro Ala Arg Gln Asn
      20      25      30
Asn Trp Phe Leu Pro Ala Ser Arg Glu Ile Pro Glu His Ser Ala Leu
      35      40      45
Thr Arg Tyr Pro Ala Gln Ile Arg Gly Cys Trp Pro His Arg Leu Thr
      50      55      60
Lys Pro Gln Thr Cys Leu Pro Gln Ala Arg Ser Tyr Leu Ser His Glu
      65      70      75      80
Val Thr Gln Ala Thr Arg Thr Cys Pro Gly Gly
      85      90

```

<210> 191
 <211> 89
 <212> PRT
 <213> mouse

<400> 191
 Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu Asp
 1 5 10 15
 Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly Pro Gly Lys
 20 25 30
 Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr Ala
 35 40 45
 Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr Pro
 50 55 60
 Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys His Tyr Pro
 65 70 75 80
 Cys Gln Pro Gly Gln Arg Val Glu Val
 85

<210> 192
 <211> 299
 <212> PRT
 <213> mouse

<220>

<400> 192
 Ala Arg Ala Gly Ala Cys Tyr Cys Pro Ala Gly Phe Leu Gly Ala Asp
 1 5 10 15
 Cys Ser Leu Ala Cys Pro Gln Gly Arg Phe Gly Pro Ser Cys Ala His
 20 25 30
 Val Cys Thr Cys Gly Gln Gly Ala Ala Cys Asp Pro Val Ser Gly Thr
 35 40 45
 Cys Ile Cys Pro Pro Gly Lys Thr Gly Gly His Cys Glu Arg Gly Cys
 50 55 60
 Pro Gln Asp Arg Phe Gly Lys Gly Cys Glu His Lys Cys Ala Cys Arg
 65 70 75 80
 Asn Gly Gly Leu Cys His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu
 85 90 95
 Gly Trp Met Gly Pro His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr
 100 105 110
 Gly Ala Ala Cys Leu Leu Glu Cys Ser Cys Gln Asn Asn Gly Ser Cys
 115 120 125
 Glu Pro Thr Ser Gly Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln
 130 135 140
 Ala Cys Glu Asp Thr Cys Pro Ala Gly Phe His Gly Ser Gly Cys Gln
 145 150 155 160
 Arg Val Cys Glu Cys Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly
 165 170 175
 Arg Cys Leu Cys Pro Ala Gly Phe Arg Gly Gln Phe Cys Glu Arg Gly
 180 185 190
 Cys Lys Pro Gly Phe Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys
 195 200 205
 Pro Thr Gly Val Pro Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro
 210 215 220
 Pro Gly Arg Ala Gly Thr Thr Cys Asp Leu Asp Cys Arg Arg Gly Arg
 225 230 235 240
 Phe Gly Pro Gly Cys Ala Leu Arg Cys Asp Cys Gly Gly Gly Ala Asp
 245 250 255
 Cys Asp Pro Ile Ser Gly Gln Cys His Cys Val Asp Ser Tyr Thr Gly

260 265 270
 Pro Thr Cys Arg Glu Val Pro Thr Gln Leu Ser Ser Ile Arg Pro Ala
 275 280 285
 Pro Gln His Ser Ser Ser Lys Ala Met Lys His
 290 295

<210> 193
 <211> 314
 <212> PRT
 <213> mouse

<220>

<400> 193

Glu Glu Pro Cys Asn Asn Gly Ser Glu Ile Leu Ala Tyr Asn Ile Asp
 1 5 10 15
 Leu Gly Asp Ser Cys Ile Thr Val Gly Asn Thr Thr Thr His Val Met
 20 25 30
 Lys Asn Leu Leu Pro Glu Thr Thr Tyr Arg Ile Arg Ile Gln Ala Ile
 35 40 45
 Asn Glu Ile Gly Val Gly Pro Phe Ser Gln Phe Ile Lys Ala Lys Thr
 50 55 60
 Arg Pro Leu Pro Pro Ser Pro Pro Arg Leu Glu Cys Ala Ala Ser Gly
 65 70 75 80
 Pro Gln Ser Leu Lys Leu Lys Trp Gly Asp Ser Asn Ser Lys Thr His
 85 90 95
 Ala Ala Gly Asp Met Val Tyr Thr Leu Gln Leu Glu Asp Arg Asn Lys
 100 105 110
 Arg Phe Ile Ser Ile Tyr Arg Gly Pro Ser His Thr Tyr Lys Val Gln
 115 120 125
 Arg Leu Thr Glu Phe Thr Cys Tyr Ser Phe Arg Ile Gln Ala Met Ser
 130 135 140
 Glu Ala Gly Glu Gly Pro Tyr Ser Glu Thr Tyr Thr Phe Ser Thr Thr
 145 150 155 160
 Lys Ser Val Pro Pro Thr Leu Lys Ala Pro Arg Val Thr Gln Leu Glu
 165 170 175
 Gly Asn Ser Cys Glu Ile Phe Trp Glu Thr Val Pro Pro Met Arg Gly
 180 185 190
 Asp Pro Val Ser Tyr Val Leu Gln Val Leu Val Gly Arg Asp Ser Glu
 195 200 205
 Tyr Lys Gln Val Tyr Lys Gly Glu Ala Thr Phe Gln Ile Ser Gly
 210 215 220
 Leu Gln Ser Asn Thr Asp Tyr Arg Phe Arg Val Cys Ala Cys Arg Arg
 225 230 235 240
 Cys Val Asp Thr SerGln Glu Leu Ser Gly Ala Phe Ser Pro Ser Ala
 245 250 255
 Ala Phe Met Leu Gln Gln Arg Glu Val Met Leu Thr Gly Asp Leu Gly
 260 265 270
 Gly Met Glu Glu Ala Lys Met Lys Gly Met Met Pro Thr Asp Glu Gln
 275 280 285
 Phe Ala Ala Leu Ile Val Leu Gly Phe Ala Thr Leu Ser Ile Leu Phe
 290 295 300
 Ala Phe Ile Leu Gln Tyr Phe Leu Met Lys
 305 310

<210> 194
 <211> 109
 <212> PRT

<213> mouse

<400> 194

Gly	Thr	Arg	Val	Gly	Thr	Pro	Tyr	Tyr	Met	Ser	Pro	Glu	Arg	Ile	His
1			5						10					15	
Glu	Asn	Gly	Tyr	Asn	Phe	Lys	Ser	Asp	Ile	Trp	Ser	Leu	Gly	Cys	Leu
		20						25					30		
Leu	Tyr	Glu	Met	Ala	Ala	Leu	Gln	Ser	Pro	Phe	Tyr	Gly	Asp	Lys	Met
		35					40					45			
Asn	Leu	Tyr	Ser	Leu	Cys	Lys	Lys	Ile	Glu	Gln	Cys	Asp	Tyr	Pro	Pro
		50				55					60				
Leu	Pro	Ser	Asp	His	Tyr	Ser	Glu	Glu	Leu	Arg	Gln	Leu	Val	Asn	Ile
65					70					75				80	
Cys	Ile	Asn	Pro	Asp	Pro	Glu	Lys	Arg	Pro	Asp	Ile	Ala	Tyr	Val	Tyr
				85					90					95	
Asp	Val	Ala	Lys	Arg	Met	His	Ala	Cys	Thr	Ala	Ser	Thr			
			100					105							

<210> 195

<211> 237

<212> PRT

<213> mouse

<400> 195

Met	Leu	Ser	Leu	Arg	Ser	Leu	Leu	Pro	His	Leu	Gly	Leu	Phe	Leu	Cys
1				5					10					15	
Leu	Ala	Leu	His	Leu	Ser	Pro	Ser	Leu	Ser	Ala	Ser	Asp	Asn	Gly	Ser
			20					25					30		
Cys	Val	Val	Leu	Asp	Asn	Ile	Tyr	Thr	Ser	Asp	Ile	Leu	Glu	Ile	Ser
		35					40					45			
Thr	Met	Ala	Asn	Val	Ser	Gly	Gly	Asp	Val	Thr	Tyr	Thr	Val	Thr	Val
		50				55					60				
Pro	Val	Asn	Asp	Ser	Val	Ser	Ala	Val	Ile	Leu	Lys	Ala	Val	Lys	Glu
65					70					75				80	
Asp	Asp	Ser	Pro	Val	Gly	Thr	Trp	Ser	Gly	Thr	Tyr	Glu	Lys	Cys	Asn
				85					90					95	
Asp	Ser	Ser	Val	Tyr	Asn	Leu	Thr	Ser	Gln	Ser	Gln	Ser	Val	Phe	
			100				105						110		
Gln	Thr	Asn	Trp	Thr	Val	Pro	Thr	Ser	Glu	Asp	Val	Thr	Lys	Val	Asn
		115				120						125			
Leu	Gln	Val	Leu	Ile	Val	Val	Asn	Arg	Thr	Ala	Ser	Lys	Ser	Ser	Val
		130				135					140				
Lys	Met	Glu	Gln	Val	Gln	Pro	Ser	Ala	Ser	Thr	Pro	Ile	Pro	Glu	Ser
145					150					155				160	
Ser	Glu	Thr	Ser	Gln	Thr	Ile	Asn	Thr	Thr	Pro	Thr	Val	Asn	Thr	Ala
				165					170					175	
Lys	Thr	Thr	Ala	Lys	Asp	Thr	Ala	Asn	Thr	Thr	Ala	Val	Thr	Thr	Ala
			180				185						190		
Asn	Thr	Thr	Ala	Asn	Thr	Thr	Ala	Val	Thr	Thr	Ala	Lys	Thr	Thr	Ala
			195				200					205			
Lys	Ser	Leu	Ala	Ile	Arg	Thr	Leu	Gly	Ser	Pro	Leu	Ala	Gly	Ala	Leu
		210				215					220				
His	Ile	Leu	Leu	Val	Phe	Leu	Ile	Ser	Lys	Leu	Leu	Phe			
225					230					235					

<210> 196

<211> 154

<212> PRT
<213> Human

<400> 196
Met Ala Leu Gly Val Pro Ile Ser Val Tyr Leu Leu Phe Asn Ala Met
1 5 10 15
Thr Ala Leu Thr Glu Glu Ala Val Thr Val Thr Pro Pro Ile Thr
20 25 30
Ala Gln Gln Gly Asn Trp Thr Val Asn Lys Thr Glu Ala His Asn Ile
35 40 45
Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu Asp His
50 55 60
Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Glu
65 70 75 80
Lys Ala Ile Cys Arg Cys Phe Thr Gly Tyr Thr Gly Glu Arg Cys Glu
85 90 95
His Leu Thr Leu Thr Ser Tyr Ala Val Asp Ser Tyr Glu Lys Tyr Ile
100 105 110
Ala Ile Gly Ile Gly Val Gly Leu Leu Ser Gly Phe Leu Val Ile
115 120 125
Phe Tyr Cys Tyr Ile Arg Lys Arg Cys Leu Lys Leu Lys Ser Pro Tyr
130 135 140
Asn Val Cys Ser Gly Glu Arg Arg Pro Leu
145 150

<210> 197
<211> 171
<212> PRT
<213> Rat

<400> 197
Met Ala Arg Pro Ala Pro Trp Trp Trp Leu Arg Pro Leu Ala Ala Leu
1 5 10 15
Ala Leu Ala Leu Ala Leu Val Arg Val Pro Ser Ala Arg Ala Gly Gln
20 25 30
Met Pro Arg Pro Ala Glu Arg Gly Pro Pro Val Arg Leu Phe Thr Glu
35 40 45
Glu Glu Leu Ala Arg Tyr Ser Gly Glu Glu Glu Asp Gln Pro Ile Tyr
50 55 60
Leu Ala Val Lys Gly Val Val Phe Asp Val Thr Ser Gly Lys Glu Phe
65 70 75 80
Tyr Gly Arg Gly Ala Pro Tyr Asn Ala Leu Ala Gly Lys Asp Ser Ser
85 90 95
Arg Gly Val Ala Lys Met Ser Leu Asp Pro Ala Asp Leu Thr His Asp
100 105 110
Ile Ser Gly Leu Thr Ala Lys Glu Leu Glu Ala Leu Asp Asp Ile Phe
115 120 125
Ser Lys Val Tyr Lys Ala Lys Tyr Pro Ile Val Gly Tyr Thr Ala Arg
130 135 140
Arg Ile Leu Asn Glu Asp Gly Ser Pro Asn Leu Asp Phe Lys Pro Glu
145 150 155 160
Asp Gln Pro His Phe Asp Ile Lys Asp Glu Phe
165 170

<210> 198
<211> 1399
<212> DNA

<213> Mouse

<400> 198

ggcaaaagact	tcggcacagag	asaacagcaa	agcagagctg	gctgcagcca	ttcactggcc	60
tcgggcgggc	gtgccacaga	ggcagttgaa	gtgaaagtga	aagagaaaac	ataagagaac	120
ggagaccaca	ggtgctaagt	gagggtgctc	acagaacccc	ctcttcagcc	agagatcact	180
agcaggggaa	ctgtggagaa	ggcagccagc	aaggaagagc	ctgagagtag	cctccatggg	240
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<210> 199

<211> 469

<212> DNA

<213> Rat

<400> 199

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agatatgcga	gtgactctct	tcaagcttct	cctgctttgg	ttggtgttaa	gtctcctggg	180
catccagctg	gcgtgggggt	tctacgggaa	cacagtgacc	gggttgatc	accgtccagg	240
gaaatggcag	caaataagc	tctcaaaact	cacagagaat	aaaggaagc	agcaggagaa	300
gggtctccag	agatatcgct	gggtctgctg	gctcctgtgc	tgtaccttgc	tgctatccag	360
accccttagg	caactgcaga	gggcttggtg	tgggggactg	gagtacctg	atgctccag	420
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<210> 200

<211> 529

<212> DNA

<213> Rat

<400> 200

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tacacggagt	ccgaggggac	cttcagcagt	ccagtcaccc	tgaagaaaac	attcaagatc	120
ccagacagac	agtatgtgct	gacagccttg	gctgcgcggg	ccaagcttag	agcctggaat	180
gatgtcgacg	ccttggtcac	cacaaagaac	tgggttggtt	acaccaagaa	gagagcacc	240
attggcttcc	atcgagttgt	ggaaattttg	cacaagaaca	gtgccccgtg	ccagatattg	300
caggaatatg	tcaatctggt	ggaagatgtg	gacacaaagt	tgaacttagc	cactaagttc	360
aagtgccatg	atgttgtcat	tgatacttgc	cgagacctga	aggatcgtca	acagttgctt	420
gcatacagga	gcaaagtaga	taaaggatct	gctgaggaag	agaaaatcga	tgtcatcctc	480

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529

<210> 201
<211> 1230
<212> DNA
<213> Rat

<400> 201

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gctgcgtcgc	ctgtggctgt	tgctggccgc	cgcttctctg	ctcgcaactgc	tgctgcagct	120
ggcgcccgcc	aggctgctac	cgagctgcgc	gctcttccag	gacctcatcc	gctacgggaa	180
gaccaagcag	tccggctcgc	ggcgcccgcc	cgctctgcag	gccttcgacg	tccccaagag	240
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ccacatcttg	ggaatgatga	tggtcttctg	gtcctctgcc	catcagtata	agtgccacgt	720
caattctcagc	aatctcagga	gaaataagaa	aggtgtggtc	atccactgcc	agcacagaat	780
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ctatgtcttc	ttcagccaag	ccttgtctgc	gttcttcaac	cacaggttct	acaaaagcac	960
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aagtacactt	tctgcagctg	gcgcccgcga	ggctgctacc	gagctgcgcg	ctcttccagg	1140
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cgggggatcc	actagttcta	gagcgccgcc				1230

<210> 202
<211> 778
<212> DNA
<213> Rat

<400> 202

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aaaataaaaa	aaaaggaaat	ttacttagcc	gcatgtcagt	cacccaaatt	ttgagtgtac	120
aaatgaaatg	gaaaacattt	attacacaaa	tttaattaca	attctaggga	ataaacatgc	180
aaatcagatg	gagctcaatc	tgcaggcgct	gacctctctc	ccctgggttg	cagtctgtgc	240
acctcctgga	ttcgcccgcg	accaggcagt	cagaggcctg	gctcttgacg	gcaggaggat	300
cactgttgta	aagaacagcg	tcacatttag	cgcatctggc	gtagtagcag	tttttaacac	360
tttgcgagg	tgcttccctt	ccccaccg	cgctttgtta	ggcttaacct	tctaaatctc	420
tgcttctctc	gcacagtaag	tgacctctcc	atgacaaagg	gccccagac	agcagttata	480
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aagttcaagg	ccagcctggg	ctacacagtg	agaccgggtc	tcaaaaacaa	aacaacaaaa	660
aacaactcct	attgaatcca	ctacaggaag	ggggggcgcg	gatcactgtc	tgcaaaactaa	720
agtgaactga	gctcctgtca	cagcctttcc	agcaagggca	agcttcttta	ttagttaa	778

<210> 203
<211> 1123
<212> DNA
<213> Rat

<400> 203

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------------	------------	------------	------------	------------	------------	----

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cgggtgccta	cagcccccac	cagcttcccc	ggggagattc	tgccgatttg	tcacgagcca	180
tgctcaggag	gcagctcgtc	tggtggcacc	tgctggcttt	gcttttcctc	ccattttgcc	240
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tggtctctct	agcgactcac	ttcagcaatc	agaacagtgg	cattatcttc	agcagtgttg	600
agaccaacat	tggaacttcc	ttcgatgtca	tgactggtag	atttggggcc	cccgtatcag	660
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<210> 204
 <211> 434
 <212> DNA
 <213> Mouse

<400> 204						
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attgttaaaa	aattgacatc	agaaaatatt	acagaaatag	atacctgttt	gaataaagtt	120
agagatgaaa	tttttgctaa	acttcaaccg	aagcttagat	gcacattagg	tgacatggaa	180
agtcctgtgt	ttgcacttcc	tgtactgtta	aagcttgaa	cccatgttga	aagcctcttt	240
acatattctt	tttcttgtaa	ttttgaatgt	tcccattgtg	gacaccagta	ccaaaacagg	300
tgtgtgaaga	gtctgggtcac	ctttaccaat	attgttccctg	agtggcatcc	actcaatgct	360
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gaaagagcgt	cgcc					434

<210> 205
 <211> 783
 <212> DNA
 <213> Mouse

<400> 205						
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catctggttg	ggaacacagc	gccggggctc	ggagaccatg	gcgggcgctg	cgggtgaagta	180
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cgtggatcaa	ctcatggagc	tgcccggtt	gagctgtgcc	acggctattg	ccaaggctta	300
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taacggaggg	gatgggctgg	tctgtgcgcg	acacdtcaaa	ctttttggtt	accagccaac	420
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gaaaatggac	attcctttcc	ttggtgaaat	gccccagag	gatgggatgt	agagaaggga	540
aacctagcgc	gaatccaacc	agacttactc	atctcactga	cggcacccaa	gaagtctgca	600
actcacttta	ctggccgata	tcattacctt	gggggtcgct	ttgtaccacc	tgctctagag	660
aagaagtacc	agctgaacct	gccatcttac	cctgacacag	agtgtgtcta	ccgtctacag	720
taaggagggt	gggtaggcag	gattctcaat	aaagacttgg	tactttctgt	cttgaaaaaa	780
aaa						783

<210> 206
 <211> 480

<212> DNA
<213> Mouse

<400> 206

aaatgaaaac	tcttggarct	cgcgcgcctg	caggctcgaca	ctagtggatc	caaagaattc	60
ggcacgagtt	aagggttttca	gactttattt	catggtattt	gacattgaca	catactgagt	120
tagtaacaag	ataccatgca	gctccctcta	gcctcggatc	accgaagcag	gaagaagggtc	180
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gatcatcatt	acaatggacc	aactgaggga	tgccctcata	ttagaccaat	taaaagttgc	420
tgtgagttaa	accaggaatg	accgcacttc	cacatcagaa	atcaaacaaa	atcaatggtt	480

<210> 207
<211> 501
<212> DNA
<213> Mouse

<400> 207

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tggaaagggc	ttgtaggtgt	cgggcttttt	gccctagccc	acgctgcctt	ttcagctgcg	120
cagcatcggt	cttatatgcg	actaacagaa	aaggaagatg	aatcattacc	aatagatata	180
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tttgactcac	tgccgcgtta	agctttttac	aaattaaata	acaggacaga	cacagaattg	480
agtattggag	tttgggggtg	a				501

<210> 208
<211> 480
<212> DNA
<213> Mouse

<400> 208

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tggtcttctc	ttttagtttt	tttacttttt	agtttagttt	gttcttttcc	ttccccaata	180
aatcattctc	acatgcttcc	atgtttgttt	ctgagagggtg	ggggctcaaa	tgtatagaaa	240
gtaggcccca	gtccataagg	aggtgtgaac	acacccctt	actgcttatc	acctatttga	300
caggaaacgc	caggagggga	gggggagggg	aagaggtgag	ttctgcacag	tcggacattt	360
ctgttgcttt	tgcatgttta	atatagacgt	tcctgtcgat	ccttgggaga	tcatggcctt	420
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<210> 209
<211> 962
<212> DNA
<213> Mouse

<400> 209

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aaatgatgcc	acagaaatcc	tttattcaca	tgtggttaaa	cctgtcccg	cacacccag	180
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gcccttgccg	gtgcttccca	actggatcgg	aggaggctac	ggaacaaagt	actggagccg	420

gaggagctct	caggagtggc	ggtgtgtcaa	cgacaagacg	cgcacccaga	ggatccagct	480
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caagaggtag	acccgtcagc	acaacgagtc	cagccacaac	tttgaaagcg	tgctgccagc	600
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ctctctcgag	cctgccattg	ctctttcctc	acttgaaagt	atatgcttcc	tgctttgatc	780
aagcccagca	ggctgtcctt	ctctgggact	agcttttctt	ttgcaagtgt	ctcaaatgt	840
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gtcatttctt	taaaagcacc	tgatgctgca	ttctgttaca	gtttaaaaaa	aaaaaaaaa	960
aa						962

<210> 210
 <211> 778
 <212> DNA
 <213> Mouse

<400> 210						
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ccacgtctat	gtccaagagt	cccccgactg	tcttggtcat	ctgtggcccc	ggaataacg	360
gaggggatgg	gctgggtctgt	gcgcgacacc	tcaaactttt	tggttaccag	ccaactatct	420
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<210> 211
 <211> 1152
 <212> DNA
 <213> Mouse

<400> 211						
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tctgtgacta	tagggagggt	agcacttttt	ctaattggaa	ttcttctctg	tctgtgtggc	180
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ctttccctga	gcctgagggt	agggcagagt	ttagagggtg	ggctaagtgt	atgttttcat	300
gtatgcattc	atgcctgtga	gtgtgtggct	tgctgtcgtg	tctcttggga	tcccaagcca	360
cgcgggtctt	ccctctgtag	atgggtctct	ggttctatca	cctgcttatt	tatgtacgag	420
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tctcagccta	gcaccacctg	tccccgagtc	ttctcagctt	gccccatcatt	ctcggcgccc	1080
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gcctgcccag	cc					1152

<210> 212
 <211> 446
 <212> DNA
 <213> Mouse

<400> 212
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 actcctggag ctggagtttag agacaatggt gagctgcctt gtggatgttg ggaattgaac 180
 ccaggtcctc tggagaaata accagtgtc ttaaccacta agccatctca acagcccaaa 240
 attatttttt taataagttg cctcggtcat gttgtcttaa tcagagcgat agaaaagtaa 300
 ctaatataga ttatttatga attcaggtgg cttaatggta tatgcatgaa ttagtagtaa 360
 aacaagaact agggccagca agtggcttaa ggtgacctgc taaccatctc agccacctga 420
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<210> 213
 <211> 2728
 <212> DNA
 <213> Mouse

<400> 213
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<210> 214

<211> 2046

<212> DNA

<213> Rat

<400> 214

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caaagg						2046

<210> 215

<211> 493

<212> DNA

<213> Mouse

<400> 215

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ggagcactgg	ccctttcttc	aacacagatg	agttggggac	tacagattct	cccctgctg	180
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<210> 216

<211> 511

<212> DNA

<213> Mouse

<400> 216

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attgctgccc	gaagcactgt	gctagccctg	cctcttgctg	accaccacac	tcagaagagc	420
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<210> 217

<211> 1107

<212> DNA

<213> Rat

<400> 217

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<210> 218

<211> 1001

<212> DNA

<213> Rat

<400> 218

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<210> 219

<211> 2206

<212> DNA

<213> Rat

<400> 219

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 <211> 376
 <212> DNA
 <213> Human

<400> 220						
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<210> 221
 <211> 433
 <212> DNA
 <213> Human

<400> 221						
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<210> 222
 <211> 530
 <212> DNA
 <213> Human

<400> 222						
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<210> 223
 <211> 550
 <212> DNA

<213> Mouse

<400> 223

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<210> 224

<211> 470

<212> DNA

<213> Mouse

<400> 224

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tgcttcctca	tcttcactca	accttaagca	gagttcaaag	actcaacttc	aacattgggtc	360
atctgggtgt	gtatttatat	gtgaataatg	atatcagatc	cagagtaaca	cctttgctgt	420
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<210> 225

<211> 1752

<212> DNA

<213> Rat

<400> 225

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<210> 226
 <211> 2165
 <212> DNA
 <213> Mouse

<400> 226						
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aaaaa						2165

<210> 227
 <211> 1348
 <212> DNA
 <213> Mouse

<220>
 <221> unsure
 <222> (644) ... (644)

<400> 227

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<210> 228
 <211> 2296
 <212> DNA
 <213> Mouse

<220>
 <221> unsure
 <222> (2255) ... (2255)

<400> 228

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aatagctatt	tcacagcagt	aacagaagct	acctgctata	ataaagacct	caacactgct	180
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tgctacaaca	ctctaccttc	agaacaacca	aataaacaat	gttgggattc	cttccgattt	420
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<210> 229

<211> 1704

<212> DNA

<213> Rat

<220>

<400> 229

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<210> 230
 <211> 2004
 <212> DNA
 <213> Rat

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gtggtggcgg	tgtgtctatg	ctccttctac	aatctcctca	cccgaacctt	ccacattgaa	1800
gagcccaaat	ccggcggcct	ggccaagcgg	ctggctaacc	tcacccggcg	tgctcgtggg	1860
gttccccctc	tctaagattc	cctttcttca	gcaactacag	cttcatactc	acctgcccga	1920
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<210> 231
 <211> 1397
 <212> DNA
 <213> Rat

<400> 231						
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gaacaaaagc	tggagctcgc	gsgctgcagg	gtcgacacta	gtggatccaa	agaattcggc	120
acgagcggca	cgagcggccc	cgaagggggc	tgacagggcg	acttggcggc	gatggctcga	180
gctccggcgg	cgacgacggg	ggccggaggc	ggcggtctct	cctccttctc	ctcctgggct	240
tggggccggc	ggtgatccga	gctggcggcc	gcccggccgc	gatgagactg	ttggcgggct	300
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cgctctcccg	ctctctgtac	gtgaacatga	ctagcggccc	tggcgggcca	gcggcggcca	420
cggggcggcg	gaaggacacg	caccagtggg	atgtgtgcaa	cagagagaaa	ttatgcgaat	480
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aatacagagt	gcttggtata	aatgaatggc	agaatacagg	gttccagtat	gatgtcatca	900
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acagtcaccc	ctggaatctg	ccctccagaa	gaggagggtg	atccagtgat	gtgaggggga	1320
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<210> 232
 <211> 861
 <212> DNA
 <213> Rat

<400> 232						
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gaagaaaaaa	aaaaaacaaa	aaaaccaaac	agtggtgact	caaataagat	aggagaaaaa	180
tgagagaaca	gaccagttc	tcgacccttg	cttctcaagg	tcctcccacc	aggctgccaa	240
agcaagatgg	tgttgctctg	atccagtcag	tattcttttg	actttttttt	ttaatctcca	300
ggtttttggt	caggctccca	tattcatacc	ctggctcatt	tagctttccc	tcattgtgtg	360
ggttcttctg	tcctcaccac	ccttactctc	cccactgata	ttcttcccag	tcaagactgt	420
ggctctggaa	gaaatatcca	ccatttgcat	agctgatgtt	ctgtagatcg	taatgttgaa	480
gcgctgggtg	tcctgggttg	cagaatcact	cctgtattac	tctgttacat	aggtgtctcc	540
tgatagactc	cctggcctta	gtcatggggt	gttttctaga	ggcagactaa	gacaggagtc	600
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tctactcagg	atcccaggtg	tttctgtaga	tgtagattgg	aatgtgtcca	taacagagag	720
gccagtgaga	gacatcccca	aggacctgcc	aggctttcct	tcgctccagg	aagacgcacc	780
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ttcttgaagt	catcgaacct	a				861

<210> 233
 <211> 445
 <212> DNA
 <213> Mouse

<400> 233						
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ggagcaagtg	cgtgagcgga	cgtgggcctg	gcagctgttg	caggagataa	aggctctctt	180
cgggaatact	gaggtgcgtc	tagctctcac	ggacgagccc	ctgaaaattt	caccataggt	240
cggccgtatt	cccagcccat	ctcttactca	ctagaagttc	ctggaagagt	catttatcct	300
cttacctgat	gccctttctc	ctcaatcaga	gtggatccct	tctctactac	ttgacttttg	360
catcaacaga	tctgacgtta	gctgtgcccc	tctgcaactc	tctggccatc	gtctttacac	420
tgattgttgg	gaaggtcctt	ggaga				445

<210> 234

<211> 565
 <212> DNA
 <213> Human

<400> 234
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 tctcgctggt tctgtctacc tggcctggat cctgttcttc gtgctctatg atttctgcat 180
 tgtttgatc accacctatg ctatcaacgt gagcctgatg tggctcagtt tccggaaggt 240
 ccaagaaccc cagggcaagg ctaagaggca ctgagccctc aaccaagcc aggctgacct 300
 ctgctttgct ttggcatgtg agccttgctt aagggggcat atctgggtcc ctagaaggcc 360
 ctatagtggt ggcttctaga ttacccctc ctctgcat acccgcat gacaatggac 420
 caaatgtgcc acacgtctgc tcttttttac acccagtgc tctgactctg tcccatggg 480
 ctggtctcca aagctcttc cattgcccag ggagggagg ttctgagcaa taaagtctt 540
 tagatcaatc aaaaaaaaa aaaaa 565

<210> 235
 <211> 476
 <212> DNA
 <213> Human

<400> 235
 ggtggctttc attggtgctg tccccggcat aggtccatct ctgcagaagc catttcagga 60
 gtacctggag gctcaacggc agaagcttca ccacaaaagc gaaatgggca caccacaggg 120
 agaaaaactgg ttgtcctgga tgtttgaaaa gttggctcgt gtcatggtgt gttacttcat 180
 cctatctatc attaaactcca tggcacaaag ttatgccaaa cgaatccagc agcgggttgaa 240
 ctgagaggag aaaactaat aagtagagaa agttttaaac tgcagaaatt ggagtggatg 300
 ggttctgcct taaattggga ggactccaag ccgggaagga aaattccctt ttccaacctg 360
 tatcaatttt tacaactttt ttctgaaaag cagtttagtc catactttgc actgacatac 420
 ttttctctc tgtgctaagg taaggatatcc accctcgatg caatccacct tgtttt 476

<210> 236
 <211> 607
 <212> DNA
 <213> Human

<400> 236
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 ggcagatgct tcagcatgtg cggcctcatg cttaaagctga agtgggtgtg ttgggtcgct 180
 gtctactgct ccttcatcag ctttgccaac tctcggagct cggaggacac gaagcaaatg 240
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 cccatgacgc ccccatgggt ataccagcct agaaggggtca cattttggac cctgtctatc 360
 cactaggcct gggctttggc tgctaaacct gctgccttca gctgccatcc tggacttccc 420
 tgaatgaggc cgtctcgggt cccccagctg gatagagggg acctggccct ttcctagggg 480
 acaccctagg cttacccctc ctgcctccct tcccctgcct gctgctgggg gagatggtgt 540
 ccatgtttct aggggtatct atttgcttct tcgttgaaac ctggtgttaa taaagtttt 600
 cactctg 607

<210> 237
 <211> 513
 <212> DNA
 <213> Mouse

<400> 237
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 ttgattcaac agattcaaac ttctacagc ctctactga tgtcttaca gctcttgctt 120

ctgtgccttt	ctcatgctat	tctttttgct	tagattgctc	tttgggtccca	gctcatgttc	180
atcactccct	tcaaagcctt	tcttccctta	tatcttctga	ctgagctctc	cctgattgac	240
atcacctcat	gcgatgacct	ccctcattct	gtgctgcctc	agcacttata	ttttgagttt	300
gtactgtggt	ccatgtactt	actaatatgt	tgctttgtaa	ttattttcta	gcactctgtg	360
ttacagtttc	atatgtgtat	ttatttccaa	aattaaattg	taagctcctt	gagggcagga	420
ataataactt	ttacatttgt	atctctgcac	ccccgagtgc	ctagtatagt	gctgagcaca	480
tagtaggcgt	ttaataaatg	cttgttgaag	tat			513

<210> 238

<211> 944

<212> DNA

<213> Rat

<400> 238

ggcacgaggg	gccgccgagt	cccgccgggt	cggtgtagct	cgctgccgac	gctgcgacgc	60
tctgtgggtgc	cgtgttcggc	ttttcctgtc	tacttcagtg	caccgctgca	gctccggcct	120
cgggtctgac	gcgccacagc	atggcttccg	ctttggagga	gttgagaaa	gacctagaag	180
agggtcaagt	gctgctggaa	aagtccacta	ggaaaagact	acgtgatact	cttacaaatg	240
aaaaatccaa	gattgagacg	gaactaagga	acaagatgca	gcagaagtca	cagaagaaac	300
cagaatttga	taatgaaaag	ccagctgctg	tggttgctcc	tcttacaaca	gggtacactg	360
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cgtgggtgga	atcccagagag	aagcaagcca	gggaagacac	agaattctga	ggctttaaaa	840
gtcctgtggg	aaccgtcatg	tggagtgtct	gtgtttccag	tagggactgt	tggtgaactg	900
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<210> 239

<211> 386

<212> DNA

<213> Rat

<400> 239

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gcgtgogggt	cctgtctctt	gtggccttcc	tggcgaccga	gctgetccct	cccttccagc	120
ggcggattca	gcccgaggag	ctgtggcttt	accggaaccc	gtacgtggag	gcggaatact	180
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ccaagtttct	gaggaaaagct	gacgccaccg	acagcaagca	agcctgcctc	gctgccagcc	300
ttgccctagc	tctgaatggt	gtctttacca	acatcataaa	actgatagtg	ggcaggccac	360
gcccagattt	cttctaccga	tgcttc				386

<210> 240

<211> 228

<212> DNA

<213> Rat

<400> 240

ttccgcgggc	gtcatgacgg	ctgcgggtgt	ctttggttgc	gccttcacgc	ccttcggggc	60
cgcgtctctc	ctttacgtct	tcaccatcgc	cactgatect	ttgcgagtea	tcttcctcat	120
cgcgggtgcc	ttcttctggg	tgggtgtctc	gctgctttcg	tctgttttct	gggttcctagt	180
gagagtcac	actgacaaca	gagatggacc	agtacagaat	tacctgct		228

<210> 241

<211> 452
 <212> DNA
 <213> Human

<400> 241
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 ttgttaggaa aatgtaggct accagtagaa aatgacattc tctattaata agatctgagg 120
 tgcgacacac ataattgtcc caatttttaa gattgatggg gagcatgaag cattttttta 180
 atgtgttggc aggcccccatt aaatgcataa actgcatagg actcatgtgg tctgaatgta 240
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 tctgagttag ctaactgaca caatgaaact gtcaggcatg tttctgctcc tctctctggc 360
 tcttttctgc tttttaacag gtgtcttcag tcaggggagga caggttgact gtggtgagtc 420
 caggacacca aggcctactg cactcgggaa cc 452

<210> 242
 <211> 1311
 <212> DNA
 <213> Mouse

<400> 242
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 ccctgggccc aatggtcaca gtcacctgct gaagacccca ctgggtggcc agaaacgcag 120
 tttttccac ctgctgccct cacctgagcc cagcccagag ggcagctacg tgggcccagca 180
 ctcccagggc ctggtgggccc actacgggga ctctacctg aagcgggaaga ggattttcta 240
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 cgtcactcct gtgttctggc ctcttgagtg cctttggagg tgtctctgac ctgtgaggat 600
 cagagacagt ccccgttttt aaacttcgac aattgacttt tatttccctt tctaattttt 660
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 ccccaaatg attccttcag ggtctggcct gccaggctc tattccacat gtgcaggctc 780
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 gtctgtgaaa ggtgaccatt gtaccaggc cactgggcct ctaccatgtt ctttcaaaacc 1200
 caggtcatta ccatccccag gctggatcac tggagcagge ctctctctg tccatgtgag 1260
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<210> 243
 <211> 399
 <212> DNA
 <213> Mouse

<400> 243
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 ctctccaaca tctcgtccat caccgacctc ggtggctttg acccagtggt gcttttcttc 180
 tgagtggcca gcccagacct gagctctgtc aatgacatcc aaggagaaaa tgagggttaat 240
 gagagacatt aattaaacac tccctcacc caccgcacca aaccagttgg gttcttctga 300
 tattctggaa tactctgggc tatgttttat gtttatttct tttttaatcg gttgtatttt 360
 ggtctttttt tttcttcttc tttttctttt gttcccaaa 399

<210> 244
 <211> 1421
 <212> DNA
 <213> Mouse

<220>
 <221> unsure
 <222> (1370)...(1370)

<221> unsure
 <222> (1395)...(1395)

<400> 244

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gtcctttttcc	cagagctgggt	tctgtgggtc	aacatgggtcc	cctgcttcct	cctgtctctg	180
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ctgccgcccc	ggactccagc	cttcagtccc	acaccaggga	ggacccagcc	cacagctccg	360
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<210> 245
 <211> 461
 <212> DNA
 <213> Mouse

<400> 245

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gctagcccca	aactcagaaa	tctgcctccc	gagtgcctggg	actaagggtg	tgaccacca	180
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ctatgtgtgc	tgggcatgga	cagagcctcc	tcacgcagc	tgatgatggc	cgggtttcca	360
ggcagccgtg	gtcctgtctg	aatattgtct	ctaactgcc	cagtttcaga	gaaaggggaa	420
caagttctcc	tttgcttctt	gccctcccag	atagaccctt	g		461

<210> 246
 <211> 1280
 <212> DNA
 <213> Mouse

<400> 246

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gaaaccttca	cagacatctt	catttcctgg	tccggcccaa	ggattggcag	gccatgggggt	180
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tcaccttaca	ccaagggggc	cagcctgctt	taccgaaagt	ttgtccaccc	atccctatcc	360
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<210> 247

<211> 833

<212> DNA

<213> Rat

<400> 247

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<210> 248

<211> 1308

<212> DNA

<213> Rat

<400> 248

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<210> 249

<211> 1212

<212> DNA

<213> Human

<400> 249

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<210> 250

<211> 453

<212> DNA

<213> Human

<400> 250

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<210> 251
 <211> 242
 <212> DNA
 <213> Human

<400> 251						
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ca						242

<210> 252
 <211> 358
 <212> DNA
 <213> Human

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gtcatccatg	ctgggagcaa	gagccaaca	gaacccatgc	ccccagggg	cagcctcaa	300
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<210> 253
 <211> 568
 <212> DNA
 <213> Human

<400> 253						
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<210> 254
 <211> 1421
 <212> DNA
 <213> Human

<400> 254						
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<210> 255

<211> 1464

<212> DNA

<213> Mouse

<400> 255

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<210> 256

<211> 2411

<212> DNA

<213> Mouse

<400> 256

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<210> 257

<211> 3516

<212> DNA

<213> Mouse

<400> 257

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gaagcactta	agttcgtcag	cttccttacc	cagggtgctgg	cgaaggcctc	caaggtgatc	720
cctgtcatga	tgatgggaaa	gctgggtgtc	cgggcgagct	atgaacactg	ggaatacctg	780
actgccgggc	tcattctccat	tggagtgtgc	atgtttcttc	tatccagtgg	accagagcct	840
agaagctctc	cagccaccac	actctctggc	ttggtcctac	tggcaggcta	tattgctttc	900
gacagcttca	cctcaaattg	gcaggatgac	ctgtttgcct	ataagatgtc	atcgggtgcag	960
atgatgtttg	gggtcaattt	attctcctgt	cttttcacag	taggctcact	actggaacag	1020
ggggccctac	tggagggggc	acgcttcatg	ggggcgacac	gtgagtttgc	gctccatgct	1080
ctcctcctct	ccatctgctc	cgccttggg	cagctcttca	tcttctacac	cattggacaa	1140
tttggagctg	ctgtcttcac	tatcatcatg	actctacgcc	aggctattgc	catcctcttc	1200
tcctgcctcc	tctatggcca	tactgtcact	gtggtggggg	gactgggagt	agctgtgggtc	1260
ttcactgccc	tcctactcag	agtctatgcc	cggggcccga	agcagcgggg	aaagaaggct	1320
gtgccactg	agcccccagt	acagaagggtg	tgagcagtg	agtaagacc	ctcatcttct	1380
gaggcactgg	ctcagtatca	gcatacagca	gaggattgga	gccctggagg	cagcctcttt	1440
tgccttaaaa	gccccactt	catggaaatg	acagctgtgg	gtgtttgggt	agaggtgacc	1500
cagagctcct	cccccaatct	ctgaaatctt	gctgtggggc	aagcaaacca	gcaccagggc	1560
tttgcctata	gcacgcaccc	ttgaggctac	caggcaccag	ctgggaagag	aatttaagag	1620
tcctgcagtt	cccctagggg	ccagtgagaa	tgggtgctgtg	ccagaaggga	caaaggcccc	1680
cagcccagtt	ggggccc					1697

<210> 265
 <211> 159
 <212> DNA
 <213> Mouse

<220>

<400> 265
 gttttcttct ccaggctgaa gacctgaacg tcaagttgga aggggagcct tccatgcgga 60
 aaccaaagca gcggccgcgg ccggagcccc tcatcatccc caccaaggcg ggcactttca 120
 tcgccccctc tgtctactcc aacatcaccc cttaccaga 159

<210> 266
 <211> 292
 <212> DNA
 <213> Mouse

<400> 266
 gtgggggtccc agacttgcca accaaagggc cattcctggt atatggttct ggcttcagct 60
 ctggtggcat ggactatggt atggttggtg gcaaggaggc tgggaccgag tctcgcttca 120
 aacagtggac ctcaatgatg gaagggtgct catctgtggc cacacaagaa gccaccatgc 180
 acaaaaacgg cgctatagt gccccctgta agaccgagg aggttcacca tacaaccagt 240
 ttgatataat cccaggtgac aacttggtg gccatacggg tctgtgctgt ga 292

<210> 267
 <211> 339
 <212> DNA
 <213> Mouse

<400> 267
 ccactgacct tcccagaagg tgacagccgg cggcggatgt tgtcaaggag ccgagatagt 60
 ccagcagtgc ctccgtaccc agaagacggg ctgtctcccc ccaaaagacg gcgacattcg 120
 atgagaagtc accacagtga tctcacattt tgcgagatta tctgtatgga gatggagtcc 180
 catgatgcag cctggccttt cctagagcct gtgaaccctc gcttggtgag tggataccga 240
 cgtgtcatca agaaccctat ggatttttcc accatgcgag aacgcctgct ccgtggaggg 300
 tacactagct cagaagagtt tgcagctgat gctctgtctg 339

<210> 268
 <211> 153
 <212> DNA
 <213> Mouse

<400> 268
 ctgaagttct ctcatccttg tctggaagac cataatagtt actgcattaa tggagcatgt 60
 gcattccacc atgagctgaa gcaagccatt tgcagatgct ttactgggta tacgggacaa 120
 cgatgtgagc atttgaccct aacttcgtat gct 153

<210> 269
 <211> 153
 <212> DNA
 <213> Human

<400> 269
 ttgaagttct cacacctttg cctggaagat cataacagtt actgcabcaa cgggtgctgt 60
 gcattccacc atgagctaga gaaagccatc tgcaggtggt ttactgggta tactggagaa 120
 aggtgtgagc acttgacttt aacttcatat gct 153

<210> 270
 <211> 288
 <212> DNA
 <213> Human

<400> 270
 gcggccgcgc tgctcctgct gctgctggcg ctgtacaccg cgcgtgtgga cgggtccaaa 60

tgcaagtgtc	cccgaaggg	acccaagatc	cgctacagcg	acgtgaagaa	gctggaatg	120
aagcgaagt	accgcactg	cgaggagaag	atggttatca	tcaccaccaa	gagcgtgtcc	180
aggtaccgag	gtcaggagca	ctgcctgcac	cccaagctgc	agagcaccaa	gcgcttcac	240
aagtggtaga	acgcctggaa	cgagaagcgc	agggctctacg	aagaatag		288

<210> 271
 <211> 234
 <212> DNA
 <213> Mouse

<400> 271						
tccaagtgt	agtgttccc	gaaggggcc	aagatccgct	acagcgacgt	gaagaagctg	60
gaaatgaagc	caaagtacc	acactgagag	gagaagatgg	ttatcgtcac	caccaagagc	120
atgtccaggt	accggggcca	ggagcactgc	ctgcacccta	agctgcagag	caccaaagcgc	180
ttcatcaagt	ggtacaatgc	ctggaacgag	aagcgcaggg	tctacgaaga	atag	234

<210> 272
 <211> 234
 <212> DNA
 <213> Human

<400> 272						
tccaaatgca	agtgttccc	gaagggacc	aagatccgct	acagcgacgt	gaagaagctg	60
gaaatgaagc	caaagtacc	gcactgcgag	gagaagatgg	ttatcatcac	caccaagagc	120
gtgtccaggt	accgaggtca	ggagcactgc	ctgcacccca	agctgcagag	caccaagcgc	180
ttcatcaagt	ggtacaacgc	ctggaacgag	aagcgcaggg	tctacgaaga	atag	234

<210> 273
 <211> 645
 <212> DNA
 <213> Mouse

<400> 273						
atgctgtcgc	tccgtctctt	gcttccacac	ctgggactgt	tcctgtgcct	ggctctgcac	60
ttatccccct	ccctctctgc	cagtgataat	gggtcctgcg	tggtccttga	taacatctac	120
acctccgaca	tcttggaat	cagcactatg	gctaactctt	ctgggtggga	tgtaacctat	180
acagtgcagg	tccccgtgaa	cgattcagtc	agtgccgtga	tcctgaaagc	agtgaaggag	240
gacgacagcc	cagtgggcac	ctggagtgga	acatatgaga	agtgaacga	cagcagtgtc	300
tactataact	tgacatocca	aagccagtcg	gtcttccaga	caaactggac	agttcctact	360
tccgaggatg	tgactaaagt	caacctgcag	gtcctcatcg	tcgtcaatcg	cacagcctca	420
aagtcatccg	tgaaaatgga	acaagtacaa	ccctcagcct	caacccttat	tcctgagagt	480
tctgagacca	gccagaccat	aaacacgact	ccaactgtga	acacagccaa	gactacagcc	540
aaggacacag	ccaacaccac	agccgtgacc	acagccaata	ccacagccaa	taccacagcc	600
grgaccacag	ccaagaccac	agccaaaagc	ctggccatcc	gcact		645

<210> 274
 <211> 63
 <212> DNA
 <213> Mouse

<400> 274						
gggtacagt	atggttacca	agtgtgtagt	aggttcggaa	gcaaagtgcc	tcagtttctg	60
aac						63

<210> 275
 <211> 388
 <212> PRT
 <213> Mouse

<400> 275
 Met Gly Leu Glu Pro Ser Trp Tyr Leu Leu Leu Cys Leu Ala Val Ser
 1 5 10 15
 Gly Ala Ala Gly Thr Asp Pro Pro Thr Ala Pro Thr Thr Ala Glu Arg
 20 25 30
 Gln Arg Gln Pro Thr Asp Ile Ile Leu Asp Cys Phe Leu Val Thr Glu
 35 40 45
 Asp Arg His Arg Gly Ala Phe Ala Ser Ser Gly Asp Arg Glu Arg Ala
 50 55 60
 Leu Leu Val Leu Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu
 65 70 75 80
 Gly Ile Thr Asp Phe Gln Gly Ser Thr Glu Thr Lys Gln Asp Ser Pro
 85 90 95
 Val Ile Phe Glu Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu
 100 105 110
 Ala Leu Leu His Ala Asp Cys Ser Gly Lys Ala Val Thr Cys Glu Ile
 115 120 125
 Ser Lys Tyr Phe Leu Gln Ala Arg Gln Glu Ala Thr Phe Glu Lys Ala
 130 135 140
 His Trp Phe Ile Ser Asn Met Gln Val Ser Arg Gly Gly Pro Ser Val
 145 150 155 160
 Ser Met Val Met Lys Thr Leu Arg Asp Ala Glu Val Gly Ala Val Arg
 165 170 175
 His Pro Thr Leu Asn Leu Pro Leu Ser Ala Gln Gly Thr Val Lys Thr
 180 185 190
 Gln Val Glu Phe Gln Val Thr Ser Glu Thr Gln Thr Leu Asn His Leu
 195 200 205
 Leu Gly Ser Ser Val Ser Leu His Cys Ser Phe Ser Met Ala Pro Asp
 210 215 220
 Leu Asp Leu Thr Gly Val Glu Trp Arg Leu Gln His Lys Gly Ser Gly
 225 230 235 240
 Gln Leu Val Tyr Ser Trp Lys Thr Gly Gln Gly Gln Ala Lys Arg Lys
 245 250 255
 Gly Ala Thr Leu Glu Pro Glu Glu Leu Leu Arg Ala Gly Asn Ala Ser
 260 265 270
 Leu Thr Leu Pro Asn Leu Thr Leu Lys Asp Glu Gly Thr Tyr Ile Cys
 275 280 285
 Gln Ile Ser Thr Ser Leu Tyr Gln Ala Gln Gln Ile Met Pro Leu Asn
 290 295 300
 Ile Leu Ala Pro Pro Lys Val Gln Leu His Leu Ala Asn Lys Asp Pro
 305 310 315 320
 Leu Pro Ser Leu Val Cys Ser Ile Ala Gly Tyr Tyr Pro Leu Asp Val
 325 330 335
 Gly Val Thr Trp Ile Arg Glu Glu Leu Gly Gly Ile Pro Ala Gln Val
 340 345 350
 Ser Gly Ala Ser Phe Ser Ser Leu Arg Gln Ser Thr Met Gly Thr Tyr
 355 360 365
 Ser Ile Ser Ser Thr Val Met Ala Asp Pro Gly Pro Thr Gly Ala Thr
 370 375 380
 Tyr Thr Cys Gln
 385

<210> 276
 <211> 151
 <212> PRT
 <213> Rat

<400> 276
 Met Ala Glu Pro Trp Ala Gly Gln Phe Leu Gln Ala Leu Pro Ala Thr
 1 5 10 15
 Val Leu Gly Ala Leu Gly Thr Leu Gly Ser Glu Phe Leu Arg Glu Trp
 20 25 30
 Glu Thr Gln Asp Met Arg Val Thr Leu Phe Lys Leu Leu Leu Trp
 35 40 45
 Leu Val Leu Ser Leu Leu Gly Ile Gln Leu Ala Trp Gly Phe Tyr Gly
 50 55 60
 Asn Thr Val Thr Gly Leu Tyr His Arg Pro Gly Lys Trp Gln Gln Met
 65 70 75 80
 Lys Leu Ser Lys Leu Thr Glu Asn Lys Gly Arg Gln Gln Glu Lys Gly
 85 90 95
 Leu Gln Arg Tyr Arg Trp Val Cys Trp Leu Leu Cys Cys Thr Leu Leu
 100 105 110
 Leu Ser Arg Pro Leu Arg Gln Leu Gln Arg Ala Trp Val Gly Gly Leu
 115 120 125
 Glu Tyr His Asp Ala Pro Arg Val Ser Leu His Cys Pro Gln Pro Cys
 130 135 140
 Leu Gln Gln Arg Gln Val Leu
 145 150

<210> 277
 <211> 163
 <212> PRT
 <213> Rat

<400> 277
 Met Pro Leu Val Thr Thr Leu Phe Tyr Ala Cys Phe Tyr His Tyr Thr
 1 5 10 15
 Glu Ser Glu Gly Thr Phe Ser Ser Pro Val Asn Leu Lys Lys Thr Phe
 20 25 30
 Lys Ile Pro Asp Arg Gln Tyr Val Leu Thr Ala Leu Ala Arg Ala
 35 40 45
 Lys Leu Arg Ala Trp Asn Asp Val Asp Ala Leu Phe Thr Thr Lys Asn
 50 55 60
 Trp Leu Gly Tyr Thr Lys Lys Arg Ala Pro Ile Gly Phe His Arg Val
 65 70 75 80
 Val Glu Ile Leu His Lys Asn Ser Ala Pro Val Gln Ile Leu Gln Glu
 85 90 95
 Tyr Val Asn Leu Val Glu Asp Val Asp Thr Lys Leu Asn Leu Ala Thr
 100 105 110
 Lys Phe Lys Cys His Asp Val Val Ile Asp Thr Cys Arg Asp Leu Lys
 115 120 125
 Asp Arg Gln Gln Leu Leu Ala Tyr Arg Ser Lys Val Asp Lys Gly Ser
 130 135 140
 Ala Glu Glu Glu Lys Ile Asp Val Ile Leu Ser Ser Ser Gln Ile Arg
 145 150 155 160
 Trp Lys Asn

<210> 278
 <211> 330
 <212> PRT
 <213> Rat

<400> 278

Met Ala Gly Trp Ala Gly Ala Glu Leu Ser Val Leu Asn Pro Leu Arg
 1 5 10 15
 Ala Leu Trp Leu Leu Leu Ala Ala Phe Leu Leu Ala Leu Leu
 20 25 30
 Gln Leu Ala Pro Ala Arg Leu Leu Pro Ser Cys Ala Leu Phe Gln Asp
 35 40 45
 Leu Ile Arg Tyr Gly Lys Thr Lys Gln Ser Gly Ser Arg Arg Pro Ala
 50 55 60
 Val Cys Arg Ala Phe Asp Val Pro Lys Arg Tyr Phe Ser His Phe Tyr
 65 70 75 80
 Val Val Ser Val Leu Trp Asn Gly Ser Leu Leu Trp Phe Leu Ser Gln
 85 90 95
 Ser Leu Phe Leu Gly Ala Pro Phe Pro Ser Trp Leu Trp Ala Leu Leu
 100 105 110
 Arg Thr Leu Gly Val Thr Gln Phe Gln Ala Leu Gly Met Glu Ser Lys
 115 120 125
 Ala Ser Arg Ile Gln Ala Gly Glu Leu Ala Leu Ser Thr Phe Leu Val
 130 135 140
 Leu Val Phe Leu Trp Val His Ser Leu Arg Arg Leu Phe Glu Cys Phe
 145 150 155 160
 Tyr Val Ser Val Phe Ser Asn Thr Ala Ile His Val Val Gln Tyr Cys
 165 170 175
 Phe Gly Leu Val Tyr Tyr Val Leu Val Gly Leu Thr Val Leu Ser Gln
 180 185 190
 Val Pro Met Asn Asp Lys Asn Val Tyr Ala Leu Gly Lys Asn Leu Leu
 195 200 205
 Leu Gln Ala Arg Trp Phe His Ile Leu Gly Met Met Met Phe Phe Trp
 210 215 220
 Ser Ser Ala His Gln Tyr Lys Cys His Val Ile Leu Ser Asn Leu Arg
 225 230 235 240
 Arg Asn Lys Lys Gly Val Val Ile His Cys Gln His Arg Ile Pro Phe
 245 250 255
 Gly Asp Trp Phe Glu Tyr Val Ser Ser Ala Asn Tyr Leu Ala Glu Leu
 260 265 270
 Met Ile Tyr Ile Ser Met Ala Val Thr Phe Gly Leu His Asn Val Thr
 275 280 285
 Trp Trp Leu Val Val Thr Tyr Val Phe Phe Ser Gln Ala Leu Ser Ala
 290 295 300
 Phe Phe Asn His Arg Phe Tyr Lys Ser Thr Phe Val Ser Tyr Pro Lys
 305 310 315 320
 His Arg Lys Ala Phe Leu Pro Phe Leu Phe
 325 330

<210> 279

<211> 61

<212> PRT

<213> Rat

<400> 279

Met Glu Asn Ile Tyr Tyr Thr Asn Leu Ile Thr Ile Leu Gly Asn Lys
 1 5 10 15
 His Ala Asn Gln Met Glu Leu Asn Leu Gln Ala Leu Ile Leu Ser Pro
 20 25 30
 Trp Phe Ala Val Cys Ala Pro Pro Gly Phe Ala Arg Asp Gln Ala Val
 35 40 45
 Arg Gly Leu Ala Leu Ala Gly Arg Arg Ile Thr Val Val
 50 55 60

<210> 280
 <211> 105
 <212> PRT
 <213> Rat

<400> 280
 Met Leu Arg Arg Gln Leu Val Trp Trp His Leu Leu Ala Leu Leu Phe
 1 5 10 15
 Leu Pro Phe Cys Leu Cys Gln Asp Glu Tyr Met Glu Ser Pro Gln Ala
 20 25 30
 Gly Gly Leu Pro Pro Asp Cys Ser Lys Cys Cys His Gly Asp Tyr Gly
 35 40 45
 Phe Arg Gly Tyr Gln Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ile
 50 55 60
 Pro Gly Asn His Gly Asn Asn Gly Asn Asn Gly Ala Thr Gly His Glu
 65 70 75 80
 Gly Ala Lys Gly Glu Lys Gly Asp Lys Gly Asp Leu Gly Pro Arg Gly
 85 90 95
 Glu Arg Gly Gln His Gly Pro Lys Gly
 100 105

<210> 281
 <211> 27
 <212> PRT
 <213> Mouse

<400> 281
 Met Leu Lys Ala Ser Leu His Ile Leu Phe Leu Gly Ile Leu Asn Val
 1 5 10 15
 Pro Ile Val Asp Thr Ser Thr Lys Thr Gly Val
 20 25

<210> 282
 <211> 169
 <212> PRT
 <213> Mouse

<400> 282
 Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly
 1 5 10 15
 Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg
 20 25 30
 Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly
 35 40 45
 Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln
 50 55 60
 Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu
 65 70 75 80
 Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr
 85 90 95
 Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly
 100 105 110
 Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe
 115 120 125
 Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu
 130 135 140

Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu
 145 150 155 160
 Gly Glu Met Pro Pro Glu Asp Gly Met
 165

<210> 283
 <211> 61
 <212> PRT
 <213> Mouse

<400> 283
 Met Glu Lys Gln Met Asp Ala Ser Val Ser Val Ile Phe Gly Ser Ile
 1 5 10 15
 Val Ile Ser Ala Phe Leu Tyr Leu Ser Leu Ala Gly Pro Trp Ala Val
 20 25 30
 Thr Val Thr Gln Met Arg Thr Ile Ile Thr Met Asp Gln Leu Arg
 35 40 45
 Asp Ala Leu Ile Leu Asp Gln Leu Lys Val Ala Val Ser
 50 55 60

<210> 284
 <211> 131
 <212> PRT
 <213> Mouse

<400> 284
 Met Ala Pro Ser Leu Trp Lys Gly Leu Val Gly Val Gly Leu Phe Ala
 1 5 10 15
 Leu Ala His Ala Ala Phe Ser Ala Ala Gln His Arg Ser Tyr Met Arg
 20 25 30
 Leu Thr Glu Lys Glu Asp Glu Ser Leu Pro Ile Asp Ile Val Leu Gln
 35 40 45
 Thr Leu Leu Ala Phe Ala Val Thr Cys Tyr Gly Ile Val His Ile Ala
 50 55 60
 Gly Glu Phe Lys Asp Met Asp Ala Thr Ser Glu Leu Lys Asn Lys Thr
 65 70 75 80
 Phe Asp Thr Leu Arg Asn His Pro Ser Phe Tyr Val Phe Asn His Arg
 85 90 95
 Gly Arg Val Leu Phe Arg Pro Ser Asp Ala Thr Asn Ser Ser Asn Leu
 100 105 110
 Asp Ala Leu Ser Ser Asn Thr Ser Leu Lys Leu Arg Lys Phe Asp Ser
 115 120 125
 Leu Arg Arg
 130

<210> 285
 <211> 78
 <212> PRT
 <213> Mouse

<400> 285
 Gly Thr Arg Lys Pro Leu Pro Met Glu Ala His Ser Arg Arg Glu Lys
 1 5 10 15
 Ala Ser Gly Leu Arg Leu Ala Trp His Tyr Glu Cys Ser Gly Val Ser
 20 25 30
 Val Trp Trp Met Cys Val Leu Gly Trp Leu Ser Phe Leu Val Phe Leu
 35 40 45

Leu Phe Ser Leu Val Cys Ser Phe Pro Ser Pro Ile Asn His Ser His
 50 55 60
 Met Leu Pro Cys Leu Phe Leu Arg Gly Gly Gly Ser Asn Val
 65 70 75

<210> 286
 <211> 206
 <212> PRT
 <213> Mouse

<400> 286
 Met Leu Pro Pro Ala Ile His Leu Ser Leu Ile Pro Leu Leu Cys Ile
 1 5 10 15
 Leu Met Arg Asn Cys Leu Ala Phe Lys Asn Asp Ala Thr Glu Ile Leu
 20 25 30
 Tyr Ser His Val Val Lys Pro Val Pro Ala His Pro Ser Ser Asn Ser
 35 40 45
 Thr Leu Asn Gln Ala Arg Asn Gly Gly Arg His Phe Ser Ser Thr Gly
 50 55 60
 Leu Asp Arg Asn Ser Arg Val Gln Val Gly Cys Arg Glu Leu Arg Ser
 65 70 75 80
 Thr Lys Tyr Ile Ser Asp Gly Gln Cys Thr Ser Ile Ser Pro Leu Lys
 85 90 95
 Glu Leu Val Cys Ala Gly Glu Cys Leu Pro Leu Pro Val Leu Pro Asn
 100 105 110
 Trp Ile Gly Gly Tyr Gly Thr Lys Tyr Trp Ser Arg Ser Ser
 115 120 125
 Gln Glu Trp Arg Cys Val Asn Asp Lys Thr Arg Thr Gln Arg Ile Gln
 130 135 140
 Leu Gln Cys Gln Asp Gly Ser Thr Arg Thr Tyr Lys Ile Thr Val Val
 145 150 155 160
 Thr Ala Cys Lys Cys Lys Arg Tyr Thr Arg Gln His Asn Glu Ser Ser
 165 170 175
 His Asn Phe Glu Ser Val Ser Pro Ala Lys Pro Ala Gln His His Arg
 180 185 190
 Glu Arg Lys Arg Ala Ser Lys Ser Ser Lys His Ser Leu Ser
 195 200 205

<210> 287
 <211> 169
 <212> PRT
 <213> Mouse

<400> 287
 Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly
 1 5 10 15
 Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg
 20 25 30
 Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly
 35 40 45
 Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln
 50 55 60
 Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu
 65 70 75 80
 Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr
 85 90 95
 Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly

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          100          105          110
Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe
          115          120          125
Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu
          130          135          140
Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu
145          150          155          160
Gly Glu Met Pro Pro Glu Asp Gly Met
          165

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<210> 288
<211> 114
<212> PRT
<213> Mouse

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<400> 288
Met Ser Val Thr Ile Gly Arg Leu Ala Leu Phe Leu Ile Gly Ile Leu
1      5      10      15
Leu Cys Pro Val Ala Pro Ser Leu Thr Arg Ser Trp Pro Gly Pro Asp
          20      25      30
Thr Cys Ser Leu Phe Leu Gln His Ser Leu Ser Leu Ser Leu Arg Leu
          35      40      45
Gly Gln Ser Leu Glu Gly Gly Leu Ser Val Cys Phe His Val Cys Ile
          50      55      60
His Ala Cys Glu Cys Val Ala Cys Cys Arg Val Leu Trp Asp Pro Lys
65          70      75      80
Pro Arg Gly Ser Ser Leu Cys Arg Trp Val Leu Gly Ser Ile Thr Cys
          85      90      95
Leu Phe Met Tyr Glu Val Gly Gly Trp Thr Gln Gly Gly Leu Ile Val
          100      105      110
Ser Leu

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<210> 289
<211> 46
<212> PRT
<213> Mouse

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<400> 289
Met His Tyr Pro Cys Leu Ala Cys Leu Phe Val Asn Val His Trp Cys
1      5      10      15
Phe Ala Trp Met Cys Ile Leu Val Lys Met Ser Glu Leu Leu Glu Leu
          20      25      30
Glu Leu Glu Thr Met Val Ser Cys Leu Val Asp Val Gly Asn
          35      40      45

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<210> 290
<211> 199
<212> PRT
<213> Mouse

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<400> 290
Met Val Leu Pro Thr Val Leu Ile Leu Leu Leu Ser Trp Ala Ala Gly
1      5      10      15
Leu Gly Gly Glu Thr Arg Pro Arg Ala Ala Thr Glu Arg Arg Ser Val
          20      25      30
Gly Pro Ser Ala Arg Arg Gly Ala Gly Pro Arg Val Ser Gly Leu Leu

```

35 40 45
 Gly Phe Cys Gln Leu Ser Gln Leu Ala Ser Ala Asp Pro Glu Arg Arg
 50 55 60
 Ser Pro Arg Ala Ile Val Pro Arg Ala Pro Arg Pro Arg Ser Arg Arg
 65 70 75 80
 Arg Pro Cys Leu Pro Gly Phe Ser Arg Arg Phe Pro Arg Glu Arg Arg
 85 90 95
 Ser Pro Gly Gln Pro Pro Ser Arg Thr Pro Gln Pro Pro Gln Pro Cys
 100 105 110
 Arg Gly Pro Ser Pro Gly Thr Ala Gln Thr Arg Ser Asn Leu Arg Gly
 115 120 125
 Trp Gln Arg Gly Gly Ser Ile Val Leu Gln Ala Ser Glu Arg Thr Arg
 130 135 140
 Ala Gly Cys Arg Thr Pro Val Cys Val Ser His Pro Ser Ala Phe Pro
 145 150 155 160
 Pro Pro Arg Ala Leu Phe Gly Val Phe Val Ala Ser Ala Pro Glu Val
 165 170 175
 Val Cys Val Cys Val Ser Val Val Leu Ser Val Cys Leu Leu Ser Pro
 180 185 190
 Arg Gly Lys Thr Leu Val Asp
 195

<210> 291

<211> 568

<212> PRT

<213> Rat

<400> 291

Met Glu Leu Leu Tyr Trp Cys Leu Leu Cys Leu Leu Leu Pro Leu Thr
 1 5 10 15
 Ser Arg Thr Gln Lys Leu Pro Thr Arg Asp Glu Glu Leu Phe Gln Met
 20 25 30
 Gln Ile Arg Asp Lys Ala Leu Phe His Asp Ser Ser Val Ile Pro Asp
 35 40 45
 Gly Ala Glu Ile Ser Ser Tyr Leu Phe Arg Asp Thr Pro Arg Arg Tyr
 50 55 60
 Phe Phe Met Val Glu Glu Asp Asn Thr Pro Leu Ser Val Thr Val Thr
 65 70 75 80
 Pro Cys Asp Ala Pro Leu Glu Trp Lys Leu Ser Leu Gln Glu Leu Pro
 85 90 95
 Glu Glu Ser Ser Ala Asp Gly Ser Gly Asp Pro Glu Pro Leu Asp Gln
 100 105 110
 Gln Lys Gln Gln Met Thr Asp Val Glu Gly Thr Glu Leu Phe Ser Tyr
 115 120 125
 Lys Gly Asn Asp Val Glu Tyr Phe Leu Ser Ser Ser Pro Ser Gly
 130 135 140
 Leu Tyr Gln Leu Glu Leu Leu Ser Thr Glu Lys Asp Thr His Phe Lys
 145 150 155 160
 Val Tyr Ala Thr Thr Thr Pro Glu Ser Asp Gln Pro Tyr Pro Asp Leu
 165 170 175
 Pro Tyr Asp Pro Arg Val Asp Val Thr Ser Ile Gly Arg Thr Thr Val
 180 185 190
 Thr Leu Ala Trp Lys Gln Ser Pro Thr Ala Ser Met Leu Lys Gln Pro
 195 200 205
 Ile Glu Tyr Cys Val Val Ile Asn Lys Glu His Asn Phe Lys Ser Leu
 210 215 220
 Cys Ala Ala Glu Thr Lys Met Ser Ala Asp Asp Ala Phe Met Val Ala

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225          230          235          240
Pro Lys Pro Gly Leu Asp Phe Ser Pro Phe Asp Phe Ala His Phe Gly
          245          250          255
Phe Pro Thr Asp Asn Leu Gly Lys Asp Arg Ser Phe Leu Ala Lys Pro
          260          265          270
Ser Pro Lys Val Gly Arg His Val Tyr Trp Arg Pro Lys Val Asp Ile
          275          280          285
Lys Lys Ile Cys Ile Gly Ser Lys Asn Ile Phe Thr Val Ser Asp Leu
          290          295          300
Lys Pro Asn Thr Gln Tyr Tyr Phe Asp Val Phe Met Val Asn Thr Asn
305          310          315          320
Thr Asn Met Asn Thr Ala Phe Val Gly Ala Phe Ala Arg Thr Lys Glu
          325          330          335
Glu Ala Lys Gln Lys Thr Val Glu Leu Lys Asp Gly Arg Val Thr Asp
          340          345          350
Val Val Val Lys Arg Lys Gly Lys Lys Phe Leu Arg Phe Ala Pro Val
          355          360          365
Ser Ser His Gln Lys Val Thr Leu Phe Ile His Ser Cys Met Asp Thr
          370          375          380
Val Gln Val Gln Val Arg Arg Asp Gly Lys Leu Leu Leu Ser Gln Asn
385          390          395          400
Val Glu Gly Ile Arg Gln Phe Gln Leu Arg Gly Lys Pro Lys Gly Lys
          405          410          415
Tyr Leu Ile Arg Leu Lys Gly Asn Lys Lys Gly Ala Ser Met Leu Lys
          420          425          430
Ile Leu Ala Thr Thr Arg Pro Ser Lys His Ala Phe Pro Ser Leu Pro
          435          440          445
Asp Asp Thr Arg Ile Lys Ala Phe Asp Lys Leu Arg Thr Cys Ser Ser
          450          455          460
Val Thr Val Ala Trp Leu Gly Thr Gln Glu Arg Arg Lys Phe Cys Ile
465          470          475          480
Tyr Arg Lys Glu Val Gly Gly Asn Tyr Ser Glu Glu Gln Lys Arg Arg
          485          490          495
Glu Arg Asn Gln Cys Leu Gly Pro Asp Thr Arg Lys Lys Ser Glu Lys
          500          505          510
Val Leu Cys Lys Tyr Phe His Ser Gln Asn Leu Gln Lys Ala Val Thr
          515          520          525
Thr Glu Thr Ile Arg Asp Leu Gln Pro Gly Lys Ser Tyr Leu Leu Asp
          530          535          540
Val Tyr Val Val Gly His Gly Gly His Ser Val Lys Tyr Gln Ser Lys
545          550          555          560
Leu Val Lys Thr Arg Lys Val Cys
          565

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<210> 292
<211> 123
<212> PRT
<213> Mouse

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<400> 292
Met Leu Thr Glu Pro Ala Gln Leu Phe Val His Lys Lys Asn Gln Pro
1          5          10          15
Pro Ser His Ser Ser Leu Arg Leu His Phe Arg Thr Leu Ala Gly Ala
          20          25          30
Leu Ala Leu Ser Ser Thr Gln Met Ser Trp Gly Leu Gln Ile Leu Pro
          35          40          45
Cys Leu Ser Leu Ile Leu Leu Leu Trp Asn Gln Val Pro Gly Leu Glu

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50 55 60
 Gly Gln Glu Phe Arg Phe Gly Ser Cys Gln Val Thr Gly Val Val Leu
 65 70 75 80
 Pro Glu Leu Trp Glu Ala Phe Trp Thr Val Lys Asn Thr Val Gln Thr
 85 90 95
 Gln Asp Asp Ile Thr Ser Ile Arg Leu Leu Lys Pro Gln Val Leu Arg
 100 105 110
 Asn Val Ser Val Ile Arg Trp Glu Gly Asp Ser
 115 120

<210> 293
 <211> 66
 <212> PRT
 <213> Mouse

<400> 293
 Met Asp Val Trp Ser Gly Leu Pro Leu Glu Thr Leu Trp Ile Tyr Glu
 1 5 10 15
 Ala Val Leu Pro Trp Leu Leu Met Gly Gln Gly His Ala Trp Val Cys
 20 25 30
 Gly Pro Ile Ala Leu Trp Val Phe Val Asn Val Pro Gly Leu Cys Tyr
 35 40 45
 His Gln Lys Pro Phe Arg Cys Pro Trp Ser Gly Leu Leu Pro Glu Ala
 50 55 60
 Leu Cys
 65

<210> 294
 <211> 294
 <212> PRT
 <213> Rat

<400> 294
 Met Thr Val Phe Arg Lys Val Thr Thr Met Ile Ser Trp Met Leu Leu
 1 5 10 15
 Ala Cys Ala Leu Pro Cys Ala Ala Asp Pro Met Leu Gly Ala Phe Ala
 20 25 30
 Arg Arg Asp Phe Gln Lys Gly Gly Pro Gln Leu Val Cys Ser Leu Pro
 35 40 45
 Gly Pro Gln Gly Pro Pro Gly Pro Pro Gly Ala Pro Gly Ser Ser Gly
 50 55 60
 Met Val Gly Arg Met Gly Phe Pro Gly Lys Asp Gly Gln Asp Gly Gln
 65 70 75 80
 Asp Gly Asp Arg Gly Asp Ser Gly Glu Glu Gly Pro Pro Gly Arg Thr
 85 90 95
 Gly Asn Arg Gly Lys Gln Gly Pro Lys Gly Lys Ala Gly Ala Ile Gly
 100 105 110
 Arg Ala Gly Pro Arg Gly Pro Lys Gly Val Ser Gly Thr Pro Gly Lys
 115 120 125
 His Gly Ile Pro Gly Lys Lys Gly Pro Lys Gly Lys Gly Glu Pro
 130 135 140
 Gly Leu Pro Gly Pro Cys Ser Cys Gly Ser Ser Arg Ala Lys Ser Ala
 145 150 155 160
 Phe Ser Val Ala Val Thr Lys Ser Tyr Pro Arg Glu Arg Leu Pro Ile
 165 170 175
 Lys Phe Asp Lys Ile Leu Met Asn Glu Gly Gly His Tyr Asn Ala Ser
 180 185 190

Ser Gly Lys Phe Val Cys Ser Val Pro Gly Ile Tyr Tyr Phe Thr Tyr
 195 200 205
 Asp Ile Thr Leu Ala Asn Lys His Leu Ala Ile Gly Leu Val His Asn
 210 215 220
 Gly Gln Tyr Arg Ile Arg Thr Phe Asp Ala Asn Thr Gly Asn His Asp
 225 230 235 240
 Val Ala Ser Gly Ser Thr Ile Leu Ala Leu Lys Glu Gly Asp Glu Val
 245 250 255
 Trp Leu Gln Ile Phe Tyr Ser Glu Gln Asn Gly Leu Phe Tyr Asp Pro
 260 265 270
 Tyr Trp Thr Asp Ser Leu Phe Thr Gly Phe Leu Ile Tyr Ala Asp Gln
 275 280 285
 Gly Asp Pro Asn Glu Val
 290

<210> 295

<211> 243

<212> PRT

<213> Rat

<400> 295

Met Arg Pro Leu Leu Ala Leu Leu Leu Gly Leu Ala Ser Gly Ser
 1 5 10 15
 Pro Pro Leu Asp Asp Asn Lys Ile Pro Ser Leu Cys Pro Gly Gln Pro
 20 25 30
 Gly Leu Pro Gly Thr Pro Gly His His Gly Ser Gln Gly Leu Pro Gly
 35 40 45
 Arg Asp Gly Arg Asp Gly Arg Asp Gly Ala Pro Gly Ala Pro Gly Glu
 50 55 60
 Lys Gly Glu Gly Gly Arg Pro Gly Leu Pro Gly Pro Arg Gly Glu Pro
 65 70 75 80
 Gly Pro Arg Gly Glu Ala Gly Pro Val Gly Ala Ile Gly Pro Ala Gly
 85 90 95
 Glu Cys Ser Val Pro Pro Arg Ser Ala Phe Ser Ala Lys Arg Ser Glu
 100 105 110
 Ser Arg Val Pro Pro Pro Ala Asp Thr Pro Leu Pro Phe Asp Arg Val
 115 120 125
 Leu Leu Asn Glu Gln Gly His Tyr Asp Ala Thr Thr Gly Lys Phe Thr
 130 135 140
 Cys Gln Val Pro Gly Val Tyr Tyr Phe Ala Val His Ala Thr Val Tyr
 145 150 155 160
 Arg Ala Ser Leu Gln Phe Asp Leu Val Lys Asn Gly Gln Ser Ile Ala
 165 170 175
 Ser Phe Phe Gln Phe Phe Gly Gly Trp Pro Lys Pro Ala Ser Leu Ser
 180 185 190
 Gly Gly Ala Met Val Arg Leu Glu Pro Glu Asp Gln Val Trp Val Gln
 195 200 205
 Val Gly Val Gly Asp Tyr Ile Gly Ile Tyr Ala Ser Ile Lys Thr Asp
 210 215 220
 Ser Thr Phe Ser Gly Phe Leu Val Tyr Ser Asp Trp His Ser Ser Pro
 225 230 235 240
 Val Phe Ala

<210> 296

<211> 444

<212> PRT

<213> Rat

<400> 296

Met	Leu	Val	Ala	Phe	Leu	Gly	Ala	Ser	Ala	Val	Thr	Ala	Ser	Thr	Gly
1				5					10					15	
Leu	Leu	Trp	Lys	Lys	Ala	His	Ala	Glu	Ser	Pro	Pro	Ser	Val	Asn	Ser
			20					25					30		
Lys	Lys	Thr	Asp	Ala	Gly	Asp	Lys	Gly	Lys	Ser	Lys	Asp	Thr	Arg	Glu
		35					40					45			
Val	Ser	Ser	His	Glu	Gly	Ser	Ala	Ala	Asp	Thr	Ala	Ala	Glu	Pro	Tyr
	50					55					60				
Pro	Glu	Glu	Lys	Lys	Lys	Lys	Arg	Ser	Gly	Phe	Arg	Asp	Arg	Lys	Val
65					70					75				80	
Met	Glu	Tyr	Glu	Asn	Arg	Ile	Arg	Ala	Tyr	Ser	Thr	Pro	Asp	Lys	Ile
				85					90					95	
Phe	Arg	Tyr	Phe	Ala	Thr	Leu	Lys	Val	Ile	Asn	Glu	Pro	Gly	Glu	Thr
			100					105					110		
Glu	Val	Phe	Met	Thr	Pro	Gln	Asp	Phe	Val	Arg	Ser	Ile	Thr	Pro	Asn
	115						120					125			
Glu	Lys	Gln	Pro	Glu	His	Leu	Gly	Leu	Asp	Gln	Tyr	Ile	Ile	Lys	Arg
	130					135					140				
Phe	Asp	Gly	Lys	Lys	Ile	Ala	Gln	Glu	Arg	Glu	Lys	Phe	Ala	Asp	Glu
145					150					155				160	
Gly	Ser	Ile	Phe	Tyr	Thr	Leu	Gly	Glu	Cys	Gly	Leu	Ile	Ser	Phe	Ser
			165					170						175	
Asp	Tyr	Ile	Phe	Leu	Thr	Thr	Val	Leu	Ser	Thr	Pro	Gln	Arg	Asn	Phe
			180					185					190		
Glu	Ile	Ala	Phe	Lys	Met	Phe	Asp	Leu	Asn	Gly	Asp	Gly	Glu	Val	Asp
	195						200					205			
Met	Glu	Glu	Phe	Glu	Gln	Val	Gln	Ser	Ile	Ile	Arg	Ser	Gln	Thr	Ser
	210					215					220				
Met	Gly	Met	Arg	His	Arg	Asp	Arg	Pro	Thr	Thr	Gly	Asn	Thr	Leu	Lys
225				230						235				240	
Ser	Gly	Leu	Cys	Ser	Ala	Leu	Thr	Thr	Tyr	Phe	Phe	Gly	Ala	Asp	Leu
			245						250					255	
Lys	Gly	Lys	Leu	Thr	Ile	Lys	Asn	Phe	Leu	Glu	Phe	Gln	Arg	Lys	Leu
		260					265						270		
Gln	His	Asp	Val	Leu	Lys	Leu	Glu	Phe	Glu	Arg	His	Asp	Pro	Val	Asp
	275						280					285			
Gly	Arg	Ile	Ser	Glu	Arg	Gln	Phe	Gly	Gly	Met	Leu	Leu	Ala	Tyr	Ser
	290					295					300				
Gly	Val	Gln	Ser	Lys	Lys	Leu	Thr	Ala	Met	Gln	Arg	Gln	Leu	Lys	Lys
305				310						315				320	
His	Phe	Lys	Asp	Gly	Lys	Gly	Leu	Thr	Phe	Gln	Glu	Val	Glu	Asn	Phe
			325						330					335	
Phe	Thr	Phe	Leu	Lys	Asn	Ile	Asn	Asp	Val	Asp	Thr	Ala	Leu	Ser	Phe
		340						345					350		
Tyr	His	Met	Ala	Gly	Ala	Ser	Leu	Asp	Lys	Val	Thr	Met	Gln	Gln	Val
	355						360					365			
Ala	Arg	Thr	Val	Ala	Lys	Val	Glu	Leu	Ser	Asp	His	Val	Cys	Asp	Val
	370					375					380				
Val	Phe	Ala	Leu	Phe	Asp	Cys	Asp	Gly	Asn	Gly	Glu	Leu	Ser	Asn	Lys
385				390						395				400	
Glu	Phe	Val	Ser	Ile	Met	Lys	Gln	Arg	Leu	Met	Arg	Gly	Leu	Glu	Lys
			405						410					415	
Pro	Lys	Asp	Met	Gly	Phe	Thr	Arg	Leu	Met	Gln	Ala	Met	Trp	Lys	Cys
			420					425					430		

Ala Gln Glu Thr Ala Trp Asp Phe Ala Leu Pro Lys
435 440

<210> 297
<211> 65
<212> PRT
<213> Human

<400> 297
Met Thr Met Leu His Leu Ala Val Ile Phe Leu Phe Ser Ala Leu Ser
1 5 10 15
Arg Ala Leu Val Gln Cys Ser Ser His Arg Ala Arg Val Val Leu Ser
20 25 30
Trp Ala Asp Tyr Leu Arg Arg Val Ala Pro Thr Ala Leu Ala Thr Ala
35 40 45
Leu Asp Val Gly Leu Ser Asn Trp Ser Phe Leu Tyr Val Thr Val Ser
50 55 60
Leu
65

<210> 298
<211> 52
<212> PRT
<213> Human

<400> 298
Met Lys Ile Asn Ile Ile Gln Gly Ser Ile Met Ile Leu Leu Ile Cys
1 5 10 15
Leu Ser Gln Thr Cys Thr Ser Leu Pro Val Gln Glu Ala Leu Ile Thr
20 25 30
Phe Cys His Leu Tyr Phe Thr Tyr Cys Tyr Ser Gly Asn Ser Asn Lys
35 40 45
Met Gln Val Leu
50

<210> 299
<211> 41
<212> PRT
<213> Human

<400> 299
Met Pro Cys Val Leu Phe Phe Phe Phe Phe Leu Ser Thr Ser Lys Ser
1 5 10 15
Met Ile Tyr Ser Ser Leu Met Leu Gly Leu Tyr Ile Pro Ser Glu Ala
20 25 30
Cys Val Leu Gly Leu Lys Phe Lys Phe
35 40

<210> 300
<211> 80
<212> PRT
<213> Mouse

<400> 300
Met Val Trp Gly Thr Leu Leu Gly Arg Val Leu Ala Ala Leu Leu Asn
1 5 10 15
Ile Val Pro Thr Glu Ser Ser Tyr Arg Ser Pro Ser Phe Leu Ala Gly

123

Val Val Glu Val Trp Ser Gln Leu Leu Ser Gln Lys His Val Gly Leu
 195 200 205
 Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu
 210 215 220
 Leu Val Ile Leu Val Ile Pro Pro Ala Val Thr Pro Gly Thr Asp Gln
 225 230 235 240
 Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Ile Leu
 245 250 255
 Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ser Gln Gln Pro
 260 265 270
 Gly Pro Asn Ala Pro Leu Ser Trp Ile Arg Ala Cys Val Gln Val Leu
 275 280 285
 Asp Pro Lys Ser Gln Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe
 290 295 300
 Tyr Gly Met Asp Tyr Ala Ala Ser Lys Asp Ala Arg Glu Pro Val Ile
 305 310 315 320
 Gly Ala Arg Ala Val Leu Lys Val Ala Leu Pro Leu Ala Val Ser Ser
 325 330 335
 Gln Gln Ile Trp Thr Leu Gly Arg Gly Gly Ser Thr Ser Ala Leu Leu
 340 345 350
 Leu Ala Gly Leu Gly Leu Ala Ser Glu Pro Cys Thr Lys Ser Glu Glu
 355 360 365
 Val Pro Lys Lys Ser Leu Leu Asp Thr Val Trp His Trp Gln Gly Glu
 370 375 380
 Pro Gly Ala Leu Cys Arg Gly Arg Leu His Thr Trp Ile Leu Val Ser
 385 390 395 400
 Ala Val Pro Gln Ala Cys Thr Cys Leu Phe Gln
 405 410

<210> 303
 <211> 617
 <212> PRT
 <213> Mouse

<400> 303

Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu Ser Leu Pro Leu Leu
 1 5 10 15
 Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala Cys Pro Cys Leu Arg
 20 25 30
 Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe
 35 40 45
 Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys
 50 55 60
 Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser
 65 70 75 80
 Phe Gln Arg Lys Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His
 85 90 95
 Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr
 100 105 110
 Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu
 115 120 125
 Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu
 130 135 140
 Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala
 145 150 155 160
 Ser Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser
 165 170 175

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Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp
      180      185      190
Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys Ile Glu Ala Ser Tyr
      195      200      205
Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser Trp
      210      215      220
Pro Glu Ala Tyr Gly Ser Asp Phe Trp Gln Ser Ile Arg Phe Thr Asp
      225      230      235      240
Tyr Ser Gln His Asn Gln Met Val Met Ala Leu Thr Leu Arg Cys Pro
      245      250      255
Leu Lys Leu Glu Ala Ser Leu Cys Trp Arg Gln Asp Pro Leu Thr Pro
      260      265      270
Cys Glu Thr Leu Pro Asn Ala Thr Ala Gln Glu Ser Glu Gly Trp Tyr
      275      280      285
Ile Leu Glu Asn Val Asp Leu His Pro Gln Leu Cys Phe Lys Phe Ser
      290      295      300
Phe Glu Asn Ser Ser His Val Glu Cys Pro His Gln Ser Gly Ser Leu
      305      310      315      320
Pro Ser Trp Thr Val Ser Met Asp Thr Gln Ala Gln Gln Leu Thr Leu
      325      330      335
His Phe Ser Ser Arg Thr Tyr Ala Thr Phe Ser Ala Ala Trp Ser Asp
      340      345      350
Pro Gly Leu Gly Pro Asp Thr Pro Met Pro Pro Val Tyr Ser Ile Ser
      355      360      365
Gln Thr Gln Gly Ser Val Pro Val Thr Leu Asp Leu Ile Ile Pro Phe
      370      375      380
Leu Arg Gln Glu Asn Cys Ile Leu Val Trp Arg Ser Asp Val His Phe
      385      390      395      400
Ala Trp Lys His Val Leu Cys Pro Asp Asp Ala Pro Tyr Pro Thr Gln
      405      410      415
Leu Leu Leu Arg Ser Leu Gly Ser Gly Arg Thr Arg Pro Val Leu Leu
      420      425      430
Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly Ala Leu
      435      440      445
Ala Glu Leu Leu Arg Thr Ala Leu Gly Gly Gly Arg Asp Val Ile Val
      450      455      460
Asp Leu Trp Glu Gly Thr His Val Ala Arg Ile Gly Pro Leu Pro Trp
      465      470      475      480
Leu Trp Ala Ala Arg Glu Arg Val Ala Arg Glu Gln Gly Thr Val Leu
      485      490      495
Leu Leu Trp Asn Cys Ala Gly Pro Ser Thr Ala Cys Ser Gly Asp Pro
      500      505      510
Gln Ala Ala Ser Leu Arg Thr Leu Leu Cys Ala Ala Pro Arg Pro Leu
      515      520      525
Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp Ile Pro Arg
      530      535      540
Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp Leu Pro Arg
      545      550      555      560
Leu Leu Arg Ala Leu Asp Ala Gln Pro Ala Thr Leu Ala Ser Ser Trp
      565      570      575
Ser His Leu Gly Ala Lys Arg Cys Leu Lys Asn Arg Leu Glu Gln Cys
      580      585      590
His Leu Leu Glu Leu Glu Ala Ala Lys Asp Asp Tyr Gln Gly Ser Thr
      595      600      605
Asn Ser Pro Cys Gly Phe Ser Cys Leu
      610      615

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<210> 304
 <211> 72
 <212> PRT
 <213> Mouse

<400> 304
 Met Ser Ala Ile Phe Asn Phe Gln Ser Leu Leu Thr Val Ile Leu Leu
 1 5 10 15
 Leu Ile Cys Thr Cys Ala Tyr Ile Arg Ser Leu Ala Pro Ser Ile Leu
 20 25 30
 Asp Arg Asn Lys Thr Gly Leu Leu Gly Ile Phe Trp Lys Cys Ala Arg
 35 40 45
 Ile Gly Glu Arg Lys Ser Pro Tyr Val Ala Ile Cys Cys Ile Val Met
 50 55 60
 Ala Phe Ser Ile Leu Phe Ile Gln
 65 70

<210> 305
 <211> 649
 <212> PRT
 <213> Mouse

<400> 305
 Met Ile Ser Pro Ala Trp Ser Leu Phe Leu Ile Gly Thr Lys Ile Gly
 1 5 10 15
 Leu Phe Phe Gln Val Ala Pro Leu Ser Val Val Ala Lys Ser Cys Pro
 20 25 30
 Ser Val Cys Arg Cys Asp Ala Gly Phe Ile Tyr Cys Asn Asp Arg Ser
 35 40 45
 Leu Thr Ser Ile Pro Val Gly Ile Pro Glu Asp Ala Thr Thr Leu Tyr
 50 55 60
 Leu Gln Asn Asn Gln Ile Asn Asn Val Gly Ile Pro Ser Asp Leu Lys
 65 70 75 80
 Asn Leu Leu Lys Val Gln Arg Ile Tyr Leu Tyr His Asn Ser Leu Asp
 85 90 95
 Glu Phe Pro Thr Asn Leu Pro Lys Tyr Val Lys Glu Leu His Leu Gln
 100 105 110
 Glu Asn Asn Ile Arg Thr Ile Thr Tyr Asp Ser Leu Ser Lys Ile Pro
 115 120 125
 Tyr Leu Glu Glu Leu His Leu Asp Asp Asn Ser Val Ser Ala Val Ser
 130 135 140
 Ile Glu Glu Gly Ala Phe Arg Asp Ser Asn Tyr Leu Arg Leu Leu Phe
 145 150 155 160
 Leu Ser Arg Asn His Leu Ser Thr Ile Pro Gly Gly Leu Pro Arg Thr
 165 170 175
 Ile Glu Glu Leu Arg Leu Asp Asp Asn Arg Ile Ser Thr Ile Ser Ser
 180 185 190
 Pro Ser Leu His Gly Leu Thr Ser Leu Lys Arg Leu Val Leu Asp Gly
 195 200 205
 Asn Leu Leu Asn Asn His Gly Leu Gly Asp Lys Val Phe Phe Asn Leu
 210 215 220
 Val Asn Leu Thr Glu Leu Ser Leu Val Arg Asn Ser Leu Thr Ala Ala
 225 230 235 240
 Pro Val Asn Leu Pro Gly Thr Ser Leu Arg Lys Leu Tyr Leu Gln Asp
 245 250 255
 Asn His Ile Asn Arg Val Pro Pro Asn Ala Phe Ser Tyr Leu Arg Gln
 260 265 270

Leu Tyr Arg Leu Asp Met Ser Asn Asn Asn Leu Ser Asn Leu Pro Gln
 275 280 285
 Gly Ile Phe Asp Asp Leu Asp Asn Ile Thr Gln Leu Ile Leu Arg Asn
 290 295 300
 Asn Pro Trp Tyr Cys Gly Cys Lys Met Lys Trp Val Arg Asp Trp Leu
 305 310 315 320
 Gln Ser Leu Pro Val Lys Val Asn Val Arg Gly Leu Met Cys Gln Ala
 325 330 335
 Pro Glu Lys Val Arg Gly Met Ala Ile Lys Asp Leu Ser Ala Glu Leu
 340 345 350
 Phe Asp Cys Lys Asp Ser Gly Ile Val Ser Thr Ile Gln Ile Thr Thr
 355 360 365
 Ala Ile Pro Asn Thr Ala Tyr Pro Ala Gln Gly Gln Trp Pro Ala Pro
 370 375 380
 Val Thr Lys Gln Pro Asp Ile Lys Asn Pro Lys Leu Ile Lys Asp Gln
 385 390 395 400
 Arg Thr Thr Gly Ser Pro Ser Arg Lys Thr Ile Leu Ile Thr Val Lys
 405 410 415
 Ser Val Thr Pro Asp Thr Ile His Ile Ser Trp Arg Leu Ala Leu Pro
 420 425 430
 Met Thr Ala Leu Arg Leu Ser Trp Leu Lys Leu Gly His Ser Pro Ala
 435 440 445
 Phe Gly Ser Ile Thr Glu Thr Ile Val Thr Gly Glu Arg Ser Glu Tyr
 450 455 460
 Leu Val Thr Ala Leu Glu Pro Glu Ser Pro Tyr Arg Val Cys Met Val
 465 470 475 480
 Pro Met Glu Thr Ser Asn Leu Tyr Leu Phe Asp Glu Thr Pro Val Cys
 485 490 495
 Ile Glu Thr Gln Thr Ala Pro Leu Arg Met Tyr Asn Pro Thr Thr Thr
 500 505 510
 Leu Asn Arg Glu Gln Glu Lys Glu Pro Tyr Lys Asn Pro Asn Leu Pro
 515 520 525
 Leu Ala Ala Ile Ile Gly Gly Ala Val Ala Leu Val Ser Ile Ala Leu
 530 535 540
 Leu Ala Leu Val Cys Trp Tyr Val His Arg Asn Gly Ser Leu Phe Ser
 545 550 555 560
 Arg Asn Cys Ala Tyr Ser Lys Gly Arg Arg Lys Asp Asp Tyr Ala
 565 570 575
 Glu Ala Gly Thr Lys Lys Asp Asn Ser Ile Leu Glu Ile Arg Glu Thr
 580 585 590
 Ser Phe Gln Met Leu Pro Ile Ser Asn Glu Pro Ile Ser Lys Glu Glu
 595 600 605
 Phe Val Ile His Thr Ile Phe Pro Pro Asn Gly Met Asn Leu Tyr Lys
 610 615 620
 Asn Asn Leu Ser Glu Ser Ser Ser Asn Arg Ser Tyr Arg Asp Ser Gly
 625 630 635 640
 Ile Pro Asp Ser Asp His Ser His Ser
 645

<210> 306

<211> 150

<212> PRT

<213> Rat

<400> 306

Met Ala Ala Pro Met Asp Arg Thr His Gly Gly Arg Ala Ala Arg Ala
 1 5 10 15

Leu Arg Arg Ala Leu Ala Leu Ala Ser Leu Ala Gly Leu Leu Leu Ser
 20 25 30
 Gly Leu Ala Gly Ala Leu Pro Thr Leu Gly Pro Gly Trp Arg Arg Gln
 35 40 45
 Asn Pro Glu Pro Pro Ala Ser Arg Thr Arg Ser Leu Leu Leu Asp Ala
 50 55 60
 Ala Ser Gly Gln Leu Arg Leu Glu Tyr Gly Phe His Pro Asp Ala Val
 65 70 75 80
 Ala Trp Ala Asn Leu Thr Asn Ala Ile Arg Glu Thr Gly Trp Ala Tyr
 85 90 95
 Leu Asp Leu Gly Thr Asn Gly Ser Tyr Lys Trp Ile Pro Arg Ala Ala
 100 105 110
 Gly Leu Cys Ser Trp Cys Gly Gly Leu Cys Val Arg Gly Ala His
 115 120 125
 Leu His Ala Leu Asp Glu His Gly Gly Gln Leu Leu Arg Pro Leu Arg
 130 135 140
 Val Arg Ser Arg Leu Leu
 145 150

<210> 307

<211> 580

<212> PRT

<213> Rat

<400> 307

Met Ala Ala Ala Met Pro Leu Gly Leu Ser Leu Leu Leu Leu Val Leu
 1 5 10 15
 Val Gly Gln Gly Cys Cys Gly Arg Val Glu Gly Pro Arg Asp Ser Leu
 20 25 30
 Arg Glu Glu Leu Val Ile Thr Pro Leu Pro Ser Gly Asp Val Ala Ala
 35 40 45
 Thr Phe Gln Phe Arg Thr Arg Trp Asp Ser Asp Leu Gln Arg Glu Gly
 50 55 60
 Val Ser His Tyr Arg Leu Phe Pro Lys Ala Leu Gly Gln Leu Ile Ser
 65 70 75 80
 Lys Tyr Ser Leu Arg Glu Leu His Leu Ser Phe Thr Gln Gly Phe Trp
 85 90 95
 Arg Thr Arg Tyr Trp Gly Pro Pro Phe Leu Gln Ala Pro Ser Gly Ala
 100 105 110
 Glu Leu Trp Val Trp Phe Gln Asp Thr Val Thr Asp Val Asp Lys Ser
 115 120 125
 Trp Lys Glu Leu Ser Asn Val Leu Ser Gly Ile Phe Cys Ala Ser Leu
 130 135 140
 Asn Phe Ile Asp Ser Thr Asn Thr Val Thr Pro Thr Ala Ser Phe Lys
 145 150 155 160
 Pro Leu Gly Leu Ala Asn Asp Thr Asp His Tyr Phe Leu Arg Tyr Ala
 165 170 175
 Val Leu Pro Arg Glu Val Val Cys Thr Glu Asn Leu Thr Pro Trp Lys
 180 185 190
 Lys Leu Leu Pro Cys Ser Ser Lys Ala Gly Leu Ser Val Leu Leu Lys
 195 200 205
 Ala Asp Arg Leu Phe His Thr Ser Tyr His Ser Gln Ala Val His Ile
 210 215 220
 Arg Pro Ile Cys Arg Asn Ala His Cys Thr Ser Ile Ser Trp Glu Leu
 225 230 235 240
 Arg Gln Thr Leu Ser Val Val Phe Asp Ala Phe Ile Thr Gly Gln Gly
 245 250 255

Lys Lys Asp Trp Ser Leu Phe Arg Met Phe Ser Arg Thr Leu Thr Glu
 260 265 270
 Ala Cys Pro Leu Ala Ser Gln Ser Leu Val Tyr Val Asp Ile Thr Gly
 275 280 285
 Tyr Ser Gln Asp Asn Glu Thr Leu Glu Val Ser Pro Pro Pro Thr Ser
 290 295 300
 Thr Tyr Gln Asp Val Ile Leu Gly Thr Arg Lys Thr Tyr Ala Val Tyr
 305 310 315 320
 Asp Leu Phe Asp Thr Ala Met Ile Asn Asn Ser Arg Asn Leu Asn Ile
 325 330 335
 Gln Leu Lys Trp Lys Arg Pro Pro Asp Asn Glu Ala Leu Pro Val Pro
 340 345 350
 Phe Leu His Ala Gln Arg Tyr Val Ser Gly Tyr Gly Leu Gln Lys Gly
 355 360 365
 Glu Leu Ser Thr Leu Leu Tyr Asn Ser His Pro Tyr Arg Ala Phe Pro
 370 375 380
 Val Leu Leu Leu Asp Ala Val Pro Trp Tyr Leu Arg Leu Tyr Val His
 385 390 395 400
 Thr Leu Thr Ile Thr Ser Lys Gly Lys Asp Asn Lys Pro Ser Tyr Ile
 405 410 415
 His Tyr Gln Pro Ala Gln Asp Arg Gln Gln Pro His Leu Leu Glu Met
 420 425 430
 Leu Ile Gln Leu Pro Ala Asn Ser Val Thr Lys Val Ser Ile Gln Phe
 435 440 445
 Glu Arg Ala Leu Leu Lys Trp Thr Glu Tyr Thr Pro Asp Pro Asn His
 450 455 460
 Gly Phe Tyr Val Ser Pro Ser Val Leu Ser Ala Leu Val Pro Ser Met
 465 470 475 480
 Val Ala Ala Lys Pro Val Asp Trp Glu Glu Ser Pro Leu Phe Asn Thr
 485 490 495
 Leu Phe Pro Val Ser Asp Gly Ser Ser Tyr Phe Val Arg Leu Tyr Thr
 500 505 510
 Glu Pro Leu Leu Val Asn Leu Pro Thr Pro Asp Phe Ser Met Pro Tyr
 515 520 525
 Asn Val Ile Cys Leu Thr Cys Thr Val Val Ala Val Cys Tyr Gly Ser
 530 535 540
 Phe Tyr Asn Leu Leu Thr Arg Thr Phe His Ile Glu Glu Pro Lys Ser
 545 550 555 560
 Gly Gly Leu Ala Lys Arg Leu Ala Asn Leu Ile Arg Arg Ala Arg Gly
 565 570 575
 Val Pro Pro Leu
 580

<210> 308

<211> 283

<212> PRT

<213> Rat

<400> 308

Met Thr Ser Gly Pro Gly Gly Pro Ala Ala Ala Thr Gly Gly Gly Lys
 1 5 10 15
 Asp Thr His Gln Trp Tyr Val Cys Asn Arg Glu Lys Leu Cys Glu Ser
 20 25 30
 Leu Gln Ser Val Phe Val Gln Ser Tyr Leu Asp Gln Gly Thr Gln Ile
 35 40 45
 Phe Leu Asn Asn Ser Ile Glu Lys Ser Gly Trp Leu Phe Ile Gln Leu
 50 55 60

Tyr His Ser Phe Val Ser Ser Val Phe Ser Leu Phe Met Ser Arg Thr
 65 70 75 80
 Ser Ile Asn Gly Leu Leu Gly Arg Gly Ser Met Phe Val Phe Ser Pro
 85 90 95
 Asp Gln Phe Gln Arg Leu Leu Lys Ile Asn Pro Asp Trp Lys Thr His
 100 105 110
 Arg Leu Leu Asp Leu Gly Ala Gly Asp Gly Glu Val Thr Lys Ile Met
 115 120 125
 Ser Pro His Phe Glu Glu Ile Tyr Ala Thr Glu Leu Ser Glu Thr Met
 130 135 140
 Ile Trp Gln Leu Gln Lys Lys Lys Tyr Arg Val Leu Gly Ile Asn Glu
 145 150 155 160
 Trp Gln Asn Thr Gly Phe Gln Tyr Asp Val Ile Ser Cys Leu Asn Leu
 165 170 175
 Leu Asp Arg Cys Asp Gln Pro Leu Thr Leu Leu Lys Asp Ile Arg Ser
 180 185 190
 Val Leu Glu Pro Thr Gln Gly Arg Val Ile Leu Ala Leu Val Leu Pro
 195 200 205
 Phe His Pro Tyr Val Glu Asn Val Gly Gly Lys Trp Glu Lys Pro Ser
 210 215 220
 Glu Ile Leu Glu Ile Lys Gly Gln Asn Trp Glu Glu Gln Val Asn Ser
 225 230 235 240
 Leu Pro Glu Val Phe Arg Lys Ala Gly Phe Val Ile Glu Ala Phe Thr
 245 250 255
 Arg Leu Pro Tyr Leu Cys Glu Gly Asp Met Tyr Asn Asp Tyr Tyr Val
 260 265 270
 Leu Asp Asp Ala Val Phe Val Leu Arg Pro Val
 275 280

<210> 309

<211> 37

<212> PRT

<213> Rat

<400> 309

Met Leu Trp Val Leu Leu Ser Leu Thr Pro Leu Leu Ser Pro Leu Ile
 1 5 10 15
 Phe Phe Pro Val Lys Thr Val Ala Leu Glu Glu Ile Ser Thr Ile Cys
 20 25 30
 Arg Ala Asp Val Leu
 35

<210> 310

<211> 70

<212> PRT

<213> Mouse

<400> 310

Met Ala Ala Ser Trp Gly Gln Val Leu Ala Leu Val Leu Val Ala Ala
 1 5 10 15
 Leu Trp Gly Gly Thr Gln Pro Leu Leu Lys Arg Ala Ser Ser Gly Leu
 20 25 30
 Glu Gln Val Arg Glu Arg Thr Trp Ala Trp Gln Leu Leu Gln Glu Ile
 35 40 45
 Lys Ala Leu Phe Gly Asn Thr Glu Val Arg Leu Ala Leu Thr Asp Glu
 50 55 60
 Pro Leu Lys Ile Ser Pro

65

70

<210> 311
 <211> 58
 <212> PRT
 <213> Human

<400> 311

Met Leu Leu Ser Ser Leu Val Ser Leu Ala Gly Ser Val Tyr Leu Ala
 1 5 10 15
 Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys Ile Thr
 20 25 30
 Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe Arg Lys Val
 35 40 45
 Gln Glu Pro Gln Gly Lys Ala Lys Arg His
 50 55

<210> 312
 <211> 52
 <212> PRT
 <213> Human

<400> 312

Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe Glu Lys
 1 5 10 15
 Leu Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile Asn Ser
 20 25 30
 Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn Ser Glu
 35 40 45
 Glu Lys Thr Lys
 50

<210> 313
 <211> 70
 <212> PRT
 <213> Human

<400> 313

Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly Leu Met Leu Lys
 1 5 10 15
 Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser Phe Ile Ser Phe
 20 25 30
 Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met Met Ser Ser Phe
 35 40 45
 Met Leu Ser Ile Ser Ala Val Val Met Ser Tyr Leu Gln Asn Pro Gln
 50 55 60
 Pro Met Thr Pro Pro Trp
 65 70

<210> 314
 <211> 58
 <212> PRT
 <213> Mouse

<400> 314

Met Phe Ile Thr Pro Phe Lys Ala Phe Leu Pro Leu Tyr Leu Leu Thr
 1 5 10 15

Glu Leu Ser Leu Ile Asp Ile Thr Ser Cys Asp Asp Leu Pro His Ser
 20 25 30
 Val Leu Pro Gln His Leu Ser Phe Glu Phe Val Leu Trp Ser Met Tyr
 35 40 45
 Leu Leu Ile Cys Cys Phe Val Ile Ile Phe
 50 55

<210> 315
 <211> 229
 <212> PRT
 <213> Rat

<400> 315
 Met Ala Ser Ala Leu Glu Glu Leu Gln Lys Asp Leu Glu Glu Val Lys
 1 5 10 15
 Val Leu Leu Glu Lys Ser Thr Arg Lys Arg Leu Arg Asp Thr Leu Thr
 20 25 30
 Asn Glu Lys Ser Lys Ile Glu Thr Glu Leu Arg Asn Lys Met Gln Gln
 35 40 45
 Lys Ser Gln Lys Lys Pro Glu Phe Asp Asn Glu Lys Pro Ala Ala Val
 50 55 60
 Val Ala Pro Leu Thr Thr Gly Tyr Thr Val Lys Ile Ser Asn Tyr Gly
 65 70 75 80
 Trp Asp Gln Ser Asp Lys Phe Val Lys Ile Tyr Ile Thr Leu Thr Gly
 85 90 95
 Val His Gln Val Pro Ala Glu Asn Val Gln Val His Phe Thr Glu Arg
 100 105 110
 Ser Phe Asp Leu Leu Val Lys Asn Leu Asn Gly Lys Asn Tyr Ser Met
 115 120 125
 Ile Val Asn Asn Leu Leu Lys Pro Ile Ser Val Glu Ser Ser Ser Lys
 130 135 140
 Lys Val Lys Thr Asp Thr Val Ile Ile Leu Cys Arg Lys Lys Ala Glu
 145 150 155 160
 Asn Thr Arg Trp Asp Tyr Leu Thr Gln Val Glu Lys Glu Cys Lys Glu
 165 170 175
 Lys Glu Lys Pro Ser Tyr Asp Thr Glu Ala Asp Pro Ser Glu Gly Leu
 180 185 190
 Met Asn Val Leu Lys Lys Ile Tyr Glu Asp Gly Asp Asp Met Lys
 195 200 205
 Arg Thr Ile Asn Lys Ala Trp Val Glu Ser Arg Glu Lys Gln Ala Arg
 210 215 220
 Glu Asp Thr Glu Phe
 225

<210> 316
 <211> 128
 <212> PRT
 <213> Rat

<400> 316
 Arg Ala Glu Phe Gly Thr Ser Gly Glu Met Gly Asn Ala Ala Leu Gly
 1 5 10 15
 Ala Glu Leu Gly Val Arg Val Leu Leu Phe Val Ala Phe Leu Ala Thr
 20 25 30
 Glu Leu Leu Pro Pro Phe Gln Arg Arg Ile Gln Pro Glu Glu Leu Trp
 35 40 45
 Leu Tyr Arg Asn Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Gly Pro

50 55 60
 Met Phe Val Ile Ala Phe Leu Thr Pro Leu Ser Leu Ile Phe Phe Ala
 65 70 75 80
 Lys Phe Leu Arg Lys Ala Asp Ala Thr Asp Ser Lys Gln Ala Cys Leu
 85 90 95
 Ala Ala Ser Leu Ala Leu Ala Leu Asn Gly Val Phe Thr Asn Ile Ile
 100 105 110
 Lys Leu Ile Val Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe
 115 120 125

<210> 317
 <211> 75
 <212> PRT
 <213> Rat

<400> 317
 Ser Ala Gly Val Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile
 1 5 10 15
 Ala Phe Gly Pro Ala Leu Ser Leu Tyr Val Phe Thr Ile Ala Thr Asp
 20 25 30
 Pro Leu Arg Val Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val
 35 40 45
 Ser Leu Leu Leu Ser Ser Val Phe Trp Phe Leu Val Arg Val Ile Thr
 50 55 60
 Asp Asn Arg Asp Gly Pro Val Gln Asn Tyr Leu
 65 70 75

<210> 318
 <211> 43
 <212> PRT
 <213> Human

<400> 318
 Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe Cys
 1 5 10 15
 Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys Gly Glu
 20 25 30
 Ser Arg Thr Pro Arg Pro Thr Ala Leu Gly Asn
 35 40

<210> 319
 <211> 86
 <212> PRT
 <213> Mouse

<400> 319
 Met Leu Gln Gly Pro Ala Pro Ser Cys Phe Trp Val Phe Ser Gly Ile
 1 5 10 15
 Cys Val Phe Trp Asp Phe Ile Phe Ile Ile Phe Phe Asn Val Leu Ser
 20 25 30
 Leu Gly Asn Arg Glu Ile Ser Ala Lys Asp Phe Ala Asp Gln Pro Ala
 35 40 45
 Gly Ala Gln Gly Met Trp Gly Ile Trp Gly His Thr Ile Thr Cys Gly
 50 55 60
 Leu Ala Pro Gly Ala Lys Pro Cys Ser Leu Lys Arg Glu Gly Pro Asp
 65 70 75 80
 Leu Leu Ser Phe Pro Pro

85

<210> 320
 <211> 60
 <212> PRT
 <213> Mouse

<400> 320
 Lys Gly Pro Glu Val Ser Cys Cys Ile Lys Tyr Phe Ile Phe Gly Phe
 1 5 10 15
 Asn Val Ile Phe Trp Phe Leu Gly Ile Thr Phe Leu Gly Ile Gly Leu
 20 25 30
 Trp Ala Trp Asn Glu Lys Gly Val Leu Ser Asn Ile Ser Ser Ile Thr
 35 40 45
 Asp Leu Gly Gly Phe Asp Pro Val Trp Leu Phe Leu
 50 55 60

<210> 321
 <211> 160
 <212> PRT
 <213> Mouse

<400> 321
 Ile Arg His Glu Ala Glu Ala Gly Arg His Gln Pro Glu Gln Leu Ala
 1 5 10 15
 Ala Asp Ser Arg Thr Glu Thr Val Gly Pro Arg Gln Ser Asn Gly Leu
 20 25 30
 Thr Gly Pro Gly Leu Pro Thr Trp Gln Leu His Pro Val Leu Phe Pro
 35 40 45
 Glu Leu Val Leu Trp Val Asn Met Val Pro Cys Phe Leu Leu Ser Leu
 50 55 60
 Leu Leu Leu Val Arg Pro Ala Pro Val Val Ala Tyr Ser Val Ser Leu
 65 70 75 80
 Pro Ala Ser Phe Leu Glu Glu Val Ala Gly Ser Gly Glu Ala Glu Gly
 85 90 95
 Ser Ser Ala Ser Ser Pro Ser Leu Leu Pro Pro Arg Thr Pro Ala Phe
 100 105 110
 Ser Pro Thr Pro Gly Arg Thr Gln Pro Thr Ala Pro Val Gly Pro Val
 115 120 125
 Pro Pro Thr Asn Leu Leu Asp Gly Ile Val Asp Phe Phe Arg Gln Tyr
 130 135 140
 Val Met Leu Ile Ala Val Val Gly Ser Leu Thr Phe Leu Ile Ser Ser
 145 150 155 160

<210> 322
 <211> 54
 <212> PRT
 <213> Mouse

<400> 322
 Arg Leu Gln Val Asp Thr Ser Gly Ser Lys Val Leu Phe Leu Phe Phe
 1 5 10 15
 Phe Phe Phe Leu Cys Val Cys Val Leu Val Cys Cys Cys Phe Gly Phe
 20 25 30
 Pro Gly Thr His Ser Val Asp Gln Ala Ser Pro Lys Leu Arg Asn Leu
 35 40 45
 Pro Pro Glu Cys Trp Asp

50

<210> 323
 <211> 280
 <212> PRT
 <213> Mouse

<400> 323
 Leu Asp Ser Arg Ala Cys Arg Ser Thr Leu Val Asp Pro Lys Asn Ser
 1 5 10 15
 Ala Arg Glu Asn Ile Arg Glu Tyr Val Arg Trp Met Met Tyr Trp Ile
 20 25 30
 Val Phe Ala Ile Phe Met Ala Ala Glu Thr Phe Thr Asp Ile Phe Ile
 35 40 45
 Ser Trp Ser Gly Pro Arg Ile Gly Arg Pro Trp Gly Trp Glu Gly Pro
 50 55 60
 His His His His His Leu Ala Ser Gly Ser His Lys Pro Leu Pro Leu
 65 70 75 80
 Leu Thr His Arg Phe Pro Phe Tyr Tyr Glu Phe Lys Met Ala Phe Val
 85 90 95
 Leu Trp Leu Leu Ser Pro Tyr Thr Lys Gly Ala Ser Leu Leu Tyr Arg
 100 105 110
 Lys Phe Val His Pro Ser Leu Ser Arg His Glu Lys Glu Ile Asp Ala
 115 120 125
 Cys Ile Val Gln Ala Lys Glu Arg Ser Tyr Glu Thr Met Leu Ser Phe
 130 135 140
 Gly Lys Arg Ser Leu Asn Ile Ala Ala Ser Ala Ala Val Gln Ala Ala
 145 150 155 160
 Thr Lys Ser Gln Gly Ala Leu Ala Gly Arg Leu Arg Ser Phe Ser Met
 165 170 175
 Gln Asp Leu Arg Ser Ile Pro Asp Thr Pro Val Pro Thr Tyr Gln Asp
 180 185 190
 Pro Leu Tyr Leu Glu Asp Gln Val Pro Arg Arg Arg Pro Pro Ile Gly
 195 200 205
 Tyr Arg Pro Gly Gly Leu Gln Gly Ser Asp Thr Glu Asp Glu Cys Trp
 210 215 220
 Ser Asp Asn Glu Ile Val Pro Gln Pro Pro Val Gly Pro Arg Glu Lys
 225 230 235 240
 Pro Leu Gly Arg Ser Gln Ser Leu Arg Val Val Lys Arg Lys Pro Leu
 245 250 255
 Thr Arg Glu Gly Thr Ser Arg Ser Leu Lys Val Arg Thr Pro Lys Lys
 260 265 270
 Ala Met Pro Ser Asp Met Asp Ser
 275 280

<210> 324
 <211> 166
 <212> PRT
 <213> Rat

<400> 324
 Ala Leu Arg Arg Val Gly Met Glu Leu Pro Ala Val Asn Leu Lys Val
 1 5 10 15
 Ile Leu Leu Val His Trp Leu Leu Thr Thr Trp Gly Cys Leu Ala Phe
 20 25 30
 Ser Gly Ser Tyr Ala Trp Gly Asn Phe Thr Ile Leu Ala Leu Gly Val
 35 40 45

Trp Ala Val Ala Gln Arg Asp Ser Val Asp Ala Ile Gly Met Phe Leu
 50 55 60
 Gly Gly Leu Val Ala Thr Ile Phe Leu Asp Ile Ile Tyr Ile Ser Ile
 65 70 75 80
 Phe Tyr Ser Ser Val Ala Val Gly Asp Thr Gly Arg Phe Ser Ala Gly
 85 90 95
 Met Ala Ile Phe Ser Leu Leu Leu Lys Pro Phe Ser Cys Cys Leu Val
 100 105 110
 Tyr His Met His Arg Glu Arg Gly Gly Glu Leu Pro Leu Arg Ser Asp
 115 120 125
 Phe Phe Gly Pro Ser Gln Glu His Ser Ala Tyr Gln Thr Ile Asp Ser
 130 135 140
 Ser Asp Ser Pro Ala Asp Pro Leu Ala Ser Leu Glu Asn Lys Gly Gln
 145 150 155 160
 Ala Ala Pro Arg Gly Tyr
 165

<210> 325

<211> 338

<212> PRT

<213> Rat

<400> 325

Ile Arg His Glu Ala Glu Ala Gly Arg His Gln Pro Glu Gln Leu Ala
 1 5 10 15
 Ala Asp Ser Arg Thr Glu Thr Val Gly Pro Arg Gln Ser Asn Gly Leu
 20 25 30
 Thr Gly Pro Gly Leu Pro Thr Trp Gln Leu His Pro Val Leu Phe Pro
 35 40 45
 Glu Leu Val Leu Trp Val Asn Met Val Pro Cys Phe Leu Leu Ser Leu
 50 55 60
 Leu Leu Leu Val Arg Pro Ala Pro Val Val Ala Tyr Ser Val Ser Leu
 65 70 75 80
 Pro Ala Ser Phe Leu Glu Glu Val Ala Gly Ser Gly Glu Ala Glu Gly
 85 90 95
 Ser Ser Ala Ser Ser Pro Ser Leu Leu Pro Pro Arg Thr Pro Ala Phe
 100 105 110
 Ser Pro Thr Pro Gly Arg Thr Gln Pro Thr Ala Pro Val Gly Pro Val
 115 120 125
 Pro Pro Thr Asn Leu Leu Asp Gly Ile Val Asp Phe Phe Arg Gln Tyr
 130 135 140
 Val Met Leu Ile Ala Val Val Gly Ser Leu Thr Phe Leu Ile Met Phe
 145 150 155 160
 Ile Val Cys Ala Ala Leu Ile Thr Arg Gln Lys His Lys Ala Thr Ala
 165 170 175
 Tyr Tyr Pro Ser Ser Phe Pro Glu Lys Lys Tyr Val Asp Gln Arg Asp
 180 185 190
 Arg Ala Gly Gly Pro His Ala Phe Ser Glu Val Pro Asp Arg Ala Pro
 195 200 205
 Asp Ser Arg Gln Glu Glu Gly Leu Asp Ser Ser Gln Gln Leu Gln Ala
 210 215 220
 Asp Ile Leu Ala Ala Thr Gln Asn Leu Arg Ser Pro Ala Arg Ala Leu
 225 230 235 240
 Pro Gly Ser Gly Glu Gly Thr Lys Gln Val Lys Gly Gly Ser Glu Glu
 245 250 255
 Glu Glu Glu Lys Glu Glu Glu Val Phe Ser Gly Gln Glu Glu Pro Arg
 260 265 270

Glu Ala Pro Val Cys Gly Val Thr Glu Glu Lys Pro Glu Val Pro Asp
 275 280 285
 Glu Thr Ala Ser Ala Glu Ala Glu Gly Val Pro Ala Ala Ser Glu Gly
 290 295 300
 Gln Gly Glu Pro Glu Gly Ser Phe Ser Leu Ala Gln Glu Pro Gln Gly
 305 310 315 320
 Ala Ala Gly Pro Ser Glu Arg Ser Cys Ala Cys Asn Arg Ile Ser Pro
 325 330 335
 Asn Val

<210> 326
 <211> 347
 <212> PRT
 <213> Human

<400> 326
 Ala Trp Ser Arg Pro Arg Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala
 1 5 10 15
 Trp Gly Ile Val Leu Glu Thr Val Ala Thr Ala Gly Val Val Thr Ser
 20 25 30
 Val Ala Phe Met Leu Thr Leu Pro Ile Leu Val Cys Lys Val Gln Asp
 35 40 45
 Ser Asn Arg Arg Lys Met Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly
 50 55 60
 Val Leu Gly Ile Phe Gly Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp
 65 70 75 80
 Gly Ser Thr Gly Pro Thr Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser
 85 90 95
 Ile Cys Phe Ser Cys Leu Leu Ala His Ala Val Ser Leu Thr Lys Leu
 100 105 110
 Val Arg Gly Arg Lys Pro Leu Ser Leu Leu Val Ile Leu Gly Leu Ala
 115 120 125
 Val Gly Phe Ser Leu Val Gln Asp Val Ile Ala Ile Glu Tyr Ile Val
 130 135 140
 Leu Thr Met Asn Arg Thr Asn Val Asn Val Phe Ser Glu Leu Ser Ala
 145 150 155 160
 Pro Arg Arg Asn Glu Asp Phe Val Leu Leu Thr Tyr Val Leu Phe
 165 170 175
 Leu Met Ala Leu Thr Phe Leu Met Ser Ser Phe Thr Phe Cys Gly Ser
 180 185 190
 Phe Thr Gly Trp Lys Arg His Gly Ala His Ile Tyr Leu Thr Met Leu
 195 200 205
 Leu Ser Ile Ala Ile Trp Val Ala Trp Ile Thr Leu Leu Met Leu Pro
 210 215 220
 Asp Phe Asp Arg Arg Trp Asp Asp Thr Ile Leu Ser Ser Ala Leu Ala
 225 230 235 240
 Ala Asn Gly Trp Val Phe Leu Leu Ala Tyr Val Ser Pro Glu Phe Trp
 245 250 255
 Leu Leu Thr Lys Gln Arg Asn Pro Met Asp Tyr Pro Val Glu Asp Ala
 260 265 270
 Phe Cys Lys Pro Gln Leu Val Lys Lys Ser Tyr Gly Val Glu Asn Arg
 275 280 285
 Ala Tyr Ser Gln Glu Glu Ile Thr Gln Gly Phe Glu Glu Thr Gly Asp
 290 295 300
 Thr Leu Tyr Ala Pro Tyr Ser Thr His Phe Gln Leu Gln Asn Gln Pro
 305 310 315 320

Pro Gln Lys Glu Phe Ser Ile Pro Arg Ala His Ala Trp Pro Ser Pro
 325 330 335
 Tyr Lys Asp Tyr Glu Val Lys Lys Glu Gly Ser
 340 345

<210> 327
 <211> 141
 <212> PRT
 <213> Human

<400> 327
 Lys Asn Ser Lys Cys Leu Leu Phe Trp Cys Arg Lys Ile Val Gly Asn
 1 5 10 15
 Arg Gln Glu Pro Met Trp Glu Phe Asn Phe Lys Phe Lys Lys Gln Ser
 20 25 30
 Pro Arg Leu Lys Ser Lys Cys Thr Gly Gly Leu Gln Pro Val Gln
 35 40 45
 Tyr Glu Asp Val His Thr Asn Pro Asp Gln Asp Cys Cys Leu Leu Gln
 50 55 60
 Val Thr Thr Leu Asn Phe Ile Phe Ile Pro Ile Val Met Gly Met Ile
 65 70 75 80
 Phe Thr Leu Phe Thr Ile Asn Val Ser Thr Asp Met Arg His His Arg
 85 90 95
 Val Arg Leu Val Phe Gln Asp Ser Pro Val His Gly Gly Arg Lys Leu
 100 105 110
 Arg Ser Glu Gln Gly Val Gln Val Ile Leu Asp Gln Cys Thr Ala Phe
 115 120 125
 Gly Ser Leu Thr Gly Gly Ile Leu Ser Thr His Ser Pro
 130 135 140

<210> 328
 <211> 71
 <212> PRT
 <213> Human

<400> 328
 Arg Glu Arg Thr Ser Leu Glu Phe Phe Val Phe Leu Phe Leu Phe Ile
 1 5 10 15
 Cys Cys Cys Leu His Ser Gly Gly Leu Gly Gly Val Pro Leu Pro Pro
 20 25 30
 Phe Pro Pro Gln Ala Gln Arg Gly Glu Gly Pro Gly Lys Trp Met Ser
 35 40 45
 Pro Pro Leu Pro Pro His Pro Val Val Ala Pro Pro Thr Pro Ser Pro
 50 55 60
 Ser Arg Gly Cys Val Leu Leu
 65 70

<210> 329
 <211> 109
 <212> PRT
 <213> Human

<400> 329
 Asp Gly Pro Ser Pro Lys Leu Ala Leu Trp Leu Pro Ser Pro Ala Pro
 1 5 10 15
 Thr Ala Ala Pro Thr Ala Leu Gly Glu Ala Gly Leu Ala Glu His Ser
 20 25 30

Gln Arg Asp Asp Arg Trp Leu Leu Val Ala Leu Leu Val Pro Thr Cys
 35 40 45
 Val Phe Leu Val Val Leu Leu Ala Leu Gly Ile Val Tyr Cys Thr Arg
 50 55 60
 Cys Gly Pro His Ala Pro Asn Lys Arg Ile Thr Asp Cys Tyr Arg Trp
 65 70 75 80
 Val Ile His Ala Gly Ser Lys Ser Pro Thr Glu Pro Met Pro Pro Arg
 85 90 95
 Gly Ser Leu Thr Gly Val Gln Thr Cys Arg Thr Ser Val
 100 105

<210> 330
 <211> 155
 <212> PRT
 <213> Human

<400> 330
 Ser Val Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu
 1 5 10 15
 Ala Ala Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu
 20 25 30
 Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys
 35 40 45
 Arg Pro Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu
 50 55 60
 Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys
 65 70 75 80
 Asp Pro Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly
 85 90 95
 Val Ser Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro
 100 105 110
 Asp Tyr Arg Met Lys Glu Trp Ser Arg Arg Glu Ala Glu Arg Leu Val
 115 120 125
 Lys Tyr Arg Glu Ala Asn Gly Leu Pro Ile Met Glu Ser Asn Cys Phe
 130 135 140
 Asp Pro Ser Lys Ile Gln Leu Pro Glu Asp Glu
 145 150 155

<210> 331
 <211> 299
 <212> PRT
 <213> Human

<400> 331
 Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
 1 5 10 15
 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
 20 25 30
 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
 35 40 45
 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
 50 55 60
 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
 65 70 75 80
 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
 85 90 95
 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser

Ala	Arg	Ala	Gly	Ala	Cys	Tyr	Cys	Pro	Ala	Gly	Phe	Leu	Gly	Ala	Asp
1				5					10					15	
Cys	Ser	Leu	Ala	Cys	Pro	Gln	Gly	Arg	Phe	Gly	Pro	Ser	Cys	Ala	His
		20						25					30		
Val	Cys	Thr	Cys	Gly	Gln	Gly	Ala	Ala	Cys	Asp	Pro	Val	Ser	Gly	Thr
		35					40					45			
Cys	Ile	Cys	Pro	Pro	Gly	Lys	Thr	Gly	Gly	His	Cys	Glu	Arg	Gly	Cys
	50					55					60				
Pro	Gln	Asp	Arg	Phe	Gly	Lys	Gly	Cys	Glu	His	Lys	Cys	Ala	Cys	Arg
65					70					75					80
Asn	Gly	Gly	Leu	Cys	His	Ala	Thr	Asn	Gly	Ser	Cys	Ser	Cys	Pro	Leu
				85					90					95	
Gly	Trp	Met	Gly	Pro	His	Cys	Glu	His	Ala	Cys	Pro	Ala	Gly	Arg	Tyr
			100					105					110		
Gly	Ala	Ala	Cys	Leu	Leu	Glu	Cys	Ser	Cys	Gln	Asn	Asn	Gly	Ser	Cys
		115					120					125			
Glu	Pro	Thr	Ser	Gly	Ala	Cys	Leu	Cys	Gly	Pro	Gly	Phe	Tyr	Gly	Gln
	130					135					140				
Ala	Cys	Glu	Asp	Thr	Cys	Pro	Ala	Gly	Phe	His	Gly	Ser	Gly	Cys	Gln
145					150					155					160
Arg	Val	Cys	Glu	Cys	Gln	Gln	Gly	Ala	Pro	Cys	Asp	Pro	Val	Ser	Gly
				165					170					175	
Arg	Cys	Leu	Cys	Pro	Ala	Gly	Phe	Arg	Gly	Gln	Phe	Cys	Glu	Arg	Gly
			180					185					190		
Cys	Lys	Pro	Gly	Phe	Phe	Gly	Asp	Gly	Cys	Leu	Gln	Gln	Cys	Asn	Cys

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      195      200      205
Pro Thr Gly Val Pro Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro
  210      215      220
Pro Gly Arg Ala Gly Thr Cys Asp Leu Asp Cys Arg Arg Gly Arg
  225      230      235      240
Phe Gly Pro Gly Cys Ala Leu Arg Cys Asp Cys Gly Gly Gly Ala Asp
      245      250      255
Cys Asp Pro Ile Ser Gly Gln Cys His Cys Val Asp Ser Tyr Thr Gly
      260      265      270
Pro Thr Cys Arg Glu Val Pro Thr Gln Leu Ser Ser Ile Arg Pro Ala
      275      280      285
Pro Gln His Ser Ser Ser Lys Ala Met Lys His
  290      295

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<210> 333
<211> 109
<212> PRT
<213> Mouse

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<400> 333
Gly Thr Arg Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His
  1      5      10      15
Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu
      20      25      30
Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met
      35      40      45
Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro
      50      55      60
Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Ile
      65      70      75      80
Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Ile Ala Tyr Val Tyr
      85      90      95
Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Thr
      100      105

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<210> 334
<211> 787
<212> PRT
<213> Mouse

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<400> 334
Lys Val Glu Gly Glu Gly Arg Gly Arg Trp Ala Leu Gly Leu Leu Arg
  1      5      10      15
Thr Phe Asp Ala Gly Glu Phe Ala Gly Trp Glu Lys Val Gly Ser Gly
      20      25      30
Gly Phe Gly Gln Val Tyr Lys Val Arg His Val His Trp Lys Thr Trp
      35      40      45
Leu Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Asp Arg Glu Arg
      50      55      60
Met Glu Leu Leu Glu Glu Ala Lys Lys Met Glu Met Ala Lys Phe Arg
      65      70      75      80
Tyr Ile Leu Pro Val Tyr Gly Ile Cys Gln Glu Pro Val Gly Leu Val
      85      90      95
Met Glu Tyr Met Glu Thr Gly Ser Leu Glu Lys Leu Leu Ala Ser Glu
      100      105      110
Pro Leu Pro Trp Asp Leu Arg Phe Arg Ile Val His Glu Thr Ala Val
      115      120      125

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Gly Met Asn Phe Leu His Cys Met Ser Pro Pro Leu Leu His Leu Asp
 130 135 140
 Leu Lys Pro Ala Asn Ile Leu Leu Asp Ala His Tyr His Val Lys Ile
 145 150 155 160
 Ser Asp Phe Gly Leu Ala Lys Cys Asn Gly Met Ser His Ser His Asp
 165 170 175
 Leu Ser Met Asp Gly Leu Phe Gly Thr Ile Ala Tyr Leu Pro Pro Glu
 180 185 190
 Arg Ile Arg Glu Lys Ser Arg Leu Phe Asp Thr Lys His Asp Val Tyr
 195 200 205
 Ser Phe Ala Ile Val Ile Trp Gly Val Leu Thr Gln Lys Lys Pro Phe
 210 215 220
 Ala Asp Glu Lys Asn Ile Leu His Ile Met Met Lys Val Val Lys Gly
 225 230 235 240
 His Arg Pro Glu Leu Pro Pro Ile Cys Arg Pro Arg Pro Arg Ala Cys
 245 250 255
 Ala Ser Leu Ile Gly Leu Met Gln Arg Cys Trp His Ala Asp Pro Gln
 260 265 270
 Val Arg Pro Thr Phe Gln Glu Ile Thr Ser Glu Thr Glu Asp Leu Cys
 275 280 285
 Glu Lys Pro Asp Glu Glu Val Lys Asp Leu Ala His Glu Pro Gly Glu
 290 295 300
 Lys Ser Ser Leu Glu Ser Lys Ser Glu Ala Arg Pro Glu Ser Ser Arg
 305 310 315 320
 Leu Lys Arg Ala Ser Ala Pro Pro Phe Asp Asn Asp Cys Ser Leu Ser
 325 330 335
 Glu Leu Leu Ser Gln Leu Asp Ser Gly Ile Ser Gln Thr Leu Glu Gly
 340 345 350
 Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Cys Lys Leu Pro Ser Ser
 355 360 365
 Ser Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val Asp Ser Ala Phe
 370 375 380
 Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg Glu Ala Ser Thr
 385 390 395 400
 Gly Asp Leu Gly Pro Thr Asp Ile Gln Lys Lys Lys Leu Val Asp Ala
 405 410 415
 Ile Ile Ser Gly Asp Thr Ser Arg Leu Met Lys Ile Leu Gln Pro Gln
 420 425 430
 Asp Val Asp Leu Val Leu Asp Ser Ser Ala Ser Leu Leu His Leu Ala
 435 440 445
 Val Glu Ala Gly Gln Glu Glu Cys Val Lys Trp Leu Leu Leu Asn Asn
 450 455 460
 Ala Asn Pro Asn Leu Thr Asn Arg Lys Gly Ser Thr Pro Leu His Met
 465 470 475 480
 Ala Val Glu Arg Lys Gly Arg Gly Ile Val Glu Leu Leu Leu Ala Arg
 485 490 495
 Lys Thr Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr Ala Leu His
 500 505 510
 Phe Ala Ala Gln Asn Gly Asp Glu Ala Ser Thr Arg Leu Leu Leu Glu
 515 520 525
 Lys Asn Ala Ser Val Asn Glu Val Asp Phe Glu Gly Arg Thr Pro Met
 530 535 540
 His Val Ala Cys Gln His Gly Gln Glu Asn Ile Val Arg Thr Leu Leu
 545 550 555 560
 Arg Arg Gly Val Asp Val Gly Leu Gln Gly Lys Asp Ala Trp Leu Pro
 565 570 575
 Leu His Tyr Ala Ala Trp Gln Gly His Leu Pro Ile Val Lys Leu Leu

580 585 590
 Ala Lys Gln Pro Gly Val Ser Val Asn Ala Gln Thr Leu Asp Gly Arg
 595 600 605
 Thr Pro Leu His Leu Ala Ala Gln Arg Gly His Tyr Arg Val Ala Arg
 610 615 620
 Ile Leu Ile Asp Leu Cys Ser Asp Val Asn Ile Cys Ser Leu Gln Ala
 625 630 635 640
 Gln Thr Pro Leu His Val Ala Ala Glu Thr Gly His Thr Ser Thr Ala
 645 650 655
 Arg Leu Leu Leu His Arg Gly Ala Gly Lys Glu Ala Leu Thr Ser Glu
 660 665 670
 Gly Tyr Thr Ala Leu His Leu Ala Ala Gln Asn Gly His Leu Ala Thr
 675 680 685
 Val Lys Leu Leu Ile Glu Glu Lys Ala Asp Val Met Ala Arg Gly Pro
 690 695 700
 Leu Asn Gln Thr Ala Leu His Leu Ala Ala Arg Gly His Ser Glu
 705 710 715 720
 Val Val Glu Glu Leu Val Ser Ala Asp Leu Ile Asp Leu Ser Asp Glu
 725 730 735
 Gln Gly Leu Ser Ala Leu His Leu Ala Ala Gln Gly Arg His Ser Gln
 740 745 750
 Thr Val Glu Thr Leu Leu Lys His Gly Ala His Ile Asn Leu Gln Ser
 755 760 765
 Leu Lys Phe Gln Gly Gly Gln Ser Ser Ala Ala Thr Leu Leu Arg Arg
 770 775 780
 Ser Lys Thr
 785

<210> 335
 <211> 194
 <212> PRT
 <213> Mouse

<400> 335
 Pro Gly Cys Lys Ser Cys Thr Val Cys Arg His Gly Leu Cys Arg Ser
 1 5 10 15
 Val Glu Lys Asp Ser Val Val Cys Glu Cys His Pro Gly Trp Thr Gly
 20 25 30
 Pro Leu Cys Asp Gln Glu Ala Arg Asp Pro Cys Leu Gly His Ser Cys
 35 40 45
 Arg His Gly Thr Cys Met Ala Thr Gly Asp Ser Tyr Val Cys Lys Cys
 50 55 60
 Ala Glu Gly Tyr Gly Gly Ala Leu Cys Asp Gln Lys Asn Asp Ser Ala
 65 70 75 80
 Ser Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
 85 90 95
 Asp Arg Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly His
 100 105 110
 His Cys Glu Gln Glu Asn Pro Cys Met Gly Glu Ile Val Arg Glu Ala
 115 120 125
 Ile Arg Arg Gln Lys Asp Tyr Ala Ser Cys Ala Thr Ala Ser Lys Val
 130 135 140
 Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Thr Thr Cys Cys Gln Pro
 145 150 155 160
 Ile Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln Cys Thr Asp Gly Ser
 165 170 175
 Ser Phe Val Glu Glu Val Glu Arg His Leu Glu Cys Gly Cys Arg Ala

Cys Ser 180 185 190
 <210> 336
 <211> 274
 <212> PRT
 <213> Human
 <400> 336
 Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu Pro Gly Ser Phe Arg
 1 5 10 15
 Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro Asn Asn Arg Ser Cys
 20 25 30
 Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro Cys Glu Gln Arg Cys
 35 40 45
 Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys His Gln Gly Tyr Glu
 50 55 60
 Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile Asp Glu Cys Ser Tyr
 65 70 75 80
 Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn Glu Pro Gly Arg Phe
 85 90 95
 Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu Ala Thr Arg Leu Cys
 100 105 110
 Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His Gln Cys Ser Glu Ala
 115 120 125
 Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg Cys Val Asp Thr Asn
 130 135 140
 Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu Asn Arg Cys Leu Cys
 145 150 155 160
 Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro Ser Ser Ile Val His
 165 170 175
 Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val Pro Ala Asp Val Phe
 180 185 190
 Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala Tyr Asn Ala Phe Gln
 195 200 205
 Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr Ile Arg Gln Ile Asn
 210 215 220
 Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro Val Thr Gly Pro Arg
 225 230 235 240
 Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met Asn Ser Leu Met Ser
 245 250 255
 Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val Phe Val Gly Ala Tyr
 260 265 270
 Thr Phe

<210> 337
 <211> 316
 <212> PRT
 <213> Mouse

<400> 337
 His Glu Glu Glu Pro Cys Asn Asn Gly Ser Glu Ile Leu Ala Tyr Asn
 1 5 10 15
 Ile Asp Leu Gly Asp Ser Cys Ile Thr Val Gly Asn Thr Thr Thr His
 20 25 30

Val Met Lys Asn Leu Leu Pro Glu Thr Thr Tyr Arg Ile Arg Ile Gln
 35 40 45
 Ala Ile Asn Glu Ile Gly Val Gly Pro Phe Ser Gln Phe Ile Lys Ala
 50 55 60
 Lys Thr Arg Pro Leu Pro Pro Ser Pro Pro Arg Leu Glu Cys Ala Ala
 65 70 75 80
 Ser Gly Pro Gln Ser Leu Lys Leu Lys Trp Gly Asp Ser Asn Ser Lys
 85 90 95
 Thr His Ala Ala Gly Asp Met Val Tyr Thr Leu Gln Leu Glu Asp Arg
 100 105 110
 Asn Lys Arg Phe Ile Ser Ile Tyr Arg Gly Pro Ser His Thr Tyr Lys
 115 120 125
 Val Gln Arg Leu Thr Glu Phe Thr Cys Tyr Ser Phe Arg Ile Gln Ala
 130 135 140
 Met Ser Glu Ala Gly Glu Gly Pro Tyr Ser Glu Thr Tyr Thr Phe Ser
 145 150 155 160
 Thr Thr Lys Ser Val Pro Pro Thr Leu Lys Ala Pro Arg Val Thr Gln
 165 170 175
 Leu Glu Gly Asn Ser Cys Glu Ile Phe Trp Glu Thr Val Pro Pro Met
 180 185 190
 Arg Gly Asp Pro Val Ser Tyr Val Leu Gln Val Leu Val Gly Arg Asp
 195 200 205
 Ser Glu Tyr Lys Gln Val Tyr Lys Gly Glu Glu Ala Thr Phe Gln Ile
 210 215 220
 Ser Gly Leu Gln Ser Asn Thr Asp Tyr Arg Phe Arg Val Cys Ala Cys
 225 230 235 240
 Arg Arg Cys Val Asp Thr Ser Gln Glu Leu Ser Gly Ala Phe Ser Pro
 245 250 255
 Ser Ala Ala Phe Met Leu Gln Gln Arg Glu Val Met Leu Thr Gly Asp
 260 265 270
 Leu Gly Gly Met Glu Glu Ala Lys Met Lys Gly Met Met Pro Thr Asp
 275 280 285
 Glu Gln Phe Ala Ala Leu Ile Val Leu Gly Phe Ala Thr Leu Ser Ile
 290 295 300
 Leu Phe Ala Phe Ile Leu Gln Tyr Phe Leu Met Lys
 305 310 315

<210> 338
 <211> 237
 <212> PRT
 <213> Mouse

<400> 338
 Met Leu Ser Leu Arg Ser Leu Leu Pro His Leu Gly Leu Phe Leu Cys
 1 5 10 15
 Leu Ala Leu His Leu Ser Pro Ser Leu Ser Ala Ser Asp Asn Gly Ser
 20 25 30
 Cys Val Val Leu Asp Asn Ile Tyr Thr Ser Asp Ile Leu Glu Ile Ser
 35 40 45
 Thr Met Ala Asn Val Ser Gly Gly Asp Val Thr Tyr Thr Val Thr Val
 50 55 60
 Pro Val Asn Asp Ser Val Ser Ala Val Ile Leu Lys Ala Val Lys Glu
 65 70 75 80
 Asp Asp Ser Pro Val Gly Thr Trp Ser Gly Thr Tyr Glu Lys Cys Asn
 85 90 95
 Asp Ser Ser Val Tyr Tyr Asn Leu Thr Ser Gln Ser Gln Ser Val Phe
 100 105 110

Gln Thr Asn Trp Thr Val Pro Thr Ser Glu Asp Val Thr Lys Val Asn
 115 120 125
 Leu Gln Val Leu Ile Val Val Asn Arg Thr Ala Ser Lys Ser Ser Val
 130 135 140
 Lys Met Glu Gln Val Gln Pro Ser Ala Ser Thr Pro Ile Pro Glu Ser
 145 150 155 160
 Ser Glu Thr Ser Gln Thr Ile Asn Thr Thr Pro Thr Val Asn Thr Ala
 165 170 175
 Lys Thr Thr Ala Lys Asp Thr Ala Asn Thr Thr Ala Val Thr Thr Ala
 180 185 190
 Asn Thr Thr Ala Asn Thr Thr Ala Val Thr Thr Ala Lys Thr Thr Ala
 195 200 205
 Lys Ser Leu Ala Ile Arg Thr Leu Gly Ser Pro Leu Ala Gly Ala Leu
 210 215 220
 His Ile Leu Leu Val Phe Leu Ile Ser Lys Leu Leu Phe
 225 230 235

<210> 339
 <211> 469
 <212> PRT
 <213> Mouse

<400> 339
 Met Leu Cys Leu Cys Leu Tyr Val Pro Ile Ala Gly Ala Ala Gln Thr
 1 5 10 15
 Glu Phe Gln Tyr Phe Glu Ser Lys Gly Leu Pro Ala Glu Leu Lys Ser
 20 25 30
 Ile Phe Lys Leu Ser Val Phe Ile Pro Ser Gln Glu Phe Ser Thr Tyr
 35 40 45
 Arg Gln Trp Lys Gln Lys Ile Val Gln Ala Gly Asp Lys Asp Leu Asp
 50 55 60
 Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr Leu Gln Asp His Glu
 65 70 75 80
 Lys Lys Leu Arg Leu Val Phe Lys Ser Leu Asp Lys Lys Asn Asp Gly
 85 90 95
 Arg Ile Asp Ala Gln Glu Ile Met Gln Ser Leu Arg Asp Leu Gly Val
 100 105 110
 Lys Ile Ser Glu Gln Ala Glu Lys Ile Leu Lys Ser Met Asp Lys
 115 120 125
 Asn Gly Thr Met Thr Ile Asp Trp Asn Glu Trp Arg Asp Tyr His Leu
 130 135 140
 Leu His Pro Val Glu Asn Ile Pro Glu Ile Ile Leu Tyr Trp Lys His
 145 150 155 160
 Ser Thr Ile Phe Asp Val Gly Glu Asn Leu Thr Val Pro Asp Glu Phe
 165 170 175
 Thr Val Glu Glu Arg Gln Thr Gly Met Trp Trp Arg His Leu Val Ala
 180 185 190
 Gly Gly Gly Ala Gly Ala Val Ser Arg Thr Cys Thr Ala Pro Leu Asp
 195 200 205
 Arg Leu Lys Val Leu Met Gln Val His Ala Ser Arg Ser Asn Asn Met
 210 215 220
 Cys Ile Val Gly Gly Phe Thr Gln Met Ile Arg Glu Gly Gly Ala Lys
 225 230 235 240
 Ser Leu Trp Arg Gly Asn Gly Ile Asn Val Leu Lys Ile Ala Pro Glu
 245 250 255
 Ser Ala Ile Lys Phe Met Ala Tyr Glu Gln Met Lys Arg Leu Val Gly
 260 265 270

Ser Asp Gln Glu Thr Leu Arg Ile His Glu Arg Leu Val Ala Gly Ser
 275 280 285
 Leu Ala Gly Ala Ile Ala Gln Ser Ser Ile Tyr Pro Met Glu Val Leu
 290 295 300
 Lys Thr Arg Met Ala Leu Arg Lys Thr Gly Gln Tyr Ser Gly Met Leu
 305 310 315 320
 Asp Cys Ala Arg Arg Ile Leu Ala Lys Glu Gly Val Ala Ala Phe Tyr
 325 330 335
 Lys Gly Tyr Ile Pro Asn Met Leu Gly Ile Ile Pro Tyr Ala Gly Ile
 340 345 350
 Asp Leu Ala Val Tyr Glu Thr Leu Lys Asn Thr Trp Leu Gln Arg Tyr
 355 360 365
 Ala Val Asn Ser Ala Asp Pro Gly Val Phe Val Leu Leu Ala Cys Gly
 370 375 380
 Thr Ile Ser Ser Thr Cys Gly Gln Leu Ala Ser Tyr Pro Leu Ala Leu
 385 390 395 400
 Val Arg Thr Arg Met Gln Ala Gln Ala Ser Ile Glu Gly Ala Pro Glu
 405 410 415
 Val Thr Met Ser Ser Leu Phe Lys Gln Ile Leu Arg Thr Glu Gly Ala
 420 425 430
 Phe Gly Leu Tyr Arg Gly Leu Ala Pro Asn Phe Met Lys Val Ile Pro
 435 440 445
 Ala Val Ser Ile Ser Tyr Val Val Tyr Glu Asn Leu Lys Ile Thr Leu
 450 455 460
 Gly Val Gln Ser Arg
 465

<210> 340
 <211> 99
 <212> PRT
 <213> Mouse

<400> 340
 Met Arg Leu Leu Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Cys
 1 5 10 15
 Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro
 20 25 30
 Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
 35 40 45
 Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Ser Met Ser
 50 55 60
 Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr
 65 70 75 80
 Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val
 85 90 95
 Tyr Glu Glu

<210> 341
 <211> 431
 <212> PRT
 <213> Mouse

<400> 341
 Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Thr Leu Pro Ser
 1 5 10 15
 Leu Gly Ala Gly Gly Glu Ser Pro Glu Ala Pro Pro Gln Ser Trp Thr

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<210> 342
<211> 51
<212> PRT
<213> Mouse
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<400> 342

Leu Lys Phe Ser His Pro Cys Leu Glu Asp His Asn Ser Tyr Cys Ile
 1 5 10 15
 Asn Gly Ala Cys Ala Phe His His Glu Leu Lys Gln Ala Ile Cys Arg
 20 25 30
 Cys Phe Thr Gly Tyr Thr Gly Gln Arg Cys Glu His Leu Thr Leu Thr
 35 40 45
 Ser Tyr Ala
 50

<210> 343

<211> 51

<212> PRT

<213> Human

<400> 343

Leu Lys Phe Ser His Leu Cys Leu Glu Asp His Asn Ser Tyr Cys Ile
 1 5 10 15
 Asn Gly Ala Cys Ala Phe His His Glu Leu Glu Lys Ala Ile Cys Arg
 20 25 30
 Cys Phe Thr Gly Tyr Thr Gly Glu Arg Cys Glu His Leu Thr Leu Thr
 35 40 45
 Ser Tyr Ala
 50

<210> 344

<211> 95

<212> PRT

<213> Human

<400> 344

Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Tyr Thr Ala Arg Val
 1 5 10 15
 Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr
 20 25 30
 Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu
 35 40 45
 Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val Ser Arg Tyr Arg Gly
 50 55 60
 Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile
 65 70 75 80
 Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu
 85 90 95

<210> 345

<211> 77

<212> PRT

<213> Mouse

<400> 345

Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr Ser Asp
 1 5 10 15
 Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu Glu Lys
 20 25 30
 Met Val Ile Val Thr Thr Lys Ser Met Ser Arg Tyr Arg Gly Gln Glu
 35 40 45
 His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile Lys Trp
 50 55 60

Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu
65 70 75

<210> 346
<211> 77
<212> PRT
<213> Human

<400> 346
Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr Ser Asp
1 5 10 15
Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu Glu Lys
20 25 30
Met Val Ile Ile Thr Thr Lys Ser Val Ser Arg Tyr Arg Gly Gln Glu
35 40 45
His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile Lys Trp
50 55 60
Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu
65 70 75

<210> 347
<211> 215
<212> PRT
<213> Mouse

<400> 347
Met Leu Ser Leu Arg Ser Leu Leu Pro His Leu Gly Leu Phe Leu Cys
1 5 10 15
Leu Ala Leu His Leu Ser Pro Ser Leu Ser Ala Ser Asp Asn Gly Ser
20 25 30
Cys Val Val Leu Asp Asn Ile Tyr Thr Ser Asp Ile Leu Glu Ile Ser
35 40 45
Thr Met Ala Asn Val Ser Gly Gly Asp Val Thr Tyr Thr Val Thr Val
50 55 60
Pro Val Asn Asp Ser Val Ser Ala Val Ile Leu Lys Ala Val Lys Glu
65 70 75 80
Asp Asp Ser Pro Val Gly Thr Trp Ser Gly Thr Tyr Glu Lys Cys Asn
85 90 95
Asp Ser Ser Val Tyr Tyr Asn Leu Thr Ser Gln Ser Gln Ser Val Phe
100 105 110
Gln Thr Asn Trp Thr Val Pro Thr Ser Glu Asp Val Thr Lys Val Asn
115 120 125
Leu Gln Val Leu Ile Val Val Asn Arg Thr Ala Ser Lys Ser Ser Val
130 135 140
Lys Met Glu Gln Val Gln Pro Ser Ala Ser Thr Pro Ile Pro Glu Ser
145 150 155 160
Ser Glu Thr Ser Gln Thr Ile Asn Thr Thr Pro Thr Val Asn Thr Ala
165 170 175
Lys Thr Thr Ala Lys Asp Thr Ala Asn Thr Thr Ala Val Thr Thr Ala
180 185 190
Asn Thr Thr Ala Asn Thr Thr Ala Val Thr Thr Ala Lys Thr Thr Ala
195 200 205
Lys Ser Leu Ala Ile Arg Thr
210 215

<210> 348
<211> 21

<212> PRT
<213> Mouse

<400> 348
Gly Tyr Ser Asp Gly Tyr Gln Val Cys Ser Arg Phe Gly Ser Lys Val
1 5 10 15
Pro Gln Phe Leu Asn

<210> 349
<211> 417
<212> DNA
<213> Mouse

<400> 349
gctagccgtg caccagctc tccggagcgc gtgcaggcga gccgagcgcc ccgtccgcgg 60
ttctcgggca ggcgtgcgg gctccccggc tccccgcgt cccgggcacc cggcggggcc 120
atgcgcccgg gctagagcgt agccgcccgg atgcccgtcc cgctgctgct cggcgcgctc 180
tgctcgcgg cctccccggc gcccgcgcgc gctgcccagc tgccgtcgga gtggagaccc 240
ttgagcgaag gctgcccggc cgagctagcc gagaccatcg tgtatgcaa ggtgctggcg 300
ctgcacccc aggtgcctgg cctctacaac tacctgccgt ggcagtacca agctggagag 360
ggagggtct tctactccgc cgagggtggag atgcttgtgt gaccaaggcg tggggca 417

<210> 350
<211> 1837
<212> DNA
<213> Mouse

<400> 350
ccccacctg cccagccaag ccgagtgcgc ccggtttgt tgcctttgtc ctccgcgacc 60
taagcgcccg gcttgaaga acgccatccc ggagagcgca cgcggcgctc caccaggtct 120
aacaacatgc ctccacttct gcttctacca gccatctaca tgctcctgtt cttcagagtg 180
tccccgacca tctctcttca ggaagtgcct gtgaaccggg agaccatggg gaagatcgct 240
gtggccagca aattaatgtg gtgctcagcc gcggtcgaca tctgttttct gttagatggc 300
tctcacagca tcgggaaggg gagcttcgag aggtccaagc gcttcgcat cgctgcctgt 360
gatgccctgg acatcagccc tggcagggtc agagtccggg ccttcagatt tggttccact 420
cctcatctgg aattccctt ggactccttc tcaactcgac aggaagtga gaaagcatc 480
aaggggatag ttttcaagg tgggcgcacc gagacgggccc tagccctgaa acgctgagc 540
agagggttcc ccggaggcag aaatggctct gtgcccaga ttcttatcat cgtcacggat 600
ggcaagtccc aggggcccgt ggctctccc gctaagcagc tgagagaaa gggcatcgtc 660
gtgtttgccc taggagtcgg ttttcccagg tgggacgagc tgctcagct ggcagtgag 720
ccgaaggacc ggcattgtgt gttggctgag caagtggagg atgccaccaa tggcctctc 780
agcaccctca gcagctccgc actctgcacc actgctgac cagactgcag ggtggaacct 840
catccctgtg agcggaggac gctggagacc gtcaggggagc tcgctggcaa tgccttgtgc 900
tggagaggat caaggcaagc agacactgtg ctggctctgc cctgtccctt ctacagctgg 960
aagagagtgt tccagacaca cctgcacaac tgctacagaa ccatctgtcc aggccctgt 1020
gactcccagc cctgcaaaa tggaggcacg tgcatccag aaggtgtgga taggtaccac 1080
tgtctctgcc cactggcatt cggaggggaa gtcaactgtg cccgaagct gagcctggaa 1140
tgcagaatcg atgtcctctt cctgtcggac agttctgcag gcaccacatt ggggggcttc 1200
cggaggggcca aggcctttgt caagcgttt gtgcaggccg tgctgaggga ggaactccga 1260
gcccgcgttg ggatagccag ttatggcagg aatctaattg tggcggtgcc ctgtcgggga 1320
gtaccagcat tgtccggac ctgatcagga gccttgacag cattcccttc agcggtgcc 1380
cgaccctaac cgggagtgc ttgtccagg tggcagagca cggctttggg agtgccagca 1440
ggactggtca ggacaggcca cgcagagtag tagttctgct cactgaatca cgtcccagg 1500
atgaggtgtc tgggccagca gctcagcaa gggctcggga gctactcctc ctgggctgtg 1560
gcagttagat cctgcaggc gagctgggtga agatcacgg tagccgaag catgtgatg 1620
tccacacaga cctcaggac ctgtcagcca aatccagagc tgcagaggag gctatgcagc 1680
cagccacggc caggctgcca ggcacagtca ctggacctgg tcttcctgtg gatgcctctg 1740

ctctgtggga cgtgagaact ttgccccaat gcagagcttc atcaggaaat gcaccctccg 1800
gtttgatgtg aatcctgatg tgacacaagt tggcctg 1837

<210> 351
<211> 941
<212> DNA
<213> Mouse

<400> 351
taagccctca ggccctccta atgctatccc cctttgttcc tgcagcgtgg acccagtcag 60
cagccaggcc atggagctct ctgatgtcac cctcattgag ggtgtgggta acgagggtgat 120
ggtggttagca ggcggtggtg cgctgactct agccctgggc ctgacctggc tctccaccta 180
tgtagcagac agtggtaaca accagctgct gggcaccatt gtgtcagcag gtgacacgtc 240
tgtttctccac ctgggcatg tggaccagct ggtaaaccaa ggcaactccag agccaaccga 300
acaccccat ccatcagggg gcaatgatga caaggctgaa gagaccagt acagtggggg 360
agacgccact ggagaacctg gagctagggg agagatggag cccagcctgg agcatctcct 420
ggacatccaa ggccctgccta aaaggcaagc aggcctgggg agcagtcgcc cagaagcccc 480
gctgggggta gatgatggct cctgcctctc tcccagcccc agcctcatca atgttcgcct 540
caagtctctc aatgacacgg aggagctagc tgtggccagg ccagaggaca ctgtgggtac 600
cctaaaaagg tgagtagggc ggagagaggc cagtgtctcg tgacttgttc ctgagatgat 660
ggtttctctga agaagctgtg catatatgtg agcacaggag ggattttaag gggaaatgga 720
gacttccata gacagacctt cagtgtcttt catgtccagg ccttgatctc tctagcctta 780
ttctttatcc agtctttcct ttcatacttg tagcaatac ttccctggac aagagaacca 840
aatgaagttg atctaccagg gtcggctgct gcaggaccca gcacgcacac tgagttccct 900
gaacattacc aacaactgcg tgatccactg ccaccgctca c 941

<210> 352
<211> 571
<212> DNA
<213> Mouse

<400> 352
gctgactgta cctataattc accatgaatt acgtctgtga gttacctccg tgagctctca 60
ttgtgatttg agtatgtgtg catgtgggtg gggctcagct gctgtgccc tgacatccac 120
atttggatgt cttttggttc cgtgaacaag tagaaattgc atgtgtctac cgtgacagt 180
gtggtgtcac tgggcccctg ggggtggtca ottacctctg attccgtctg tgggaaagtc 240
ccagtgtacc caaatgtggc attgttgcac gccttgggtg tgtgtgggag attgtctctg 300
tctctcagac cctttgtggc tttgtctgtt gaaagagaca gagaccctt gtggttttct 360
cagctgagaa ccttccctcc tgggatgttg ggtgtaaact taactgcttt gcaaagcctg 420
cccctcctca tgcagacct tcaatatctg gcagtgcatt gttcccaagc ccccttctg 480
tatgggaatg tcagggtctc ctcacctga cagctgataa ttccattcct cgactcttga 540
gaactggccc ttgctttgtt ttctctgcct g 571

<210> 353
<211> 467
<212> DNA
<213> Rat

<400> 353
cggagaatga gcgggtggcc gtggctgcag ctgctgccc ggcactgaca ggacacgagc 60
tctatgcctt tccggtgctt tatcccgctc ggcctcgtgt gcgtgctgct gccctgcac 120
catggtgcgc caggccccga aggcaccgag cccgacccc cccactacag ggagcgagtc 180
aaggccatgt tctaccacgc ctacgacagt tacctggaaa atgcctttcc ctacgatgag 240
ctgagacctc tcacctgtga cgggcacgac acctggggca gttttctct gacactgatt 300
gatgccttg acaccttgct gattttgggg aatacctctg aattccaaag agtgggtggag 360
gttctccagg acaaactgag actttgatat cgacgtcaat gcctctgtgt tcgaaaccaa 420
catccgagtg gtaggaggac tcctttctgc tcactctctg tcaaga 467

<210> 354

<211> 528

<212> DNA

<213> Rat

<400> 354

gtgactcctg	ctgtaggacc	ctccaggaag	cactggcctc	tcctacagag	tcctccacct	60
agcaccggcc	ttaatgctaa	agccaaatgt	ggtttctgcc	ctgcagcgtg	cccctggtaa	120
tctcgagttg	ccactcccaa	gccagccccc	actggccata	tggcatcata	tctgggggtc	180
aggagggcct	gtgcaggctt	tggacagcca	cttgccacag	cagaggagag	agtgaggttt	240
ccaggagcag	caggaaggaa	gaccccagaa	ttccccaggg	ctctttgagt	ggtaatgttg	300
acttctggag	agtctgcccc	ccttgtgctc	acacaagcat	ggacaggaca	ctgggacttt	360
tatctctgtt	ttaagctgtt	tccacagaag	cccgttcagg	tagttacttc	accacatttg	420
gccctatagc	cagaggagtg	ccctggctaa	ctgcagtgtg	agcttgtaag	caacagaagt	480
gcccaggagc	tgacccccaa	ggccaggaag	gctcgagctt	gccacttt		528

<210> 355

<211> 473

<212> DNA

<213> Mouse

<400> 355

ggcagcagga	ccgcggtcac	tgagcctctg	caggtgtcaa	caaggctcaa	ggagcaggat	60
ggatctcgat	gtggttaaca	tgtttgtgat	tgcgggtggg	accctggcca	ttccaatcct	120
ggcatttggt	gcgtctttcc	tcctgtggcc	ttcagcactg	ataagaatct	attattggta	180
ctggcggagg	acactgggca	tgcaagttec	ctacgcacac	catgaggact	atcagttctg	240
ttactccttc	cggggcaggc	caggacacaa	gccatccatc	cttatgctcc	atggattctc	300
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<210> 356

<211> 431

<212> DNA

<213> Rat

<400> 356

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ttgcaatgaa	atctagaagg	ggacctcatg	tcctgtgggg	acacaatgcc	ccgaaggact	360
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tccttgcaga	t					431

<210> 357

<211> 1206

<212> DNA

<213> Mouse

<400> 357

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<210> 358
 <211> 1052
 <212> DNA
 <213> Rat

<400> 358						
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<210> 359
 <211> 1134
 <212> DNA
 <213> Rat

<400> 359						
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accccggt	caagccaaca	agagctctga	agatatccgg	tgc aaatgca	tctgtcccc	240
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<210> 360
 <211> 876
 <212> DNA
 <213> Mouse

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cgagaggagc	ctgcagggga	ggagaggcgg	cgcccagaca	ctttgcagtt	gtggcaggaa	840
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<210> 361
 <211> 495
 <212> DNA
 <213> Mouse

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caacttgccg	ggaaggaaac	tcggggaagt	ccctcagtgt	gtttggagaa	taaatgtgga	180
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<210> 362
 <211> 349
 <212> DNA
 <213> Mouse

<400> 362	tctctgtcta	tcttgctgc	tgtgagggtg	tcacccaggc	ccacttatcc	atctacagcg	60
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accaaggcca	gatgcgagcc	accagaagt	taattaaacc	aggttcacg	ggagtttgct	300
gaaatgtaa	gcatactctg	ttctagagag	ggagtgaaga	aaggggcca		349

<210> 363
 <211> 380
 <212> DNA
 <213> Mouse

<400> 363						
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<210> 364
 <211> 351
 <212> DNA
 <213> Mouse

<400> 364						
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<210> 365
 <211> 854
 <212> DNA
 <213> Rat

<400> 365						
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<210> 366
 <211> 257

<212> DNA

<213> Rat

<400> 366

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cggttcgggt	catgcattgc	ctccgttcaa	gacctcaacc	aagattccta	caatgacgtg	180
gtggtggggg	cccctcagga	ggacagccac	agagggggca	tctacatctt	ccatggcttc	240
caaaccaaca	tcctgaa					257

<210> 367

<211> 475

<212> DNA

<213> Rat

<400> 367

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<210> 368

<211> 392

<212> DNA

<213> Mouse

<400> 368

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cggccttctt	tccttcaggc	tcggtcggcg	ccttgcttgc	cccagggttg	ctccccggcc	180
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gcccagggtg	cgccgggtgc	cgcggtgggc	cttggtgcgt	ttcagctcgg	ggtcgcgcga	360
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<210> 369

<211> 824

<212> DNA

<213> Rat

<400> 369

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<210> 370
 <211> 1663
 <212> DNA
 <213> Mouse

<400> 370
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<210> 371
 <211> 568
 <212> DNA
 <213> Human

<400> 371
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<210> 372
 <211> 5583

<212> DNA

<213> Rat

<400> 372

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<210> 373

<211> 83

<212> PRT

<213> Mouse

<400> 373

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Met Pro Leu Pro Leu Leu Leu Ala Ala Leu Cys Leu Ala Ala Ser Pro
  1             5             10             15
Ala Pro Ala Arg Ala Cys Gln Leu Pro Ser Glu Trp Arg Pro Leu Ser
             20             25             30
Glu Gly Cys Arg Ala Glu Leu Ala Glu Thr Ile Val Tyr Ala Lys Val
             35             40             45
Leu Ala Leu His Pro Glu Val Pro Gly Leu Tyr Asn Tyr Leu Pro Trp

```

50 55 60
 Gln Tyr Gln Ala Gly Glu Gly Gly Leu Phe Tyr Ser Ala Glu Val Glu
 65 70 75 80
 Met Leu Val

<210> 374
 <211> 405
 <212> PRT
 <213> Mouse

<400> 374
 Met Pro Pro Leu Leu Leu Leu Pro Ala Ile Tyr Met Leu Leu Phe Phe
 1 5 10 15
 Arg Val Ser Pro Thr Ile Ser Leu Gln Glu Val His Val Asn Arg Glu
 20 25 30
 Thr Met Gly Lys Ile Ala Val Ala Ser Lys Leu Met Trp Cys Ser Ala
 35 40 45
 Ala Val Asp Ile Leu Phe Leu Leu Asp Gly Ser His Ser Ile Gly Lys
 50 55 60
 Gly Ser Phe Glu Arg Ser Lys Arg Phe Ala Ile Ala Cys Asp Ala
 65 70 75 80
 Leu Asp Ile Ser Pro Gly Arg Val Arg Val Gly Ala Leu Gln Phe Gly
 85 90 95
 Ser Thr Pro His Leu Glu Phe Pro Leu Asp Ser Phe Ser Thr Arg Gln
 100 105 110
 Glu Val Lys Glu Ser Ile Lys Gly Ile Val Phe Lys Gly Gly Arg Thr
 115 120 125
 Glu Thr Gly Leu Ala Leu Lys Arg Leu Ser Arg Gly Phe Pro Gly Gly
 130 135 140
 Arg Asn Gly Ser Val Pro Gln Ile Leu Ile Ile Val Thr Asp Gly Lys
 145 150 155 160
 Ser Gln Gly Pro Val Ala Leu Pro Ala Lys Gln Leu Arg Glu Arg Gly
 165 170 175
 Ile Val Val Phe Ala Val Gly Val Arg Phe Pro Arg Trp Asp Glu Leu
 180 185 190
 Leu Thr Leu Ala Ser Glu Pro Lys Asp Arg His Val Leu Leu Ala Glu
 195 200 205
 Gln Val Glu Asp Ala Thr Asn Gly Leu Leu Ser Thr Leu Ser Ser Ser
 210 215 220
 Ala Leu Cys Thr Thr Ala Asp Pro Asp Cys Arg Val Glu Pro His Pro
 225 230 235 240
 Cys Glu Arg Arg Thr Leu Glu Thr Val Arg Glu Leu Ala Gly Asn Ala
 245 250 255
 Leu Cys Trp Arg Gly Ser Arg Gln Ala Asp Thr Val Leu Ala Leu Pro
 260 265 270
 Cys Pro Phe Tyr Ser Trp Lys Arg Val Phe Gln Thr His Pro Ala Asn
 275 280 285
 Cys Tyr Arg Thr Ile Cys Pro Gly Pro Cys Asp Ser Gln Pro Cys Gln
 290 295 300
 Asn Gly Gly Thr Cys Ile Pro Glu Gly Val Asp Arg Tyr His Cys Leu
 305 310 315 320
 Cys Pro Leu Ala Phe Gly Gly Glu Val Asn Cys Ala Pro Lys Leu Ser
 325 330 335
 Leu Glu Cys Arg Ile Asp Val Leu Phe Leu Leu Asp Ser Ser Ala Gly
 340 345 350
 Thr Thr Leu Gly Gly Phe Arg Arg Ala Lys Ala Phe Val Lys Arg Phe

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          355          360          365
Val Gln Ala Val Leu Arg Glu Asp Ser Arg Ala Arg Val Gly Ile Ala
          370          375          380
Ser Tyr Gly Arg Asn Leu Met Val Ala Val Pro Cys Arg Gly Val Pro
385          390          395          400
Ala Leu Cys Arg Thr
          405

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<210> 375
<211> 180
<212> PRT
<213> Mouse

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<400> 375
Met Glu Leu Ser Asp Val Thr Leu Ile Glu Gly Val Gly Asn Glu Val
  1          5          10          15
Met Val Val Ala Gly Val Val Ala Leu Thr Leu Ala Leu Val Leu Ala
          20          25          30
Trp Leu Ser Thr Tyr Val Ala Asp Ser Gly Asn Asn Gln Leu Leu Gly
          35          40          45
Thr Ile Val Ser Ala Gly Asp Thr Ser Val Leu His Leu Gly His Val
          50          55          60
Asp Gln Leu Val Asn Gln Gly Thr Pro Glu Pro Thr Glu His Pro His
65          70          75          80
Pro Ser Gly Gly Asn Asp Asp Lys Ala Glu Glu Thr Ser Asp Ser Gly
          85          90          95
Gly Asp Ala Thr Gly Glu Pro Gly Ala Arg Gly Glu Met Glu Pro Ser
          100          105          110
Leu Glu His Leu Leu Asp Ile Gln Gly Leu Pro Lys Arg Gln Ala Gly
          115          120          125
Leu Gly Ser Ser Arg Pro Glu Ala Pro Leu Gly Leu Asp Asp Gly Ser
          130          135          140
Cys Leu Ser Pro Ser Pro Ser Leu Ile Asn Val Arg Leu Lys Phe Leu
145          150          155          160
Asn Asp Thr Glu Glu Leu Ala Val Ala Arg Pro Glu Asp Thr Val Gly
          165          170          175
Thr Leu Lys Arg
          180

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<210> 376
<211> 68
<212> PRT
<213> Mouse

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```

<400> 376
Met Cys Leu Pro Val Thr Val Trp Cys His Trp Ala Leu Trp Val Ala
  1          5          10          15
His Leu Pro Leu Ile Pro Ser Val Gly Lys Ser Gln Cys Thr Gln Met
          20          25          30
Trp His Cys Cys Met Pro Trp Val Cys Val Gly Asp Cys Leu Cys Leu
          35          40          45
Ser Asp Pro Leu Trp Leu Cys Leu Leu Lys Glu Thr Glu Thr Pro Cys
          50          55          60
Gly Phe Leu Ser
65

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<210> 377

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<211> 107

<212> PRT

<213> Rat

<400> 377

Met	Pro	Phe	Arg	Leu	Leu	Ile	Pro	Leu	Gly	Leu	Val	Cys	Val	Leu	Leu
1				5					10					15	
Pro	Leu	His	His	Gly	Ala	Pro	Gly	Pro	Glu	Gly	Thr	Ala	Pro	Asp	Pro
			20					25					30		
Ala	His	Tyr	Arg	Glu	Arg	Val	Lys	Ala	Met	Phe	Tyr	His	Ala	Tyr	Asp
		35					40					45			
Ser	Tyr	Leu	Glu	Asn	Ala	Phe	Pro	Tyr	Asp	Glu	Leu	Arg	Pro	Leu	Thr
	50					55					60				
Cys	Asp	Gly	His	Asp	Thr	Trp	Gly	Ser	Phe	Ser	Leu	Thr	Leu	Ile	Asp
65					70				75					80	
Ala	Leu	Asp	Thr	Leu	Leu	Ile	Leu	Gly	Asn	Thr	Ser	Glu	Phe	Gln	Arg
				85					90					95	
Val	Val	Glu	Val	Leu	Gln	Asp	Lys	Arg	Gly	Leu					
			100					105							

<210> 378

<211> 95

<212> PRT

<213> Rat

<400> 378

Met	Trp	Phe	Leu	Pro	Cys	Ser	Val	Pro	Leu	Val	Ile	Ser	Ser	Cys	His
1				5					10					15	
Ser	Gln	Ala	Ser	Pro	His	Trp	Pro	Tyr	Gly	Ile	Ile	Ser	Gly	Gln	
			20					25					30		
Glu	Gly	Leu	Cys	Arg	Leu	Trp	Thr	Ala	Thr	Cys	His	Ser	Arg	Gly	Glu
		35					40					45			
Ser	Glu	Val	Ser	Arg	Ser	Ser	Arg	Lys	Glu	Asp	Pro	Arg	Ile	Pro	Gln
	50					55					60				
Gly	Ser	Leu	Ser	Gly	Asn	Val	Asp	Phe	Trp	Arg	Val	Cys	Pro	Pro	Cys
65					70				75					80	
Ala	His	Thr	Ser	Met	Asp	Arg	Thr	Leu	Gly	Leu	Leu	Ser	Cys	Cys	
				85					90					95	

<210> 379

<211> 138

<212> PRT

<213> Mouse

<400> 379

Met	Asp	Leu	Asp	Val	Val	Asn	Met	Phe	Val	Ile	Ala	Gly	Gly	Thr	Leu
1				5					10					15	
Ala	Ile	Pro	Ile	Leu	Ala	Phe	Val	Ala	Ser	Phe	Leu	Leu	Trp	Pro	Ser
			20					25					30		
Ala	Leu	Ile	Arg	Ile	Tyr	Tyr	Trp	Tyr	Trp	Arg	Arg	Thr	Leu	Gly	Met
		35					40					45			
Gln	Val	Arg	Tyr	Ala	His	His	Glu	Asp	Tyr	Gln	Phe	Cys	Tyr	Ser	Phe
	50					55					60				
Arg	Gly	Arg	Pro	Gly	His	Lys	Pro	Ser	Ile	Leu	Met	Leu	His	Gly	Phe
65					70				75					80	
Ser	Ala	His	Lys	Asp	Met	Trp	Leu	Ser	Val	Val	Lys	Phe	Leu	Pro	Lys
				85					90					95	

Asn Leu His Leu Val Cys Val Asp Met Pro Gly His Glu Gly Thr Thr
 100 105 110
 Arg Ser Ser Leu Asp Asp Leu Ser Ile Val Gly Gln Val Lys Arg Ile
 115 120 125
 His Gln Phe Val Glu Cys Leu Lys Leu Asn
 130 135

<210> 380
 <211> 81
 <212> PRT
 <213> Rat

<400> 380
 Met Ala Ser Ser Ser Asn Trp Leu Ser Gly Val Asn Val Val Leu Val
 1 5 10 15
 Met Ala Tyr Gly Ser Leu Val Phe Val Leu Leu Phe Ile Phe Val Lys
 20 25 30
 Arg Gln Ile Met Arg Phe Ala Met Lys Ser Arg Arg Gly Pro His Val
 35 40 45
 Pro Val Gly His Asn Ala Pro Lys Asp Leu Lys Glu Ile Asp Ile
 50 55 60
 Arg Leu Ser Arg Val Gln Asp Ile Lys Tyr Glu Pro Gln Leu Leu Ala
 65 70 75 80
 Asp

<210> 381
 <211> 257
 <212> PRT
 <213> Mouse

<400> 381
 Met Arg Ser Gly Ala Leu Trp Pro Leu Leu Trp Gly Ala Leu Val Trp
 1 5 10 15
 Thr Val Gly Ser Val Gly Ala Val Met Gly Ser Glu Asp Ser Val Pro
 20 25 30
 Gly Gly Val Cys Trp Leu Gln Gln Gly Arg Glu Ala Thr Cys Ser Leu
 35 40 45
 Val Leu Lys Thr Arg Val Ser Arg Glu Glu Cys Cys Ala Ser Gly Asn
 50 55 60
 Ile Asn Thr Ala Trp Ser Asn Phe Thr His Pro Gly Asn Lys Ile Ser
 65 70 75 80
 Leu Leu Gly Phe Leu Gly Leu Val His Cys Leu Pro Cys Lys Asp Ser
 85 90 95
 Cys Asp Gly Val Glu Cys Gly Pro Gly Lys Ala Cys Arg Met Leu Gly
 100 105 110
 Gly Arg Pro Thr Leu Arg Ser Cys Val Pro Asn Cys Glu Gly Leu Pro
 115 120 125
 Ala Gly Phe Gln Val Cys Gly Ser Asp Gly Ala Thr Tyr Arg Asp Glu
 130 135 140
 Cys Glu Leu Arg Thr Ala Arg Cys Arg Gly His Pro Asp Leu Arg Val
 145 150 155 160
 Met Tyr Arg Gly Arg Cys Gln Lys Ser Cys Ala Gln Val Val Cys Pro
 165 170 175
 Arg Pro Gln Ser Cys Leu Val Asp Gln Thr Gly Ser Ala His Cys Val
 180 185 190
 Val Cys Arg Ala Ala Pro Cys Pro Val Pro Ser Asn Pro Gly Gln Glu

```

      195      200      205
Leu Cys Gly Asn Asn Asn Val Thr Tyr Ile Ser Ser Cys His Leu Arg
  210      215      220
Gln Ala Thr Cys Phe Leu Gly Arg Ser Ile Gly Val Arg His Pro Gly
  225      230      235      240
Ile Cys Thr Gly Gly Pro Lys Val Pro Ala Glu Glu Glu Glu Asn Phe
      245      250      255
Val

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<210> 382
<211> 285
<212> PRT
<213> Rat

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      <400> 382
Met Ile Ser Trp Met Leu Leu Ala Cys Ala Leu Pro Cys Ala Ala Asp
  1      5      10      15
Pro Met Leu Gly Ala Phe Ala Arg Arg Asp Phe Gln Lys Gly Gly Pro
      20      25      30
Gln Leu Val Cys Ser Leu Pro Gly Pro Gln Gly Pro Pro Gly Pro Pro
  35      40      45
Gly Ala Pro Gly Ser Ser Gly Met Val Gly Arg Met Gly Phe Pro Gly
  50      55      60
Lys Asp Gly Gln Asp Gly Gln Asp Gly Asp Arg Gly Asp Ser Gly Glu
  65      70      75      80
Glu Gly Pro Pro Gly Arg Thr Gly Asn Arg Gly Lys Gln Gly Pro Lys
      85      90      95
Gly Lys Ala Gly Ala Ile Gly Arg Ala Gly Pro Arg Gly Pro Lys Gly
      100      105      110
Val Ser Gly Thr Pro Gly Lys His Gly Ile Pro Gly Lys Lys Gly Pro
      115      120      125
Lys Gly Lys Lys Gly Glu Pro Gly Leu Pro Gly Pro Cys Ser Cys Gly
      130      135      140
Ser Ser Arg Ala Lys Ser Ala Phe Ser Val Ser Val Thr Lys Ser Tyr
  145      150      155      160
Pro Arg Glu Arg Leu Pro Ile Lys Phe Asp Lys Ile Leu Met Asn Glu
      165      170      175
Gly Gly His Tyr Asn Ala Ser Ser Gly Lys Phe Val Cys Ser Val Pro
      180      185      190
Gly Ile Tyr Tyr Phe Thr Tyr Asp Ile Thr Leu Ala Asn Lys His Leu
      195      200      205
Ala Ile Gly Leu Val His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp
      210      215      220
Ala Asn Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr Ile Leu Ala
  225      230      235      240
Leu Lys Glu Gly Asp Glu Val Trp Leu Gln Ile Phe Tyr Ser Glu Gln
      245      250      255
Asn Gly Leu Phe Tyr Asp Pro Tyr Trp Thr Asp Ser Leu Phe Thr Gly
      260      265      270
Phe Leu Ile Tyr Ala Asp Gln Gly Asp Pro Asn Glu Val
      275      280      285

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<210> 383
<211> 183
<212> PRT
<213> Rat

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<400> 383
 Met Lys Leu Leu Cys Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
 1 5 10 15
 Pro Ala Gln Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
 20 25 30
 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
 35 40 45
 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 50 55 60
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
 65 70 75 80
 Glu Glu Arg Ser Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 85 90 95
 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
 100 105 110
 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
 115 120 125
 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
 130 135 140
 Ile Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
 145 150 155 160
 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
 165 170 175
 Asp Arg His Lys Met Leu Ser
 180

<210> 384
 <211> 292
 <212> PRT
 <213> Mouse

<400> 384
 Cys Gln Leu Pro Leu Arg Val Leu Ile Ile Ser Asn Asn Lys Leu Gly
 1 5 10 15
 Ala Leu Pro Pro Asp Ile Ser Thr Leu Gly Ser Leu Arg Gln Leu Asp
 20 25 30
 Val Ser Ser Asn Glu Leu Gln Ser Leu Pro Val Glu Leu Cys Ser Leu
 35 40 45
 Arg Ser Leu Arg Asp Leu Asn Val Arg Arg Asn Gln Leu Ser Thr Leu
 50 55 60
 Pro Asp Glu Leu Gly Asp Leu Pro Leu Val Arg Leu Asp Phe Ser Cys
 65 70 75 80
 Asn Arg Ile Ser Arg Ile Pro Val Ser Phe Cys Arg Leu Arg His Leu
 85 90 95
 Gln Val Val Leu Leu Asp Ser Asn Pro Leu Gln Ser Pro Pro Ala Gln
 100 105 110
 Ile Cys Leu Lys Gly Lys Leu His Ile Phe Lys Tyr Leu Thr Met Glu
 115 120 125
 Ala Gly Arg Arg Gly Ala Ala Leu Gly Asp Leu Val Pro Ser Arg Pro
 130 135 140
 Pro Ser Phe Ser Pro Cys Pro Ala Glu Asp Leu Phe Pro Gly Arg Arg
 145 150 155 160
 Tyr Asp Gly Gly Leu Asp Ser Gly Phe His Ser Val Asp Ser Gly Ser
 165 170 175
 Lys Arg Trp Ser Gly Asn Glu Ser Thr Asp Asp Phe Ser Glu Leu Ser
 180 185 190

Phe Arg Ile Ser Glu Leu Ala Arg Asp Pro Arg Gly Pro Arg Gln Pro
 195 200 205
 Arg Glu Asp Gly Ala Gly Asp Gly Asp Leu Glu Gln Ile Asp Phe Ile
 210 215 220
 Asp Ser His Val Pro Gly Glu Asp Glu Asp Arg Ser Ala Ala Glu Glu
 225 230 235 240
 Gln Leu Pro Ser Glu Leu Ser Leu Val Ala Gly Asp Val Glu Lys Pro
 245 250 255
 Ser Ser Ser Arg Arg Glu Glu Pro Ala Gly Glu Glu Arg Arg Arg Pro
 260 265 270
 Asp Thr Leu Gln Leu Trp Gln Glu Arg Glu Arg Lys Gln Gln Gln Gln
 275 280 285
 Ser Gly Gly Trp
 290

<210> 385
 <211> 164
 <212> PRT
 <213> Mouse

<400> 385
 Ser Arg Gln Leu Arg Ala Pro Arg Phe Asp Pro Arg Ala Gly Phe His
 1 5 10 15
 Ala Glu Gly Lys Asp Arg Gly Pro Ser Val Pro Gln Gly Leu Leu Lys
 20 25 30
 Ala Ala Arg Ser Ser Gly Gln Leu Asn Leu Ala Gly Arg Asn Leu Gly
 35 40 45
 Glu Val Pro Gln Cys Val Trp Arg Ile Asn Val Asp Ile Pro Glu Glu
 50 55 60
 Ala Asn Gln Asn Leu Ser Phe Ser Ser Thr Glu Arg Trp Trp Asp Gln
 65 70 75 80
 Thr Asp Leu Thr Lys Leu Ile Ile Ser Ser Asn Lys Leu Gln Ser Leu
 85 90 95
 Ser Asp Asp Leu Arg Leu Leu Pro Ala Leu Thr Val Leu Asp Ile His
 100 105 110
 Asp Asn Gln Leu Thr Ser Leu Pro Ser Ala Ile Arg Glu Leu Asp Asn
 115 120 125
 Leu Gln Lys Leu Asn Val Ser His Asn Lys Leu Lys Ile Leu Pro Glu
 130 135 140
 Glu Ile Thr Ser Leu Lys Asn Leu Arg Thr Leu His Leu Gln His Asn
 145 150 155 160
 Glu Leu Thr Cys

<210> 386
 <211> 71
 <212> PRT
 <213> Mouse

<400> 386
 Ser Leu Ser Ile Leu Pro Ala Val Arg Val Ser Pro Arg Pro Thr Tyr
 1 5 10 15
 Pro Ser Thr Ala Ser Ser Met Ala Ala Phe Leu Val Thr Gly Phe Phe
 20 25 30
 Phe Ser Leu Phe Val Val Leu Gly Met Glu Pro Arg Ala Leu Phe Arg
 35 40 45
 Pro Asp Lys Ala Leu Pro Leu Ser Cys Ala Lys Pro Thr Ser Leu Cys

50 55 60
 Val Gln Ser Ser Phe Leu Gly
 65 70

<210> 387
 <211> 126
 <212> PRT
 <213> Mouse

<400> 387
 Glu Tyr Glu Ala Arg Val Leu Glu Lys Ser Leu Arg Lys Glu Ser Arg
 1 5 10 15
 Asn Lys Glu Thr Asp Lys Val Lys Leu Thr Trp Arg Asp Arg Phe Pro
 20 25 30
 Ala Tyr Phe Thr Asn Leu Val Ser Ile Ile Phe Met Ile Ala Val Thr
 35 40 45
 Phe Ala Ile Val Leu Gly Val Ile Ile Tyr Arg Ile Ser Thr Ala Ala
 50 55 60
 Ala Leu Ala Met Asn Ser Ser Pro Ser Val Arg Ser Asn Ile Arg Val
 65 70 75 80
 Thr Val Thr Ala Thr Ala Val Ile Ile Asn Leu Val Val Ile Ile Leu
 85 90 95
 Leu Asp Glu Val Tyr Gly Cys Ile Ala Arg Trp Leu Thr Lys Ile Gly
 100 105 110
 Glu Cys His Val Gln Asp Ser Ile Gly Ser Met Gly Leu Gly
 115 120 125

<210> 388
 <211> 84
 <212> PRT
 <213> Rat

<400> 388
 Ala Ala Glu Asn Glu Met Pro Val Ala Val Gly Pro Tyr Gly Gln Ser
 1 5 10 15
 Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly Phe Val Met Gly Cys
 20 25 30
 Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly Thr Phe Ser Cys Leu
 35 40 45
 Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly Gly Ile Gly Lys Thr
 50 55 60
 Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe Met Ala Ile Gly Met
 65 70 75 80
 Gly Ile Arg Cys

<210> 389
 <211> 284
 <212> PRT
 <213> Rat

<400> 389
 Gly Gly Ser Ser Val Ser His Val Leu Arg Gly Ser Gly Gln Glu Arg
 1 5 10 15
 Ser Pro Pro Pro Ala Ser Met Gln Pro Pro Trp Gly Leu Ala Leu Pro
 20 25 30
 Leu Leu Leu Pro Trp Val Ala Gly Gly Val Gly Thr Ser Pro Arg Asp

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      35      40      45
Tyr Trp Leu Pro Ala Leu Ala His Gln Pro Gly Val Cys His Tyr Gly
  50      55      60
Thr Lys Thr Ala Cys Cys Tyr Gly Trp Lys Arg Asn Ser Lys Gly Val
  65      70      75      80
Cys Glu Ala Val Cys Glu Pro Arg Cys Lys Phe Gly Glu Cys Val Gly
      85      90      95
Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser
  100      105      110
Gln Asp Val Asn Glu Cys Ala Phe Lys Pro Arg Pro Cys Gln His Arg
  115      120      125
Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His
  130      135      140
Met Leu Leu Pro Asp Ala Thr Cys Ser Asn Ser Arg Thr Cys Ala Arg
  145      150      155      160
Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Ala Glu Gly Pro Arg Cys
      165      170      175
Val Cys Pro Ser Ser Gly Leu Arg Leu Gly Pro Asn Gly Arg Val Cys
  180      185      190
Leu Asp Ile Asp Glu Cys Ala Ser Ser Lys Ala Val Cys Pro Ser Asn
  195      200      205
Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile
  210      215      220
Gly Phe Glu Leu Lys Tyr Ile Ser Arg Arg Tyr Asp Cys Val Asp Ile
  225      230      235      240
Asn Glu Cys Thr Leu Asn Thr Arg Thr Cys Ser Pro His Ala Asn Cys
      245      250      255
Leu Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Arg
  260      265      270
Gly Asn Gly Leu Gln Cys Ser Val Ile Pro Glu His
  275      280

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<210> 390
 <211> 85
 <212> PRT
 <213> Rat

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      <400> 390
Gly Ala Pro Met Tyr Phe Ser Glu Gly Arg Glu Arg Gly Lys Val Tyr
  1      5      10      15
Val Tyr Asn Leu Arg Gln Asn Arg Phe Val Phe Asn Gly Thr Leu Lys
      20      25      30
Asp Ser His Ser Tyr Gln Asn Ala Arg Phe Gly Ser Cys Ile Ala Ser
      35      40      45
Val Gln Asp Leu Asn Gln Asp Ser Tyr Asn Asp Val Val Gly Ala
  50      55      60
Pro Gln Glu Asp Ser His Arg Gly Ala Ile Tyr Ile Phe His Gly Phe
  65      70      75      80
Gln Thr Asn Ile Leu
      85

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<210> 391
 <211> 158
 <212> PRT
 <213> Rat

<400> 391

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Phe Gln Thr Asn Ile Leu Lys Lys Pro Val Gln Arg Ile Ser Ala Ser
 1          5          10          15
Glu Leu Ala Pro Gly Leu Gln His Phe Gly Cys Ser Ile His Gly Gln
          20          25          30
Leu Asp Leu Asn Glu Asp Gly Leu Val Asp Leu Ala Val Gly Ala Leu
          35          40          45
Gly Asn Ala Val Val Leu Trp Ala Arg Pro Val Val Gln Ile Asn Ala
          50          55          60
Ser Leu His Phe Glu Pro Ser Lys Ile Asn Ile Phe His Lys Asp Cys
65          70          75          80
Lys Arg Asn Gly Arg Asp Ala Thr Cys Leu Ala Ala Phe Leu Cys Phe
          85          90          95
Gly Pro Ile Phe Leu Ala Pro His Phe His Thr Ala Thr Val Gly Ile
          100          105          110
Arg Tyr Asn Ala Thr Met Asp Glu Arg Arg Tyr Met Pro Arg Ala His
          115          120          125
Leu Asp Glu Gly Ala Asp Gln Phe Thr Asn Arg Ala Val Leu Leu Ser
130          135          140
Ser Gly Gln Glu His Cys Gln Arg Ile Asn Phe His Val Leu
145          150          155

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<210> 392
<211> 124
<212> PRT
<213> Mouse

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<400> 392
Ala Ala Glu Gln Glu Ala Ser Ser Arg Arg Arg Gly Gly Ala Gly
 1          5          10          15
Pro Ala Leu Phe Ser Ser Gly Ser Leu Arg Ser Glu Pro Gln Pro Arg
          20          25          30
Leu Pro Gln Ala Arg Ser Arg Pro Arg Pro Ser Phe Leu Gln Ala Arg
          35          40          45
Ser Arg Pro Cys Leu Ser Gln Ala Cys Ser Pro Ala Ala Ser Val Leu
          50          55          60
Ser Ser Ser Ser Leu Cys Gly Arg Ser His Leu Leu Pro Gly Ser Leu
65          70          75          80
Pro Ala Thr Ala Phe Leu Leu Leu Leu Pro Gly Ser Leu Pro Gly Arg
          85          90          95
Arg Pro Ser Ala Ala Gln Ala Ala Pro Val Leu Ala Trp Gly Leu Val
          100          105          110
Ala Phe Gln Leu Gly Val Ala Ala Gly Ala Gly Arg
          115          120

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<210> 393
<211> 242
<212> PRT
<213> Rat

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<400> 393
Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys Gly Gln
 1          5          10          15
Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ser Ser His Leu Val
          20          25          30
Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Thr Gly Pro Glu Glu
          35          40          45
Ser His Cys Leu Gln Cys Arg Lys Gly Trp Ala Leu His His Leu Lys

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50 55 60
 Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gln Ala Thr Cys Gly Ala
 65 70 75 80
 Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg Asp Cys
 85 90 95
 Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Pro Cys Lys
 100 105 110
 Lys Cys Ser Arg Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu Asp Val
 115 120 125
 Asp Glu Cys Glu Thr Val Val Cys Pro Gly Glu Asn Glu Gln Cys Glu
 130 135 140
 Asn Thr Glu Gly Ser Tyr Arg Cys Val Cys Ala Glu Gly Phe Arg Gln
 145 150 155 160
 Glu Asp Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala Gly Phe
 165 170 175
 Phe Ala Glu Met Thr Glu Asp Glu Met Val Val Leu Gln Gln Met Phe
 180 185 190
 Phe Gly Val Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys Gly Asp
 195 200 205
 Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met Thr Gly
 210 215 220
 Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe Ile Lys
 225 230 235 240
 Gly Arg

<210> 394
 <211> 99
 <212> PRT
 <213> Mouse

<400> 394
 Met Arg Leu Leu Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Cys
 1 5 10 15
 Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro
 20 25 30
 Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
 35 40 45
 Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Ser Met Ser
 50 55 60
 Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr
 65 70 75 80
 Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val
 85 90 95
 Tyr Glu Glu

<210> 395
 <211> 103
 <212> PRT
 <213> Human

<400> 395
 Met Ala Leu Gly Val Pro Ile Ser Val Tyr Leu Leu Phe Asn Ala Met
 1 5 10 15
 Thr Ala Leu Thr Glu Glu Ala Ala Val Thr Val Thr Pro Pro Ile Thr
 20 25 30

Ala Gln Gln Gly Asn Trp Thr Val Asn Lys Thr Glu Ala Asp Asn Ile
 35 40 45
 Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu Asp His
 50 55 60
 Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Glu
 65 70 75 80
 Lys Ala Ile Cys Arg Cys Leu Lys Leu Lys Ser Pro Tyr Asn Val Cys
 85 90 95
 Ser Gly Glu Arg Arg Pro Leu
 100

<210> 396
 <211> 1529
 <212> PRT
 <213> Rat

<400> 396
 Met Ser Gly Ile Gly Trp Gln Thr Leu Ser Leu Ser Leu Ala Leu Val
 1 5 10 15
 Leu Ser Ile Leu Asn Lys Val Ala Pro His Ala Cys Pro Ala Gln Cys
 20 25 30
 Ser Cys Ser Gly Ser Thr Val Asp Cys His Gly Leu Ala Leu Arg Ser
 35 40 45
 Val Pro Arg Asn Ile Pro Arg Asn Thr Glu Arg Leu Asp Leu Asn Gly
 50 55 60
 Asn Asn Ile Thr Arg Ile Thr Lys Thr Asp Phe Ala Gly Leu Arg His
 65 70 75 80
 Leu Arg Val Leu Gln Leu Met Glu Asn Lys Ile Ser Thr Ile Glu Arg
 85 90 95
 Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn Arg
 100 105 110
 Asn Asn Leu Gln Leu Phe Pro Glu Leu Leu Phe Leu Gly Thr Ala Lys
 115 120 125
 Leu Tyr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Ala Ile Pro Arg
 130 135 140
 Lys Ala Phe Arg Gly Ala Val Asp Ile Lys Asn Leu Gln Leu Asp Tyr
 145 150 155 160
 Asn Gln Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu Arg Asp
 165 170 175
 Leu Glu Val Leu Thr Leu Asn Asn Asn Asn Ile Thr Arg Leu Ser Val
 180 185 190
 Ala Ser Phe Asn His Met Pro Lys Leu Arg Thr Phe Arg Leu His Ser
 195 200 205
 Asn Asn Leu Tyr Cys Asp Cys His Leu Ala Trp Leu Ser Asp Trp Leu
 210 215 220
 Arg Gln Arg Pro Arg Val Gly Leu Tyr Thr Gln Cys Met Gly Pro Ser
 225 230 235 240
 His Leu Arg Gly His Asn Val Ala Glu Val Gln Lys Arg Glu Phe Val
 245 250 255
 Cys Ser Gly His Gln Ser Phe Met Ala Pro Ser Cys Ser Val Leu His
 260 265 270
 Cys Pro Ile Ala Cys Thr Cys Ser Asn Asn Ile Val Asp Cys Arg Gly
 275 280 285
 Lys Gly Leu Thr Glu Ile Pro Thr Asn Leu Pro Glu Thr Ile Thr Glu
 290 295 300
 Ile Arg Leu Glu Gln Asn Ser Ile Arg Val Ile Pro Pro Gly Ala Phe
 305 310 315 320

Ser Pro Tyr Lys Lys Leu Arg Arg Leu Asp Leu Ser Asn Asn Gln Ile
 325 330 335
 Ser Glu Leu Ala Pro Asp Ala Phe Gln Gly Leu Arg Ser Leu Asn Ser
 340 345 350
 Leu Val Leu Tyr Gly Asn Lys Ile Thr Glu Leu Pro Lys Ser Leu Phe
 355 360 365
 Glu Gly Leu Phe Ser Leu Gln Leu Leu Leu Asn Ala Asn Lys Ile
 370 375 380
 Asn Cys Leu Arg Val Asp Ala Phe Gln Asp Leu His Asn Leu Asn Leu
 385 390 395 400
 Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Val Ala Lys Gly Thr Phe
 405 410 415
 Ser Ala Leu Arg Ala Ile Gln Thr Met His Leu Ala Gln Asn Pro Phe
 420 425 430
 Ile Cys Asp Cys His Leu Lys Trp Leu Ala Asp Tyr Leu His Thr Asn
 435 440 445
 Pro Ile Glu Thr Ser Gly Ala Arg Cys Thr Ser Pro Arg Arg Leu Ala
 450 455 460
 Asn Lys Arg Ile Gly Gln Ile Lys Ser Lys Lys Phe Arg Cys Ser Ala
 465 470 475 480
 Lys Glu Gln Tyr Phe Ile Pro Gly Thr Glu Asp Tyr Arg Ser Lys Leu
 485 490 495
 Ser Gly Asp Cys Phe Ala Asp Leu Ala Cys Pro Glu Lys Cys Arg Cys
 500 505 510
 Glu Gly Thr Thr Val Asp Cys Ser Asn Gln Lys Leu Asn Lys Ile Pro
 515 520 525
 Asp His Ile Pro Gln Tyr Thr Ala Glu Leu Arg Leu Asn Asn Asn Glu
 530 535 540
 Phe Thr Val Leu Glu Ala Thr Gly Ile Phe Lys Lys Leu Pro Gln Leu
 545 550 555 560
 Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Thr Asp Ile Glu Glu Gly
 565 570 575
 Ala Phe Glu Gly Ala Ser Gly Val Asn Glu Ile Leu Leu Thr Ser Asn
 580 585 590
 Arg Leu Glu Asn Val Gln His Lys Met Phe Lys Gly Leu Glu Ser Leu
 595 600 605
 Lys Thr Leu Met Leu Arg Ser Asn Arg Ile Ser Cys Val Gly Asn Asp
 610 615 620
 Ser Phe Thr Gly Leu Gly Ser Val Arg Leu Leu Ser Leu Tyr Asp Asn
 625 630 635 640
 Gln Ile Thr Thr Val Ala Pro Gly Ala Phe Gly Thr Leu His Ser Leu
 645 650 655
 Ser Thr Leu Asn Leu Leu Ala Asn Pro Phe Asn Cys Asn Cys His Leu
 660 665 670
 Ala Trp Leu Gly Glu Trp Leu Arg Arg Lys Arg Ile Val Thr Gly Asn
 675 680 685
 Pro Arg Cys Gln Lys Pro Tyr Phe Leu Lys Glu Ile Pro Ile Gln Asp
 690 695 700
 Val Ala Ile Gln Asp Phe Thr Cys Asp Asp Gly Asn Asp Asp Asn Ser
 705 710 715 720
 Cys Ser Pro Leu Ser Arg Cys Pro Ser Glu Cys Thr Cys Leu Asp Thr
 725 730 735
 Val Val Arg Cys Ser Asn Lys Gly Leu Lys Val Leu Pro Lys Gly Ile
 740 745 750
 Pro Arg Asp Val Thr Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu
 755 760 765
 Val Pro Lys Glu Leu Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu

770		775		780
Ser Asn Asn Arg Ile	Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met			
785	790	795	800	
Thr Gln Leu Leu Thr	Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile			
	805	810	815	
Pro Pro Arg Thr Phe	Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu			
	820	825	830	
His Gly Asn Asp Ile	Ser Val Val Pro Glu Gly Ala Phe Gly Asp Leu			
	835	840	845	
Ser Ala Leu Ser His	Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp			
	850	855	860	
Cys Asn Met Gln Trp	Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu			
	865	870	875	880
Pro Gly Ile Ala Arg	Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu			
	885	890	895	
Leu Leu Thr Thr Pro	Ser Lys Lys Phe Thr Cys Gln Gly Pro Val Asp			
	900	905	910	
Val Thr Ile Gln Ala	Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys			
	915	920	925	
Asn Asp Gly Thr Cys	Asn Asn Asp Pro Val Asp Phe Tyr Arg Cys Thr			
	930	935	940	
Cys Pro Tyr Gly Phe	Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala			
	945	950	955	960
Cys Ile Ser Asn Pro	Cys Lys His Gly Gly Thr Cys His Leu Lys Glu			
	965	970	975	
Gly Glu Asn Asp Gly	Phe Trp Cys Thr Cys Ala Asp Gly Phe Glu Gly			
	980	985	990	
Glu Ser Cys Asp Ile	Asn Ile Asp Asp Cys Glu Asp Asn Asp Cys Glu			
	995	1000	1005	
Asn Asn Ser Thr Cys	Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys			
	1010	1015	1020	
Pro Pro Glu Tyr Thr	Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys			
	1025	1030	1035	104
Ala Gln Asp Leu Asn	Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr			
	1045	1050	1055	
Pro Lys Gly Phe Lys	Cys Asp Cys Thr Pro Gly Tyr Ile Gly Glu His			
	1060	1065	1070	
Cys Asp Ile Asp Phe	Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly			
	1075	1080	1085	
Ala His Cys Thr Asp	Ala Val Asn Gly Tyr Thr Cys Val Cys Pro Glu			
	1090	1095	1100	
Gly Tyr Ser Gly Leu	Phe Cys Glu Phe Ser Pro Pro Met Val Leu Leu			
	1105	1110	1115	112
Arg Thr Ser Pro Cys	Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys			
	1125	1130	1135	
Ile Ile Arg Val Asn	Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Leu			
	1140	1145	1150	
Gly Glu Lys Cys Glu	Lys Leu Val Ser Val Asn Phe Val Asn Lys Glu			
	1155	1160	1165	
Ser Tyr Leu Gln Ile	Pro Ser Ala Lys Val Arg Pro Gln Thr Asn Ile			
	1170	1175	1180	
Thr Leu Gln Ile Ala	Thr Asp Glu Asp Ser Gly Ile Leu Leu Tyr Lys			
	1185	1190	1195	120
Gly Asp Lys Asp His	Ile Ala Val Glu Leu Tyr Arg Gly Arg Val Arg			
	1205	1210	1215	
Ala Ser Tyr Asp Thr	Gly Ser His Pro Ala Ser Ala Ile Tyr Ser Val			
	1220	1225	1230	

Glu Thr Ile Asn Asp Gly Asn Phe His Ile Val Glu Leu Leu Thr Leu
 1235 1240 1245
 Asp Ser Ser Leu Ser Leu Ser Val Asp Gly Gly Ser Pro Lys Ile Ile
 1250 1255 1260
 Thr Asn Leu Ser Lys Gln Ser Thr Leu Asn Phe Asp Ser Pro Leu Tyr
 1265 1270 1275 128
 Val Gly Gly Met Pro Gly Lys Asn Asn Val Ala Ser Leu Arg Gln Ala
 1285 1290 1295
 Pro Gly Gln Asn Gly Thr Ser Phe His Gly Cys Ile Arg Asn Leu Tyr
 1300 1305 1310
 Ile Asn Ser Glu Leu Gln Asp Phe Arg Lys Val Pro Met Gln Thr Gly
 1315 1320 1325
 Ile Leu Pro Gly Cys Glu Pro Cys His Lys Lys Val Cys Ala His Gly
 1330 1335 1340
 Thr Cys Gln Pro Ser Ser Gln Ser Gly Phe Thr Cys Glu Cys Glu Glu
 1345 1350 1355 136
 Gly Trp Met Gly Pro Leu Cys Asp Gln Arg Thr Asn Asp Pro Cys Leu
 1365 1370 1375
 Gly Asn Lys Cys Val His Gly Thr Cys Leu Pro Ile Asn Ala Phe Ser
 1380 1385 1390
 Tyr Ser Cys Lys Cys Leu Glu Gly His Gly Gly Val Leu Cys Asp Glu
 1395 1400 1405
 Glu Glu Asp Leu Phe Asn Pro Cys Gln Val Ile Lys Cys Lys His Gly
 1410 1415 1420
 Lys Cys Arg Leu Ser Gly Leu Gly Gln Pro Tyr Cys Glu Cys Ser Ser
 1425 1430 1435 144
 Gly Phe Thr Gly Asp Ser Cys Asp Arg Glu Ile Ser Cys Arg Gly Glu
 1445 1450 1455
 Arg Ile Arg Asp Tyr Tyr Gln Lys Gln Gln Gly Tyr Ala Ala Cys Gln
 1460 1465 1470
 Thr Thr Lys Lys Val Ser Arg Leu Glu Cys Arg Gly Gly Cys Ala Gly
 1475 1480 1485
 Gly Gln Cys Cys Gly Pro Leu Arg Ser Lys Arg Arg Lys Tyr Ser Phe
 1490 1495 1500
 Glu Cys Thr Asp Gly Ser Ser Phe Val Asp Glu Val Glu Lys Val Val
 1505 1510 1515 152
 Lys Cys Gly Cys Thr Arg Cys Ala Ser
 1525

<210> 397
 <211> 8
 <212> PRT
 <213> Mouse

<400> 397
 Trp Tyr Asn Ala Trp Asn Glu Lys
 1 5

<210> 398
 <211> 7
 <212> PRT
 <213> Mouse

<400> 398
 Met Val Ile Ile Thr Thr Lys
 1 5

<210> 399
 <211> 2206
 <212> DNA
 <213> Rat

<400> 399
 gtttcgtctt aacgccctct ctgctgtggc agaactggcc gtgggctccc gctggtacca 60
 tggaaacatct cagcccacac agactaagcg gagactgatg ttggtggcgt tcctcggagc 120
 atcccggttg actgcaagta ccggtctcct gtggaagaag gctcacgcag aatctccacc 180
 gagcgtcaac agcaagaaga ctgacgtggc agataagggg aagagcaagg acaccggga 240
 agtgtccagc catgaaggaa gcgctgcaga cactgcggcc gagccttacc cagaggagaa 300
 gaagaagaag cgttctggat tcagagacag aaaagtaatg gagtatgaga ataggatccg 360
 agcctactcc acaccagaca aaatcttccg gtattttgcc accttgaaag taatcaacga 420
 acctggtgaa actgaagtgt tcatgacccc acaggacttt gtgcgctcca taacacccaa 480
 tgagaagcag ccagaacact tgggcctgga tcagtacata ataaagcgt tcgatggaaa 540
 gaaaattggc caggaacgag aaaagtttgc tgacgaaggc agcatcttct atacccttg 600
 agagtgtgga ctcatctcct tctctgacta catcttctc acaacgggtg tctccactcc 660
 tcagagaaat ttcgaaattg ccttcaagat gtttgacttg aatggagatg gagaagtaga 720
 catggaggag tttgagcagg ttcaaagcat cattcgctcc cagaccagca tgggcatgcg 780
 tcacagagat cgtccaacta ctgggaacac cctcaagctt ggcttatgtt cgccctcac 840
 gacctacttt tttggagctg atctcaaagg gaaactgacc attaaaaact tcctggaatt 900
 tcagcgtaaa ctgcagcatg acgttctaaa gctggagttt gaacgccatg acccggtaga 960
 cgggagaatc tctgagaggc agttcggtag catgctgctg gcctacagtg gaggtcagtc 1020
 caagaagctg accgccatgc agaggcagct gaagaagcac ttcaaggatg ggaagggcct 1080
 gactttccag gaggtggaga acttcttcac tttcctgaag aacattaatg acgtggacac 1140
 tgcgttaagc ttttaccaca tggctggagc atccctcgat aaagtgaaca tgcagcaagt 1200
 ggccaggaca gtggcgaaag tcgagctgtc ggaccacgtg tgtgacgtgg tgtttgact 1260
 ctttgactgc gacggcaatg gggagctgag caataaggag tttgtctcca tcatgaagca 1320
 gcggctgatg agaggcctgg agaagcccaa ggacatgggc ttaccctgc tcatgcaggc 1380
 catgtggaaa tgtgcccaag aaaccgcctg ggactttgct ctacccaaat agtaccacac 1440
 ctctctgacc ttagcaccac gcaatcctgg agtggccttc atgctgctga tgcttctggg 1500
 agtagtgccc acatcccat ctttctggaa gtgacctctg gcctcagctg gctgacctct 1560
 ccactctccc ctgaccagct cagtgttccg ctaggctctg aatctgcagt cagatcaaa 1620
 gtctaagaca ggaacaagtc ttcaaagcag agaccatagc tcccttaacc agtgccccgt 1680
 gggtaaatgc ggggagccct cccacactgg cagccccagg aggcattctc gcagtctctc 1740
 actgtggatt taagtaacac aaacgtccct gccatcttcc tcccactgtt ttaaagctgc 1800
 aagtttggaa atactctggc agggcaaagg aagtctgtga tgaacggtaa tgcagatgac 1860
 cctggtaccc tgatctggca gggcacctgg tcagggggaa ggtctgcgtc agacaccagc 1920
 ggcaccagga aggtctcttg ccaccagcac agctcccgat tcaaagtcgc tgccttgagc 1980
 ggctctccag aacctcctgc tctttttttt ttctcccggt ctccctgcga tgctctctct 2040
 gggactctgc ttacttagag ccagggtgga gccctgttct cttgtgtctt gtccctctct 2100
 tatagacctg cagagcgag cttagagcct atctgcctc tgtctaatac actcgtaaat 2160
 atcactttaa ttatagcact ttgcaggaaa taccctaaaa aaaaaa 2206

<210> 400
 <211> 160
 <212> DNA
 <213> Mouse

<400> 400
 tcgcaggacg ctactggac agcttgggct tttttcagtt gattttatgg ttgcatctt 60
 tctctttctc tttttctgtt tcttgttccc ctttccctt ttctggtga gaaagcacat 120
 attactgagc cattgcaagc aatgggaggg gtccacaatg 160

<210> 401
 <211> 430
 <212> DNA

<213> Rat

<400> 401

ggcaccagcc	cggtctctgt	gtctccgtca	gtctccagcg	atccctccct	acctccgccc	60
tccatggggt	cgctcctgtg	ctgtgggcct	aagctggccg	cctgtggcat	cgctcctcagc	120
gcctggggag	tgatcatgtt	gataatgctc	gggatatatt	tcaatgtcca	ttctgctgtg	180
ttaatggagg	atgtccctt	cacagagaaa	gattttgaga	acggccctca	gaacatatac	240
aacctgtacg	agcaagtcag	ctaacaactgt	ttcatcgccg	cgggcctcta	cctcctcctc	300
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agcgcagtcc	gactctcccc	attccctccc	ttattttaaag	actcctcagt	ccatctgttc	420
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<210> 402

<211> 190

<212> DNA

<213> Rat

<400> 402

ccgaatacgc	ggcgcgctcg	acatactgcc	tgtagagtta	gtattttctgt	tttttatatg	60
ttgcacactg	aattgaagaa	atgttggttt	ttcttggttt	gttttagttt	gtttctttgg	120
ttttgttttt	ggttttgctt	ttacttccc	aggtttgact	atttgccaat	gccgtcgacg	180
cggccgcgaa						190

<210> 403

<211> 1774

<212> DNA

<213> Mouse

<400> 403

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tgcgccatgt	gcactggaag	acgtgggctcg	cgatcaagtg	ctcgcccagt	ctgcacgtcg	180
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gatacattct	actgtgtac	ggcatatgcc	aggaacctgt	cggtctgggtc	atggagtaca	300
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tgtcgacct	agacctgaag	ccagcgaaca	tctgtctgga	tgcctactac	catgtcaaga	480
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aggccagcac	aaggctgctg	ctagagaaga	atgcttctgt	caatgagggt	gactttgagg	1620
gccgaacacc	catgcatgta	gcctgccagc	atggacagga	gaacattgtg	cgcacctgc	1680

tccgccgtgg tgtggatgtg ggcctgcagg gaaaggatgc ctggttcct ctgcactatg 1740
ctgcctggca aggccacctt cccattggta agct 1774

<210> 404
<211> 372
<212> DNA
<213> Mouse

<400> 404
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gactgcccgc ctctggggct tccttttagag gagacagtct ttacccatct agactcctgc 120
caccctgact gctgacttac agctatgagg tcccggcttc tgctgcccgt gcccatttg 180
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gcgtccccc gcctggatga ctacgtcagg tgtatctgtc agctggcaca gccacacctca 300
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cgagagaaga gg 372

<210> 405
<211> 396
<212> DNA
<213> Mouse

<400> 405
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ccttccatgc ggaaacccaa gcagcggccg cgcccgagc ccctcatcat cccacccaag 180
gccccgactt tcatcgcccc tctgtctac tccaacatca ccccttacca gagccacctg 240
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<210> 406
<211> 444
<212> PRT
<213> Rat

<400> 406
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1 5 10 15
Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser
20 25 30
Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu
35 40 45
Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr
50 55 60
Pro Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val
65 70 75 80
Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile
85 90 95
Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr
100 105 110
Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn
115 120 125
Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg
130 135 140
Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu
145 150 155 160

Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser
 165 170 175
 Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe
 180 185 190
 Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp
 195 200 205
 Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser
 210 215 220
 Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys
 225 230 235 240
 Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu
 245 250 255
 Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu
 260 265 270
 Gln His Asp Val Leu Lys Leu Glu Phe Glu Arg His Asp Pro Val Asp
 275 280 285
 Gly Arg Ile Ser Glu Arg Gln Phe Gly Gly Met Leu Leu Ala Tyr Ser
 290 295 300
 Gly Val Gln Ser Lys Lys Leu Thr Ala Met Gln Arg Gln Leu Lys Lys
 305 310 315 320
 His Phe Lys Asp Gly Lys Gly Leu Thr Phe Gln Glu Val Glu Asn Phe
 325 330 335
 Phe Thr Phe Leu Lys Asn Ile Asn Asp Val Asp Thr Ala Leu Ser Phe
 340 345 350
 Tyr His Met Ala Gly Ala Ser Leu Asp Lys Val Thr Met Gln Gln Val
 355 360 365
 Ala Arg Thr Val Ala Lys Val Glu Leu Ser Asp His Val Cys Asp Val
 370 375 380
 Val Phe Ala Leu Phe Asp Cys Asp Gly Asn Gly Glu Leu Ser Asn Lys
 385 390 395 400
 Glu Phe Val Ser Ile Met Lys Gln Arg Leu Met Arg Gly Leu Glu Lys
 405 410 415
 Pro Lys Asp Met Gly Phe Thr Arg Leu Met Gln Ala Met Trp Lys Cys
 420 425 430
 Ala Gln Glu Thr Ala Trp Asp Phe Ala Leu Pro Lys
 435 440

<210> 407
 <211> 53
 <212> PRT
 <213> Mouse

<400> 407
 Arg Arg Thr Leu Thr Gly Gln Leu Gly Leu Phe Ser Val Asp Phe Met
 1 5 10 15
 Val Cys Ile Phe Leu Phe Leu Phe Phe Cys Phe Leu Phe Pro Phe Pro
 20 25 30
 Leu Phe Leu Val Arg Lys His Ile Leu Leu Ser His Cys Lys Gln Trp
 35 40 45
 Glu Gly Ser Thr Met
 50

<210> 408
 <211> 119
 <212> PRT
 <213> Rat

<400> 408
 Gly Thr Ser Pro Ala Ser Val Leu Arg Ser Val Ser Ser Asp Pro Ser
 1 5 10 15
 Leu Pro Pro Pro Ser Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu
 20 25 30
 Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile
 35 40 45
 Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu Ile Glu Asp
 50 55 60
 Val Pro Phe Thr Glu Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr
 65 70 75 80
 Asn Leu Tyr Glu Gln Val Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu
 85 90 95
 Tyr Leu Leu Leu Gly Gly Phe Ser Phe Cys Gln Val Arg Leu Asn Lys
 100 105 110
 Arg Lys Glu Tyr Met Val Arg
 115

<210> 409
 <211> 590
 <212> PRT
 <213> Mouse

<400> 409
 Lys Val Glu Gly Glu Gly Arg Gly Arg Trp Ala Leu Gly Leu Leu Arg
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 Thr Phe Asp Ala Gly Glu Phe Ala Gly Trp Glu Lys Val Gly Ser Gly
 20 25 30
 Gly Phe Gly Gln Val Tyr Lys Val Arg His Val His Trp Lys Thr Trp
 35 40 45
 Leu Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Asp Arg Glu Arg
 50 55 60
 Met Glu Leu Leu Glu Glu Ala Lys Lys Met Glu Met Ala Lys Phe Arg
 65 70 75 80
 Tyr Ile Leu Pro Val Tyr Gly Ile Cys Gln Glu Pro Val Gly Leu Val
 85 90 95
 Met Glu Tyr Met Glu Thr Gly Ser Leu Glu Lys Leu Leu Ala Ser Glu
 100 105 110
 Pro Leu Pro Trp Asp Leu Arg Phe Arg Ile Val His Glu Thr Ala Val
 115 120 125
 Gly Met Asn Phe Leu His Cys Met Ser Pro Pro Leu Leu His Leu Asp
 130 135 140
 Leu Lys Pro Ala Asn Ile Leu Leu Asp Ala His Tyr His Val Lys Ile
 145 150 155 160
 Ser Asp Phe Gly Leu Ala Lys Cys Asn Gly Met Ser His Ser His Asp
 165 170 175
 Leu Ser Met Asp Gly Leu Phe Gly Thr Ile Ala Tyr Leu Pro Pro Glu
 180 185 190
 Arg Ile Arg Glu Lys Ser Arg Leu Phe Asp Thr Lys His Asp Val Tyr
 195 200 205
 Ser Phe Ala Ile Val Ile Trp Gly Val Leu Thr Gln Lys Lys Pro Phe
 210 215 220
 Ala Asp Glu Lys Asn Ile Leu His Ile Met Met Lys Val Val Lys Gly
 225 230 235 240
 His Arg Pro Glu Leu Pro Pro Ile Cys Arg Pro Arg Pro Arg Ala Cys
 245 250 255
 Ala Ser Leu Ile Gly Ile Met Gln Arg Cys Trp His Ala Asp Pro Gln

260 265 270
 Val Arg Pro Thr Phe Gln Glu Ile Thr Ser Glu Thr Glu Asp Leu Cys
 275 280 285
 Glu Lys Pro Asp Glu Glu Val Lys Asp Leu Ala His Glu Pro Gly Glu
 290 295 300
 Lys Ser Ser Leu Glu Ser Lys Ser Glu Ala Arg Pro Glu Ser Ser Arg
 305 310 315 320
 Leu Lys Arg Ala Ser Ala Pro Pro Phe Asp Asn Asp Cys Ser Leu Ser
 325 330 335
 Glu Leu Leu Ser Gln Leu Asp Ser Gly Ile Ser Gln Thr Leu Glu Gly
 340 345 350
 Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Cys Lys Leu Pro Ser Ser
 355 360 365
 Ser Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val Asp Ser Ala Phe
 370 375 380
 Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg Glu Ala Ser Thr
 385 390 395 400
 Gly Asp Leu Gly Pro Thr Asp Ile Gln Lys Lys Lys Leu Val Asp Ala
 405 410 415
 Ile Ile Ser Gly Asp Thr Ser Arg Leu Met Lys Ile Leu Gln Pro Gln
 420 425 430
 Asp Val Asp Leu Val Leu Asp Ser Ser Ala Ser Leu Leu His Leu Ala
 435 440 445
 Val Glu Ala Gly Gln Glu Glu Cys Val Lys Trp Leu Leu Leu Asn Asn
 450 455 460
 Ala Asn Pro Asn Leu Thr Asn Arg Lys Gly Ser Thr Pro Leu His Met
 465 470 475 480
 Ala Val Glu Arg Lys Gly Arg Gly Ile Val Glu Leu Leu Leu Ala Arg
 485 490 495
 Lys Thr Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr Ala Leu His
 500 505 510
 Phe Ala Ala Gln Asn Gly Asp Glu Ala Ser Thr Arg Leu Leu Leu Glu
 515 520 525
 Lys Asn Ala Ser Val Asn Glu Val Asp Phe Glu Gly Arg Thr Pro Met
 530 535 540
 His Val Ala Cys Gln His Gly Gln Glu Asn Ile Val Arg Thr Leu Leu
 545 550 555 560
 Arg Arg Gly Val Asp Val Gly Leu Gln Gly Lys Asp Ala Trp Leu Pro
 565 570 575
 Leu His Tyr Ala Ala Trp Gln Gly His Leu Pro Ile Gly Lys
 580 585 590

<210> 410

<211> 339

<212> DNA

<213> Human

<400> 410

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aacaaaacag	aagctgacaa	catagaagga	cccatagcct	tgaagttctc	acacctttgc	180
ctggaagatc	ataacagtta	ctgcatcaac	ggtgcttggtg	cattccacca	tgagctagag	240
aaagccatct	gcaggtgttt	tactggttat	actggagaaa	ggtgtctaaa	attgaaatcg	300
ccttacaatg	tctgttctgg	agaaagacga	ccactgtga			339

<210> 411

<211> 285

<212> DNA
<213> Human

<400> 411
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gaagaggcag ccgtgactgt aacacctcca atcacagccc agcaagctga caacatagaa 120
ggacccatag ccttgaagtt ctcacacctt tgcctggaag atcataacag ttactgcac 180
aacggtgctt gtgcattcca ccatgagcta gagaaagcca tctgcagggtg tctaaaattg 240
aatcgccctt acaatgtctg ttctggagaa agacgaccac tgtga 285

<210> 412
<211> 460
<212> DNA
<213> Human

<400> 412
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cttttattca acgctgacaa catagaagga cccatagcct tgaagttctc acacctttgc 120
ctggaagatc ataacagtta ctgcacaaac ggtgcttgtg cattccacca tgagctagag 180
aaagccatct gcaggtgtct aaaattgaaa tgcctttaca atgtctgttc tggagaaaga 240
cgaccactgt gaggcctttg tgaagaattt tcatcaaggc atctgtagag atcagtgagc 300
ccaaaattaa agttttcaga tgaaacaaca aaacttgtca agctgactag actcgaaaat 360
aatgaaagtt gggatcacaa tgaatgaga agataaaatt cagcgtttgc ctttagactt 420
tgccatcctt aaggagtgtat ggaagccaag tgaacaagcc 460

<210> 413
<211> 112
<212> PRT
<213> Human

<400> 413
Met Ala Leu Gly Val Pro Ile Ser Val Tyr Leu Leu Phe Asn Ala Met
1 5 10 15
Thr Ala Leu Thr Glu Glu Ala Ala Val Thr Val Thr Pro Pro Ile Thr
20 25 30
Ala Gln Gln Gly Asn Trp Thr Val Asn Lys Thr Glu Ala Asp Asn Ile
35 40 45
Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu Asp His
50 55 60
Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Glu
65 70 75 80
Lys Ala Ile Cys Arg Cys Phe Thr Gly Tyr Thr Gly Glu Arg Cys Leu
85 90 95
Lys Leu Lys Ser Pro Tyr Asn Val Cys Ser Gly Glu Arg Arg Pro Leu
100 105 110

<210> 414
<211> 94
<212> PRT
<213> Human

<400> 414
Met Ala Leu Gly Val Pro Ile Ser Val Tyr Leu Leu Phe Asn Ala Met
1 5 10 15
Thr Ala Leu Thr Glu Glu Ala Ala Val Thr Val Thr Pro Pro Ile Thr
20 25 30
Ala Gln Gln Ala Asp Asn Ile Glu Gly Pro Ile Ala Leu Lys Phe Ser


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      35              40              45
His Leu Cys Leu Glu Asp His Asn Ser Tyr Cys Ile Asn Gly Ala Cys
      50              55              60
Ala Phe His His Glu Leu Glu Lys Ala Ile Cys Arg Cys Leu Lys Leu
      65              70              75              80
Lys Ser Pro Tyr Asn Val Cys Ser Gly Glu Arg Arg Pro Leu
      85              90

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<210> 415
 <211> 73
 <212> PRT
 <213> Human

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      <400> 415
Met Ala Leu Gly Val Pro Ile Ser Val Tyr Leu Leu Phe Asn Ala Asp
      1              5              10              15
Asn Ile Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu
      20              25              30
Asp His Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu
      35              40              45
Leu Glu Lys Ala Ile Cys Arg Cys Leu Lys Leu Lys Ser Pro Tyr Asn
      50              55              60
Val Cys Ser Gly Glu Arg Arg Pro Leu
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<210> 416
 <211> 312
 <212> DNA
 <213> Human

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      <400> 416
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ggacccatag ccttgaagtt ctcacacctt tgcctgggag atcataacag ttactgcac      180
aacggtgctt gtgcattcca ccatgagcta gagaaagcca tctgcaggtg ttttactggt      240
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cgaccactgt ga                                     312

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<210> 417
 <211> 103
 <212> PRT
 <213> Human

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      <400> 417
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      1              5              10              15
Thr Ala Leu Thr Glu Glu Ala Ala Val Thr Val Thr Pro Pro Ile Thr
      20              25              30
Ala Gln Gln Ala Asp Asn Ile Glu Gly Pro Ile Ala Leu Lys Phe Ser
      35              40              45
His Leu Cys Leu Gly Asp His Asn Ser Tyr Cys Ile Asn Gly Ala Cys
      50              55              60
Ala Phe His His Glu Leu Glu Lys Ala Ile Cys Arg Cys Phe Thr Gly
      65              70              75              80
Tyr Thr Gly Glu Arg Cys Leu Lys Leu Lys Ser Pro Tyr Asn Val Cys
      85              90              95
Ser Gly Glu Arg Arg Pro Leu

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100

<210> 418

<211> 846

<212> DNA

<213> Rat

<400> 418

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aacaaaaaaa	ccaaacagtg	ggtagctcaa	taagatagga	gaaaaatgag	agaacagacc	180
cagttctcga	cccttgcttc	tcaaggctct	cccaccaggc	tgccaaagca	agatggtgtt	240
gctctgatcc	agtcagtatt	cttttgactt	ttttttttaa	tctccagggt	ttgggttcagg	300
ctcccatatt	cataccctgg	ctcatattagc	ttccctcat	gttggtgggtt	cttctgtccc	360
tcacccctt	actctcccca	ctgatattct	tccagtcac	gactgtggct	ctggaagaaa	420
tatccacat	ttgcagagct	gatgttctgt	agatcgtaat	gttgaagcgc	tgggtgtcct	480
ggttggcaga	atcactcctg	tattactctg	gtacataggt	gtctcctgat	agactccctg	540
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cgagtgtttc	tgtagatgta	gattgggaatg	tgtccataac	agagaggcca	gtgagagaca	720
tccccaagga	cctggcaggc	tttccttcgc	tccaggaaga	cgcaccatca	ctcaaaaggg	780
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gaacct						846

<210> 419

<211> 960

<212> DNA

<213> Mouse

<400> 419

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cgacaagggtg	aagctgacct	ggagggaccg	attcccagcc	tatttcacca	atcttgtctc	120
catcatcttc	atgatcgag	tgacatttgc	aatcgctctc	ggagttatca	tctatagaat	180
ctccacagct	gcagccttgg	ccatgaactc	ctcccgtct	gtgcgggtcca	acatccgggt	240
tacagtcacg	gccaccgctg	ttatcatcaa	cctcgtggtc	atcattctgc	tggatgaagt	300
ttaccggctgc	attgccaggt	ggctcaccaa	gattgggtgag	tgccatgtgc	aggacagcat	360
aggcagcatg	ggcctagggc	agggccagcc	ttgaagtggg	cagcctggtc	acagaactgt	420
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agtaccgtat	gtctctctc	agaggtccca	aagacagaga	agagctttga	ggagaggcta	540
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cggatggagg	agtgtgcccc	ggcgggctgc	ctcatggagc	tctgtatcca	gctgagcatc	720
attatgctgg	gcaagcagct	aatccagaac	aatctcttcg	agattggcat	cccgaagatg	780
aaaaagttca	tccgtacct	gaagctgcgc	agacagagcc	cctcagaccg	tgaagagtac	840
gtgaagcgga	agcagcgcta	tgaggtggac	ttcaacctcg	aacctttcgc	cggcctcacg	900
cccaggtaca	tggaatgat	cattcagttc	ggctttgtca	ccctgtttgt	tgcgtccttc	960

<210> 420

<211> 1330

<212> DNA

<213> Mouse

<400> 420

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tatgtcatgt	gtcatttgaa	tagtttcagt	cacacacact	ttgtatttct	ctaagtgtaa	180
cgcattgtga	gtgggtgggt	gtagtatgat	ttctccgtct	ttcttgtttg	aatgtttgga	240

cttgtgcacg	tgtgcacatg	tgtgtgtgtg	tgtgtgtgtg	tgtgtgtgtg	tgtgtgtatt	300
tgctcctgtg	gctatgtgca	tgtgccatgt	gggtgtgtgt	gcttgtgggg	gccagaggtt	360
aggtagcttc	ctctatctct	ccaccctggt	ggtttttgtt	ttgttttgtt	ttgttttggg	420
ccaggtctat	cactgataag	ctaggttggg	tggcttctga	gaagagtctg	cctctctgtc	480
cccctgcccc	tyctccccc	agccctcagg	ttacagataa	gtgccacaag	tccttgtcct	540
ttcaagtagc	ctctagggat	ccaggctcat	atccttgtgc	ttactgactg	agccacctct	600
cagctccctc	agcccggttt	tacacgttaa	ctttgtctcc	tgcttatgcc	tgctctcttc	660
agtgacccct	tccgttttcc	tttcactctt	ttctctgaat	agatttgtgt	gcgagagact	720
attatcatat	ggatgcataa	atatcatctg	caaagtcaat	cgcaggaaag	acttagagtc	780
tcttttagctt	tatgactgta	aaggattccg	cttcttgcca	ttgattcagc	ttttttgcca	840
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ggatagatgg	atttaactgc	ttttctcaag	acgcttttac	tctctcgttg	aattcttttt	1020
aaacttttaa	ttgacattgt	acttgcattc	ttatgggaaa	cagggtgacc	cacacacatg	1080
tgtacacagg	tacacacaca	gtcaggtcag	catagctggt	atgttgttgt	ttatgttggg	1140
gacagtcaga	ttggtattgt	ttttgcactg	tgctgtggaa	cattggaaaa	ccttatctga	1200
tggtagccct	gtgcctacta	acagccctca	ctaggataca	ttttggagtc	tctggcaacc	1260
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aaaaaaaa						1330

<210> 421
 <211> 880
 <212> DNA
 <213> Mouse

<400> 421			
aggaccttga	ccgacatcca gaccacggga cccgactgga tgtctcacc	tgccctgca	60
ggccctgtcc	cttccaaaac aggcacttct gtcacaggat acttttttt	ttaacttaaa	120
tttgcttggg	ggaggggagc agttctagtt ccattgaggca caaatggagg	tcaaagagca	180
acttgccgat	gtctcttctc tcctccact gtgtgggtag taggaattga	atcaggttat	240
cgatcttggg	gctgagccat ctctgtggcc cacagagcac ttatatgttg	ttacttgttg	300
ctctcacatt	gtcagtgtac agcttgggtg cctttgtcac tggcatgctc	tgtgacactg	360
ttgtgataaa	aatgttggatg agtttacaca aatctagtaa attgaacca	agagccaagt	420
gtggtgggtg	acccttaatt ccagcacttt gggggcaagt tcaggtagtt	ctctgaattt	480
gagagcctcc	tggccacat agtgagttcc atggctgctg agttgcaaaa	gaacaccaac	540
acctttcccc	cacaaataga attgtactga aggtcacagt cagagaaagc	atagcaagga	600
tggctgctct	gagccctcc tgtgcacttc ttagaccta gcccgggtgt	ctaaatggag	660
tctgatttta	gcacctgcac ttgactgctg tgctccacc tgaccgcct	tytctgac	720
ccagattgct	agaactttga ccaaatggg acttaattgg agttgtgatt	ggkatgttca	780
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aaaaaaaa	aaaaaaaa	aaaaaaaa	880

<210> 422
 <211> 533
 <212> DNA
 <213> Mouse

<400> 422			
cctaaatgct	gggattaaag gctgcccga ctactgccag gctgttttt	ttttttttt	60
ttttttatta	atgatctgc agacaaagag atgtccttt	tggtgcaaaa	120
gcttgaagtc	actatatttg attagctctg taactgatac	acaaataaaa	180
tggataatac	attatctatt attatttato tcttgttcat	ttttgcaatt	240
actcccagtt	gagtacaagg tgcccttggg gggttttcaa	ggatcttgag	300
attgctgatg	atgtctgttg aaagcattgt atggaggcct	gaggtatatt	360
gcagagtttt	taaaatagag cctgctggaa aagctagctg	gagcttctga	420
aaggcactgt	ttgaagcaca ggccatgaag taagacttgc	ttctagttta	480
ttttgttttt	ttaagtcwtt agtgtataga gatttcctac	attttttgtg	533

<210> 423
 <211> 738
 <212> DNA
 <213> Rat

<400> 423

ataaggcaca	tttgcttcat	aaaataaaaa	aaaaggaaat	ttacttagcc	gcatgtcagt	60
cacccaaatt	ttgagtgtac	aaatgaaatg	gaaaacattt	attacacaaa	tttaattaca	120
attctagggg	ataaacatgc	aaatcagatg	gagctcaatc	tgacggcgct	gatcctctcc	180
ccctgggttg	cagtctgtgc	acctcctgga	ttcgcccgcg	accaggcagt	cagaggcctg	240
gctcttgtag	gcaggaggat	cactgttgta	aagaacagcg	tcacatttag	cgcatctggc	300
gtagtacag	tttttaacac	tttgcgcagg	tgctctccct	ccccaccg	cgctttgtta	360
ggtctacctc	tctaaatctc	tgctctcttc	gcacagtaag	tgacctctcc	atgacaaagg	420
gccccagac	agcagttata	aatcaatgtg	ttttgggttt	gtttgtttgt	ttgttttgtt	480
ttaaagaaaa	accgggcat	gcttggtggc	acttgctttt	aatagtagcg	cttggttagac	540
agaggcaagc	ggttctctgt	aagtccaagg	ccagcctggt	ctacacagtg	agaccgggtc	600
tcaaaaaaaa	aacaacaaaa	aacaactcct	attgaatcca	ctacaggaag	ggggggcgcg	660
gatcactgtc	tgcaactaa	agtgacttga	gctcctgtca	cagcctttcc	agcaagggca	720
agcttcttta	ttagttat					738

<210> 424
 <211> 1035
 <212> DNA
 <213> Rat

<400> 424

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ccggggagat	tctgccgatt	tgtcacagc	catgctcagg	aggcagctcg	tctgggtggc	120
cctgctggct	ttgcttttcc	tcccattttg	cctgtgtcaa	gatgaataca	tggagtctcc	180
acaagctgga	ggactgcccc	cagactgcag	caagtgttgc	catggagatt	atggattccg	240
tggtttacaa	gggccccctg	gacccccagg	tctctctggc	attccaggaa	accatggaaa	300
caatggaaat	aacggagcca	ctggccacga	agggggccaag	ggtgagaaag	gagacaaagg	360
cgacctgggg	cctcgagggg	aacgggggca	gcattggccc	aaaggataga	agggataccc	420
aggggtgcca	ccagagctgc	agattgctgt	catggcttct	ctagcgactc	acttcagcaa	480
tcagaacagt	ggcattatct	tcagcagtgt	tgagaccaac	attggaaact	tcttcgatgt	540
catgactggt	agattttggg	cccccgatc	aggcgtgtat	ttcttcacct	tcagcatgat	600
gaagcatgag	gacgtggagg	aagtgtatgt	gtaccttatg	cacaatggta	acacgggtgt	660
cagcatgtac	agctatgaaa	caaaggga	atcagatata	tccagcaacc	atgcagtgtc	720
gaagttggcc	aaaggagatg	aagtctggct	aagaatgggc	aacggtgccc	tccatgggga	780
ccaccagcgc	ttctctacct	tcgcaggctt	tctgcttttt	gaaactaagt	gatgaggaag	840
tcaggatagc	tccatgctaa	gggcgatttg	taggtgagct	aggggtgtta	ggaactgagg	900
ggtgttgagg	ttgggcttct	ctatggagta	tttaactgtt	acattgggtc	cactgtact	960
cattctaagt	gcataccaat	tatgttggat	acttttaggg	ctaggaagaa	tagaccacaa	1020
ggtaatatcc	ccaga					1035

<210> 425
 <211> 835
 <212> DNA
 <213> Rat

<400> 425

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tcactggctg	ttgacaacct	ggggctgctt	ggcgttctca	ggctcctatg	cttggggcaa	120
cttcactatc	ctggccctgg	gtgctgtggg	ctgtggccca	gcgggactct	gttgatgcca	180
ttggcatggt	tcttggtggc	ttgggtggca	ccatcttctc	ggacattatc	tacattagca	240
tcttctactc	aagcgttgcc	gttggggaca	ctggccgctt	cagtgcgggc	atggccatct	300

tcagcttgct	gctgcaagcc	cttctcctgc	tgcctcgtct	accacatgca	ccgggcagcg	360
agggggtgag	ctcccgctcc	gctcggatct	cttcggacct	tctcaggaac	atagtgcccta	420
ccagacaatt	gactcgtcag	actcacctgc	agacccctt	gcaagcctgg	agaacaagg	480
ccaagctgcc	ccccgggggt	actgaagctg	tccctggccg	tccctggggcc	cagcaggatg	540
cttgctcacct	tctttactgg	acctacaatg	gggtatcctc	cattccctgc	cacagagggtg	600
gcctgagtca	tgtgccctcg	gagggtccag	ctgagaagag	cccagtccta	attctccatg	660
ctgccctccc	attcaagaca	cctgttaacc	cctgggctag	aactgtgggt	ggtttcttcc	720
cctcctcccc	atcactataa	cacacaaccg	ccgagctgtg	cagagtgttc	agggccatcc	780
aggccttatg	ggccaatgat	cactgcctct	caggctaccc	caaggtgacc	cagcc	835

<210> 426

<211> 1337

<212> DNA

<213> Mouse

<220>

<221> unsure

<222> (626) ... (626)

<400> 426

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cttatatgta	catgtgctta	tatccgatcc	ctggcaccga	gcacccctga	cagaaataaa	120
actggactat	tgggaatatt	ttggaagtgt	gcccgaattg	gggaacgcaa	gagtccttat	180
gtcgccatat	gctgtatagt	gatggccttc	agcatcctct	tcatacagta	gcttttgaaa	240
ctaccagcat	gtgcttgcta	tcagactgta	aacaaggact	tgccctccaga	aaataatggg	300
aagaatgggt	aagccatttg	tctctgaaca	tggaaatgaga	taaacttcaa	gatgctgttc	360
tctattttta	tgctattgga	ccaatgagct	gaatgaataa	ttaagatgta	acagttcaat	420
acacaggaat	gtgattgtat	ccatcaacct	cagttctctc	actccagtat	tacattctgc	480
aaatgtcatt	ctgttggtgc	aggactgctt	ttcataaggt	tcttcgggca	cgaagtagaa	540
accagtggtc	aaattccaag	gctcctttga	ctagggtctc	aaaataatgt	cttcacagaa	600
tggtacctct	agcgactgtc	ctattnttat	tgagaaaaaa	acttgttcta	tttttgttgt	660
tgttactgtt	cttatggatt	gcattcatat	ttaaaccttt	tggattgcta	accagagtac	720
ctctatttct	ggcaaatccc	gcagtttatt	acaggtgttt	aaagtatttt	aaacaaaact	780
ctgaatttct	ttagttagcc	taagagttgg	cttctagtca	caaagataca	gctgccacac	840
tgtgacgaag	agcaccttag	aaagaaaagc	agcaagttag	cggtgagcaa	gtaagcaccg	900
tgcagtcttc	gtgcaagtaa	gcaccgtgca	gtcttcgttc	tctgtagtct	tgtcttccaa	960
atagaacgtc	catcgtagtt	acccaaaggt	ggtattttgt	gtgttcttaa	tgcagtgcct	1020
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taaacatatc	tcatatctgc	tttagtctgg	gtactatgct	ctaagtacat	ttcagctttg	1140
acacagaatg	tgaatagacg	aatatcaaa	gatacttaca	agtttgatc	caacatttct	1200
tcagggttcag	ctgaaaatca	gttactgttt	caaaacaaag	aggaattaaa	tcctagtctga	1260
aaactataca	tagcatttat	taattaatta	ctgggtttaa	ctgctctttt	taaaagtgtg	1320
aaaaaaaaaa	aaaaaaaa					1337

<210> 427

<211> 780

<212> DNA

<213> Mouse

<400> 427

gctagtgcga	tgtccgggct	gcggacgctg	ctggggctgg	ggctgctggg	tgccgggctcg	60
cgcctgccac	gggtcatcag	ccagcagagt	gtgtgtcgtg	caaggcccat	ctgggtggga	120
acacagcgcc	ggggctcgga	gaccatggcg	ggcgctgcgg	tgaagtactt	aagtcaggag	180
gaggctcagg	ccgtggacca	agagcttttt	aacgagtatc	agttcagcgt	ggatcaactc	240
atggagctgg	ccgggttgag	ctgtgccacg	gctattgcca	aggcttatcc	ccccacgtct	300
atgtccaaga	gtccccgac	tgtcttggtc	atctgtggcc	ccggaaataa	cggaggggat	360
gggdtggtct	gtgcgcgaca	cctcaaaact	tttggttacc	agccaactat	ctattacccc	420

aaaagaccta	acaagcccct	cttactgagg	ctagtactc	agtgtcagaa	aatggacatt	480
cctttccttg	gtgaaatgcc	cccagaggat	gggatgtaga	gaagggaaac	cctagcggaa	540
tccaaccaga	cttactcatc	tactgacgg	caccaagaa	gtctgcaact	cactttactg	600
gccgatatca	ttaccttggg	ggctgctttg	taccacctgc	tctagagaag	aagtaccagc	660
tgaacctgcc	atcttaccct	gacacagagt	gtgtctaccg	tctaagataa	gggaggtggg	720
taggcaggat	tctcaataaa	gacttggtac	tttctgtctt	gaaaaaaaaa	aaaaaaaaaa	780

<210> 428
 <211> 460
 <212> DNA
 <213> Mouse

<400> 428						
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cgctgccttt	tcagctgcgc	agcatcggtc	ttatatgcga	ctaacagaaa	aggaagatga	120
atcattacca	atagatatag	ttcttcagac	acttctggcc	tttgcagtta	cctgttatgg	180
catagtctcat	atcgacgggg	agttcaaaga	catggatgcc	acttcagaat	taaagaataa	240
gacatttgat	accttaagga	atcacccatc	tttttatgtg	tttaaccatc	gtggctcagt	300
gctgttcggg	ccttcagatg	caacaaatc	ttcaaaccta	gatgcattgt	cctctaatac	360
atcgttgaag	ttacgaaagt	ttgactcact	gcgcggttaa	gctttttaca	aattaaataa	420
caggacagac	acagaattga	gtattggagt	ttgggggtga			460

<210> 429
 <211> 472
 <212> DNA
 <213> Mouse

<400> 429						
gaagcctctt	cccattggaag	cacactctag	gagagagaag	gcctctgggc	tccgcctggc	60
ctggcattat	gaatgcagtg	gggtcagtg	gtgggtggatg	tgtgtactgg	gttggctttc	120
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tcacatgctt	ccatgtttgt	ttctgagagg	tgggggctca	aatgtataga	aagtaggccc	240
cagtcataaa	ggagggtgtga	acacaccccc	ttactgctta	tcaccatttt	gacaggaagc	300
cccaggaggg	gagggggagg	ggaagagggtg	agttctgcac	agtcggacat	ttctgttgc	360
tttgcatgtt	taatatagac	gttcctgtcg	atccttggga	gatcatggcc	ttcagatatg	420
cacacgacct	ttgaattgtg	cctactaatt	atagcagggg	acttgggtac	cc	472

<210> 430
 <211> 954
 <212> DNA
 <213> Mouse

<400> 430						
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ccacagaaat	cctttattca	catgtgggta	aacctgtccc	ggcacacccc	agcagcaaca	180
gcaccctgaa	tcaagccagg	aatggaggca	ggcattttcag	tagcactgga	ctggatcgaa	240
acagtcgagt	tcaagtgggc	tgagggaac	tgcggtccac	caaatacatt	tcggacggcc	300
agtgcaccag	catcagccct	ctgaaggagc	tgggtgtgctc	gggcgagtgc	ttgcccctgc	360
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gtttgcagtg aaagccaggc atcctgtagt ttccatcccc tcccccatcc cagtcatttc 900
 tttaaaagca cctgatgctg cattctgtta cagtttaaaa aaaaaaaaaa aaaa 954

<210> 431
 <211> 780
 <212> DNA
 <213> Mouse

<400> 431
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 cgcttgcac gggtcatcag ccagcagagt gtgtgtcgtg caaggcccat ctggtgggga 120
 acacagcgcc ggggctcgga gaccatggcg ggcgctgcgg tgaagtactt aagtcaggag 180
 gaggctcagg ccgtggacca agagcttttt aacgagtatc agttcagcgt ggatcaactc 240
 atggagctgg ccgggttgag ctgtgccacg gctattgcca aggcctatcc cccacgtct 300
 atgtccaaga gtccccgac tgtcttggtc atctgtggcc ccggaataa cggaggggat 360
 gggctggtct gtgcgcgaca cctcaaatct tttggttacc agccaactat ctattacccc 420
 aaaagacctt acaagcccct cttcactggg ctagtgtact agtgtcagaa aatggacatt 480
 cctttccttg gtgaaatgcc ccagaggat gggatgtaga gaagggaac cctagcggaa 540
 tccaaccaga ctactcatc tcaactgacg caccacaaga gtctgcaact cactttactg 600
 gccgatata ttaccttggg ggtcgctttg taccacctgc tctagagaag aagtaccagc 660
 tgaacctgcc atcttaccct gacacagagt gtgtctaccg tctacagtaa gggaggtggg 720
 taggcaggat tctcaataaa gacttggtag tttctgtctt gaaaaaaaaa aaaaaaaaaa 780

<210> 432
 <211> 1144
 <212> DNA
 <213> Mouse

<400> 432
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 gccacaggaa gctgctgact ggccacttga caccctcccc cttaaagctaa tgtctgtgac 120
 tatagggagg ttagcacttt ttctaattgg aattcttctc tgtcctgtgg ccccatccct 180
 caccgcctct tggcctggac cagatacatg cagcctcttt ctccagcaca gcctttccct 240
 gaggctgagg ttagggcaga gtttagaggg tgggctaagt gtatgttttc atgtatgcat 300
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 gtggaccag ggtgggttga ttgtctcttt gtaaggaagt atgtgtcggg ggtgacacga 480
 ggctaagccc gagaaacccc gggagacagc actgcataag aaactggttt ccmagactgc 540
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 agcc 1144

<210> 433
 <211> 438
 <212> DNA
 <213> Mouse

<400> 433
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ttaatgtgca	ctggtgtttt	gcctggatgt	gtatacttgt	gaagatgtca	gaactcctgg	120
agctggagtt	agagacaatg	gtgagctgcc	ttgtggatgt	tgggaattga	acccaggtcc	180
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tttaataagt	tgcctcggtc	atgttgtctt	aatcagagcg	atagaaaagt	aactaatata	300
gattatttat	gaattcaggt	ggcttaatgg	tatatgcatg	aattagtagt	aaaacaagaa	360
ctagggccag	caagtggcct	aaggggtgct	gctaaccatc	tcagccacct	gagttcagtc	420
tccaggaacc	acacagtg					438

<210> 434
 <211> 383
 <212> DNA
 <213> Mouse

<400> 434	
cccacgtcta	tggttcacctt
gtctgctttg	gacacttcaa
acagatgccg	tgagctccag
tctgcgaaat	acatcgctca
gctcctggga	gctcaggcga
atgcctcctg	atggcctcac
aatgagattc	accagtaagg
ggt	
	60
	120
	180
	240
	300
	360
	383

<210> 435
 <211> 405
 <212> DNA
 <213> Rat

<220>
 <221> unsure
 <222> (114)...(114)

<221> unsure
 <222> (346)...(346)

<221> unsure
 <222> (353)...(353)

<221> unsure
 <222> (387)...(388)

<400> 435	
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cggctctgcg	tttgtggcct
ttcagcccca	cgagctgtgg
cgggcccat	gtttgtcatt
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ctagcgctaa	atgggtgtctt
aaattgcttc	taccgagtgt
	60
	120
	180
	240
	300
	360
	405

<210> 436
 <211> 151
 <212> DNA
 <213> Rat

<400> 436	
atactgcctg	tagagttagt
gttggttttt	cttggttttt
	60
	120

tacttcccag gtttgactat ttgccaatgc c 151

<210> 437

<211> 1715

<212> DNA

<213> Mouse

<400> 437

cagaatatgg	ctctgggggt	tctgatagca	gtctgcctct	tgttcaaagc	aatgaaggca	60
gcactgagcg	agaagcaga	gggtgatccct	cctagcacag	cacagcagag	caactggaca	120
tttaacaaca	ccgaagctga	ctacatagaa	gaacctgtag	ctctgaagtt	ctctcatcct	180
tgtctggaag	accataatag	ttactgcatt	aatggagcat	gtgcattcca	ccatgagctg	240
aagcaagcca	tttgacagatg	ctttactggg	tatacgggac	aacgatgtga	gcatttgacc	300
ctaacttcgt	atgctgtgga	ttcttatgaa	aaatacattg	cgattgggat	tggcgctcgg	360
ttgctaatta	gtgcttttct	tgctgtcttc	tattgtctaca	taagaaaaag	gtgtataaat	420
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<210> 438

<211> 1627

<212> DNA

<213> Mouse

<400> 438

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 <213> Mouse

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 <211> 1379
 <212> DNA
 <213> Mouse

<220>
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<210> 441
 <211> 1214
 <212> DNA
 <213> Rat

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<400> 441
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 <211> 1977
 <212> DNA
 <213> Rat

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<210> 443
 <211> 1744
 <212> DNA
 <213> Rat

<400> 443

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<210> 444

<211> 2157

<212> DNA

<213> Mouse

<400> 444

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<210> 445

<211> 2250

<212> DNA

<213> Mouse

<220>

<221> unsure

<222> (2219)... (2219)

<400> 445

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<210> 446
<211> 1685
<212> DNA
<213> Rat

<220>
<221> unsure
<222> (1482) ... (1482)

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<210> 447
<211> 1890
<212> DNA
<213> Rat

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<400> 447
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<210> 448

<211> 1272

<212> DNA

<213> Rat

<400> 448

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<210> 449
 <211> 936
 <212> DNA
 <213> Rat

<400> 449						
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 <211> 433
 <212> DNA
 <213> Mouse

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 <211> 1225
 <212> DNA
 <213> Mouse

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 <211> 445
 <212> DNA
 <213> Mouse

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<210> 453
 <211> 2792
 <212> DNA
 <213> Mouse

<400> 453						
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<210> 454
 <211> 1808
 <212> DNA
 <213> Mouse

<400> 454						
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<210> 455

<211> 1121

<212> DNA

<213> Rat

<220>

<221> unsure

<222> (1095)... (1095)

<400> 455

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<210> 456

<211> 75

<212> PRT

<213> Mouse

<400> 456

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			20					25						30	
Met	Cys	Val	Leu	Gly	Trp	Leu	Ser	Phe	Leu	Val	Phe	Leu	Leu	Phe	Ser
		35					40					45			
Leu	Val	Cys	Ser	Phe	Pro	Ser	Pro	Ile	Asn	His	Ser	His	Met	Leu	Pro
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<210> 457

<211> 49

<212> PRT

<213> Rat

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 Phe Cys Phe Trp Phe Cys Phe Leu Leu Pro Arg Phe Asp Tyr Leu Pro
 35 40 45
 Met

<210> 458
 <211> 296
 <212> PRT
 <213> Mouse

<400> 458
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 1 5 10 15
 Ala Cys Pro Gln Gly Arg Phe Gly Pro Ser Cys Ala His Val Cys Thr
 20 25 30
 Cys Gly Gln Gly Ala Ala Cys Asp Pro Val Ser Gly Thr Cys Ile Cys
 35 40 45
 Pro Pro Gly Lys Thr Gly Gly His Cys Glu Arg Gly Cys Pro Gln Asp
 50 55 60
 Arg Phe Gly Lys Gly Cys Glu His Lys Cys Ala Cys Arg Asn Gly Gly
 65 70 75 80
 Leu Cys His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu Gly Trp Met
 85 90 95
 Gly Pro His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr Gly Ala Ala
 100 105 110
 Cys Leu Leu Glu Cys Ser Cys Gln Asn Asn Gly Ser Cys Glu Pro Thr
 115 120 125
 Ser Gly Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln Ala Cys Glu
 130 135 140
 Asp Thr Cys Pro Ala Gly Phe His Gly Ser Gly Cys Gln Arg Val Cys
 145 150 155 160
 Glu Cys Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly Arg Cys Leu
 165 170 175
 Cys Pro Ala Gly Phe Arg Gly Gln Phe Cys Glu Arg Gly Cys Lys Pro
 180 185 190
 Gly Phe Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys Pro Thr Gly
 195 200 205
 Val Pro Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro Pro Gly Arg
 210 215 220
 Ala Gly Thr Thr Cys Asp Leu Asp Cys Arg Arg Gly Arg Phe Gly Pro
 225 230 235 240
 Gly Cys Ala Leu Arg Cys Asp Cys Gly Gly Gly Ala Asp Cys Asp Pro
 245 250 255
 Ile Ser Gly Gln Cys His Cys Val Asp Ser Tyr Thr Gly Pro Thr Cys
 260 265 270
 Arg Glu Val Pro Thr Gln Leu Ser Ser Ile Arg Pro Ala Pro Gln His
 275 280 285
 Ser Ser Ser Lys Ala Met Lys His
 290 295

<210> 459

<211> 106
 <212> PRT
 <213> Mouse

<400> 459
 Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His Glu Asn Gly
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 Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu Leu Tyr Glu
 20 25 30
 Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met Asn Leu Tyr
 35 40 45
 Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Leu Pro Ser
 50 55 60
 Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Ile Cys Ile Asn
 65 70 75 80
 Pro Asp Pro Glu Lys Arg Pro Asp Ile Ala Tyr Val Tyr Asp Val Ala
 85 90 95
 Lys Arg Met His Ala Cys Thr Ala Ser Thr
 100 105

<210> 460
 <211> 53
 <212> PRT
 <213> Mouse

<400> 460
 Met Cys Ala Gly His Gly Gln Ser Leu Leu Ile Ala Ser Asp Asp Gly
 1 5 10 15
 Arg Val Ser Arg Gln Pro Trp Ser Cys Leu Asn Ile Val Ser Asn Cys
 20 25 30
 His Ser Phe Arg Glu Arg Gly Thr Ser Ser Pro Leu Leu Leu Ala Leu
 35 40 45
 Pro Asp Arg Pro Leu
 50

<210> 461
 <211> 261
 <212> PRT
 <213> Mouse

<400> 461
 Asn Ile Arg Glu Tyr Val Arg Trp Met Met Tyr Trp Ile Val Phe Ala
 1 5 10 15
 Ile Phe Met Ala Ala Glu Thr Phe Thr Asp Ile Phe Ile Ser Trp Ser
 20 25 30
 Gly Pro Arg Ile Gly Arg Pro Trp Gly Trp Glu Gly Pro His His His
 35 40 45
 His His Leu Ala Ser Gly Ser His Lys Pro Leu Pro Leu Leu Thr His
 50 55 60
 Arg Phe Pro Phe Tyr Tyr Glu Phe Lys Met Ala Phe Val Leu Trp Leu
 65 70 75 80
 Leu Ser Pro Tyr Thr Lys Gly Ala Ser Leu Leu Tyr Arg Lys Phe Val
 85 90 95
 His Pro Ser Leu Ser Arg His Glu Lys Glu Ile Asp Ala Cys Ile Val
 100 105 110
 Gln Ala Lys Glu Arg Ser Tyr Glu Thr Met Leu Ser Phe Gly Lys Arg
 115 120 125

Ser Leu Asn Ile Ala Ala Ser Ala Ala Val Gln Ala Ala Thr Lys Ser
 130 135 140
 Gln Gly Ala Leu Ala Gly Arg Leu Arg Ser Phe Ser Met Gln Asp Leu
 145 150 155 160
 Arg Ser Ile Pro Asp Thr Pro Val Pro Thr Tyr Gln Asp Pro Leu Tyr
 165 170 175
 Leu Glu Asp Gln Val Pro Arg Arg Arg Pro Pro Ile Gly Tyr Arg Pro
 180 185 190
 Gly Gly Leu Gln Gly Ser Asp Thr Glu Asp Glu Cys Trp Ser Asp Asn
 195 200 205
 Glu Ile Val Pro Gln Pro Pro Val Gly Pro Arg Glu Lys Pro Leu Gly
 210 215 220
 Arg Ser Gln Ser Leu Arg Val Val Lys Arg Lys Pro Leu Thr Arg Glu
 225 230 235 240
 Gly Thr Ser Arg Ser Leu Lys Val Arg Thr Pro Lys Lys Ala Met Pro
 245 250 255
 Ser Asp Met Asp Ser
 260

<210> 462
 <211> 138
 <212> PRT
 <213> Mouse

<400> 462
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 Lys Ser Lys Cys Thr Gly Gly Leu Gln Pro Pro Val Gln Tyr Glu Asp
 35 40 45
 Val His Thr Asn Pro Asp Gln Asp Cys Cys Leu Leu Gln Val Thr Thr
 50 55 60
 Leu Asn Phe Ile Phe Ile Pro Ile Val Met Gly Met Ile Phe Thr Leu
 65 70 75 80
 Phe Thr Ile Asn Val Ser Thr Asp Met Arg His His Arg Val Arg Leu
 85 90 95
 Val Phe Gln Asp Ser Pro Val His Gly Arg Lys Leu Arg Ser Glu
 100 105 110
 Gln Gly Val Gln Val Ile Leu Asp Gln Cys Thr Ala Phe Gly Ser Leu
 115 120 125
 Thr Gly Gly Ile Leu Ser Thr His Ser Pro
 130 135

<210> 463
 <211> 314
 <212> PRT
 <213> Mouse

<400> 463
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 1 5 10 15
 Leu Gly Asp Ser Cys Ile Thr Val Gly Asn Thr Thr Thr His Val Met
 20 25 30
 Lys Asn Leu Leu Pro Glu Thr Thr Tyr Arg Ile Arg Ile Gln Ala Ile
 35 40 45
 Asn Glu Ile Gly Val Gly Pro Phe Ser Gln Phe Ile Lys Ala Lys Thr

50	55	60
Arg Pro Leu Pro Pro Ser Pro Pro Arg Leu Glu Cys Ala Ala Ser Gly		
65	70	75
Pro Gln Ser Leu Lys Leu Lys Trp Gly Asp Ser Asn Ser Lys Thr His		80
	85	90
Ala Ala Gly Asp Met Val Tyr Thr Leu Gln Leu Glu Asp Arg Asn Lys		95
	100	105
Arg Phe Ile Ser Ile Tyr Arg Gly Pro Ser His Thr Tyr Lys Val Gln		110
	115	120
Arg Leu Thr Glu Phe Thr Cys Tyr Ser Phe Arg Ile Gln Ala Met Ser		125
	130	135
Glu Ala Gly Glu Gly Pro Tyr Ser Glu Thr Tyr Thr Phe Ser Thr Thr		140
	145	150
Lys Ser Val Pro Pro Thr Leu Lys Ala Pro Arg Val Thr Gln Leu Glu		155
	160	165
Gly Asn Ser Cys Glu Ile Phe Trp Glu Thr Val Pro Pro Met Arg Gly		170
	175	180
Asp Pro Val Ser Tyr Val Leu Gln Val Leu Val Gly Arg Asp Ser Glu		185
	190	195
Tyr Lys Gln Val Tyr Lys Gly Glu Glu Ala Thr Phe Gln Ile Ser Gly		200
	205	210
Leu Gln Ser Asn Thr Asp Tyr Arg Phe Arg Val Cys Ala Cys Arg Arg		215
	220	225
Cys Val Asp Thr Ser Gln Glu Leu Ser Gly Ala Phe Ser Pro Ser Ala		230
	235	240
Ala Phe Met Leu Gln Gln Arg Glu Val Met Leu Thr Gly Asp Leu Gly		245
	250	255
Gly Met Glu Glu Ala Lys Met Lys Gly Met Met Pro Thr Asp Glu Gln		260
	265	270
Phe Ala Ala Leu Ile Val Leu Gly Phe Ala Thr Leu Ser Ile Leu Phe		275
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Ala Phe Ile Leu Gln Tyr Phe Leu Met Lys		290
	295	300
305	310	

<210> 464
 <211> 1663
 <212> DNA
 <213> Mouse

<400> 464

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<210> 465

<211> 99

<212> PRT

<213> Mouse

<400> 465

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      20             25             30
Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
      35             40             45
Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Ser Met Ser
      50             55             60
Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr
      65             70             75             80
Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val
      85             90             95
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<211> 886

<212> DNA

<213> Rat

<400> 466

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<211> 1076

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<211> 448

<212> DNA

<213> Human

<400> 468

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<211> 1500

<212> DNA

<213> Human

<400> 469

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<400> 474

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<210> 475

<211> 2795

<212> DNA

<213> Rat

<400> 475

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<210> 476

<211> 1953

<212> DNA

<213> Rat

<400> 476

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<210> 477

<211> 1714

<212> DNA

<213> Rat

<400> 477

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<210> 478

<211> 3134

<212> DNA

<213> Mouse

<400> 478

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<210> 479

<211> 2100

<212> DNA

<213> Rat

<400> 479

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<210> 480

<211> 1183

<212> DNA

<213> Rat

<400> 480

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<210> 481

<211> 3102

<212> DNA

<213> Rat

<400> 481

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<210> 482

<211> 441

<212> DNA

<213> Rat

<400> 482

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ttccacgac	gtcgtgggg	cacagtgtgt	gatgacggct	gggacaagaa	ggatggggac	180

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atcttccact	gccagttctc	caaattggggc	gtgacaaatt	gtgggcatgc	tgaggacgct	360
ggagtgactt	gtactgccct	ctgaaagtgg	ccacagccca	aggctagggc	actgcctcag	420
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<210> 483

<211> 376

<212> DNA

<213> Human

<400> 483

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<210> 484

<211> 2580

<212> DNA

<213> Rat

<400> 484

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gtagatgttt	tccaggatac	accgggaaga	cctgcagtca	agacgtgaat	gagtgtgcat	360
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<210> 485

<211> 1274

<212> DNA

<213> Mouse

<400> 485

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caaaatgaag	tttacaacaa	aacagagcaa	ctggctgaac	tctcaaaggg	tgttcaagaa	180
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ctggatgagc	tgcgaaagga	ttctagcaac	ccatgtgttg	acctaagga	cctcattctt	360
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aaaaaaaaaa	aaaa					1274

<210> 486

<211> 858

<212> DNA

<213> Human

<400> 486

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<210> 487
 <211> 2128
 <212> DNA
 <213> Mouse

<400> 487						
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<210> 488
 <211> 95
 <212> PRT
 <213> Rat

<400> 488
 Met Trp Phe Leu Pro Cys Ser Val Pro Leu Val Ile Ser Ser Cys His

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Ser Gln Ala Ser Pro His Trp Pro Tyr Gly Ile Ile Ser Gly Gly Gln
      20           25           30
Glu Gly Leu Cys Arg Leu Trp Thr Ala Thr Cys His Ser Arg Gly Glu
      35           40           45
Ser Glu Val Ser Arg Ser Ser Arg Lys Glu Asp Pro Arg Ile Pro Gln
      50           55           60
Gly Ser Leu Ser Gly Asn Val Asp Phe Trp Arg Val Cys Pro Pro Cys
      65           70           75           80
Ala His Thr Ser Met Asp Arg Thr Leu Gly Leu Leu Ser Cys Cys
      85           90           95

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<210> 489
 <211> 207
 <212> PRT
 <213> Human

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      <400> 489
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      1           5           10           15
Leu Pro Met Ser Leu Ala Phe Leu Phe Leu Phe Pro Ser Ala Ile
      20           25           30
Leu Thr Leu Ile Val Cys His Ile Asn Ser Pro Gly Cys Val Phe Phe
      35           40           45
Ser Arg Lys Lys Leu Lys Gly Lys Thr Lys Pro Lys Lys Pro Glu Thr
      50           55           60
Thr Asn Lys Asn Gly Asn Asp Asn Gly Cys Leu Ser Phe Phe Cys His
      65           70           75           80
Asp Phe Pro Asp Leu Val Cys Ser Leu Cys Leu Arg Glu Ala Gly Asp
      85           90           95
Val Asp Glu Ala Val Phe Phe Phe Leu Phe Leu Val Phe Glu Thr Arg
      100          105          110
Val Ser Leu Cys His Pro Gly Trp Ser Val Thr Trp His Asp Leu Ser
      115          120          125
Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Arg Leu Ser Cys Leu Ser
      130          135          140
Leu Leu Ser Ser Trp Asp Tyr Arg His Ala Pro Leu Cys Pro Asp Asn
      145          150          155          160
Phe Phe Val Phe Leu Val Glu Thr Gly Phe His His Val Gly Gln Ala
      165          170          175
Gly Leu Glu Leu Leu Thr Ser Gly Tyr Pro Pro Thr Leu Ala Ser Gln
      180          185          190
Ser Ala Gly Ile Ile Gly Met Asn His Arg Ala Trp Pro Lys Met
      195          200          205

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<210> 490
 <211> 81
 <212> PRT
 <213> Human

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      <400> 490
Met Ser Gln Val Gln Val Ile Leu Leu Thr Leu Val Ser Gln Ser Val
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Gly Ile Ile Gly Met Ser His Cys Ile Lys Pro Val Lys Ser Ile Tyr
      20           25           30
Ile Lys Leu Asp Cys Arg Lys Arg Arg Asp Lys Thr Ser Leu Leu Phe
      35           40           45

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Cys Pro Gln Gly Pro Arg Asn Pro Val Ser Lys Ala Pro His Gln Leu
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 Gln Cys Val Pro Val Ser Arg Val Pro Thr Gly Thr Glu Ser Ser Gly
 65 70 75 80
 Thr

<210> 491
 <211> 193
 <212> PRT
 <213> Human

<400> 491
 Met Ala Pro Leu Leu Ser Leu Ser Cys Phe Trp Ala Asn Leu Leu Ala
 1 5 10 15
 Ile Arg Ser Trp Leu Thr Arg Lys His Ile Gln Arg Leu His Ala Ala
 20 25 30
 Ala Thr Val Ile Lys Arg Ala Trp Gln Lys Trp Arg Ile Arg Met Ala
 35 40 45
 Cys Leu Ala Ala Lys Glu Leu Asp Gly Val Glu Glu Lys His Phe Ser
 50 55 60
 Gln Ala Pro Cys Ser Leu Ser Thr Ser Pro Leu Gln Thr Arg Leu Leu
 65 70 75 80
 Glu Ala Ile Ile Arg Leu Trp Pro Leu Gly Leu Val Leu Ala Asn Thr
 85 90 95
 Ala Met Gly Val Gly Ser Phe Gln Arg Lys Leu Val Val Trp Ala Cys
 100 105 110
 Leu Gln Leu Pro Arg Gly Ser Pro Ser Ser Tyr Thr Val Gln Thr Ala
 115 120 125
 Gln Asp Gln Ala Gly Val Thr Ser Ile Arg Ala Leu Pro Gln Gly Ser
 130 135 140
 Ile Lys Phe His Cys Arg Lys Ser Pro Leu Arg Tyr Ala Asp Ile Cys
 145 150 155 160
 Pro Glu Pro Ser Pro Tyr Ser Ile Thr Gly Phe Asn Gln Ile Leu Leu
 165 170 175
 Glu Arg His Arg Leu Ile His Val Thr Ser Ser Ala Phe Thr Gly Leu
 180 185 190
 Gly

<210> 492
 <211> 104
 <212> PRT
 <213> Human

<400> 492
 Met Pro Pro Asn Pro His Leu Thr Leu Ile Leu Ile Thr Ala Leu Trp
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 Glu Ala Val Val Gly Gly Ser Leu Lys Pro Arg Arg Leu Arg Leu Glu
 20 25 30
 Cys Cys Thr Ile Ala Pro Leu His Ser Thr Ala Trp Ala Thr Glu Gly
 35 40 45
 Asp Pro Val Ser Lys Lys Arg Glu Thr Ala Val Ala Ile Ile Val Val
 50 55 60
 Arg Asn Asn Thr Glu Arg Ser Leu Val Leu Ser Ala Gln Leu Phe Leu
 65 70 75 80
 Thr Val Ser Leu Cys Arg Thr Pro Gln Ser His Thr Arg Thr Trp Thr

85 90 95
 Leu Met Pro Ser Gly Gly Leu Thr
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 <210> 493
 <211> 254
 <212> PRT
 <213> Human
 <400> 493
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 Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr Gly Pro Pro Leu
 20 25 30
 Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu Thr Ala Asp Ser Asp
 35 40 45
 Val Asp Glu Phe Leu Asp Lys Phe Leu Ser Ala Gly Val Lys Gln Ser
 50 55 60
 Asp Leu Pro Arg Lys Glu Thr Glu Gln Pro Pro Ala Pro Gly Ser Met
 65 70 75 80
 Glu Glu Ser Val Arg Gly Tyr Asp Trp Ser Pro Arg Asp Ala Arg Arg
 85 90 95
 Ser Pro Asp Gln Gly Arg Gln Gln Ala Glu Arg Arg Ser Val Leu Arg
 100 105 110
 Gly Phe Cys Ala Asn Ser Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala
 115 120 125
 Phe Asp Asp Ile Pro Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp
 130 135 140
 Arg His Gly Ala Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn
 145 150 155 160
 Trp Lys Arg Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly
 165 170 175
 Ala Pro Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn
 180 185 190
 Ala Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys
 195 200 205
 Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys Phe
 210 215 220
 Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe Arg Ser
 225 230 235 240
 Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe Ala
 245 250

<210> 494
 <211> 215
 <212> PRT
 <213> Rat

<400> 494
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 Pro Arg Asp Ala Pro Ser Thr Ser Ser Val Ala Pro Ala Ser Arg Ala
 20 25 30
 Val His Thr Pro Pro Leu Gly Pro Ile Leu Lys Lys Thr Ala Gly Leu
 35 40 45
 Gly Phe Cys Ala Val Phe Leu Tyr Phe Ile Thr Ala Leu Ile Phe Pro
 50 55 60

Ala Ile Ser Thr Asn Ile Gln Pro Met His Lys Gly Thr Gly Ser Pro
 65 70 75 80
 Trp Thr Ser Lys Phe Tyr Val Pro Leu Thr Val Phe Leu Leu Phe Asn
 85 90 95
 Phe Ala Asp Leu Cys Gly Arg Gln Val Thr Ala Trp Ile Gln Val Pro
 100 105 110
 Gly Pro Arg Ser Lys Leu Leu Pro Ile Leu Ala Val Ser Arg Val Cys
 115 120 125
 Leu Val Pro Leu Phe Leu Leu Cys Asn Tyr Gln Pro Arg Ser His Leu
 130 135 140
 Thr Leu Val Leu Phe Gln Ser Asp Ile Tyr Pro Ile Leu Phe Thr Cys
 145 150 155 160
 Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Val Leu Met Tyr
 165 170 175
 Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Ser Val Val
 180 185 190
 Met Leu Phe Tyr Met Ser Leu Gly Leu Met Leu Gly Ser Ala Cys Ala
 195 200 205
 Ala Leu Leu Glu His Phe Ile
 210 215

<210> 495
 <211> 91
 <212> PRT
 <213> Human

<400> 495
 Met Ile Gln Pro Ser Leu Ser Val Leu Cys Gly Leu Gly Cys Ala Phe
 1 5 10 15
 Leu Trp Ala Thr Ser Ser Phe Ala Ala Val Ser Pro Pro Ala Cys Ala
 20 25 30
 Pro Ala Thr Ser Pro Ser Pro Val Val His Leu Arg Ser Thr Gln Pro
 35 40 45
 Gly Gln Ser Cys Phe Val Leu Leu His Arg Leu Gly Leu Pro Cys Val
 50 55 60
 Leu Ser Ser Ser Gly Ser Phe Ser Ser Pro His Leu Phe Cys Phe Leu
 65 70 75 80
 Pro Val Leu Val Ser Pro Cys Ala Leu Gly Pro
 85 90

<210> 496
 <211> 224
 <212> PRT
 <213> Human

<400> 496
 Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu
 1 5 10 15
 Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn
 20 25 30
 Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His
 35 40 45
 Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
 50 55 60
 Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
 65 70 75 80
 Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu

				85					90					95			
Cys	Lys	Thr	Asp	Leu	Asp	Ile	Ala	Tyr	Lys	Phe	Gly	Lys	Thr	Val	Val		
			100						105					110			
Ser	Cys	Glu	Gly	Tyr	Glu	Ser	Ser	Glu	Asp	Gln	Tyr	Val	Leu	Arg	Gly		
		115						120					125				
Ser	Cys	Gly	Leu	Glu	Tyr	Asn	Leu	Asp	Tyr	Thr	Glu	Leu	Gly	Leu	Gln		
		130					135				140						
Lys	Leu	Lys	Glu	Ser	Gly	Lys	Gln	His	Gly	Phe	Ala	Ser	Phe	Ser	Asp		
145					150					155					160		
Tyr	Tyr	Tyr	Lys	Trp	Ser	Ser	Ala	Asp	Ser	Cys	Asn	Met	Ser	Gly	Leu		
			165						170					175			
Ile	Thr	Ile	Val	Val	Leu	Leu	Gly	Ile	Ala	Phe	Val	Val	Tyr	Lys	Leu		
			180					185						190			
Phe	Leu	Ser	Asp	Gly	Gln	Tyr	Ser	Pro	Pro	Pro	Tyr	Ser	Glu	Tyr	Pro		
		195					200					205					
Pro	Phe	Ser	His	Arg	Tyr	Gln	Arg	Phe	Thr	Asn	Ser	Ala	Gly	Pro	Pro		
		210				215						220					

<210> 497

<211> 766

<212> PRT

<213> Rat

<400> 497

Met	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Ala	Cys	Pro	Leu	Leu	Ser			
1				5				10				15					
Ala	Arg	Met	Phe	Pro	Gly	Asn	Ala	Gly	Gly	Glu	Leu	Val	Thr	Pro	His		
			20					25				30					
Trp	Val	Leu	Asp	Gly	Lys	Thr	Trp	Leu	Lys	Val	Thr	Leu	Lys	Glu	Gln		
		35				40						45					
Ile	Ser	Lys	Pro	Asp	Ser	Gly	Leu	Val	Ala	Leu	Lys	Ala	Glu	Gly	Gln		
		50				55					60						
Asp	Leu	Leu	Leu	Glu	Leu	Glu	Lys	Asn	His	Arg	Leu	Leu	Ala	Pro	Gly		
65				70					75					80			
Tyr	Thr	Glu	Thr	Tyr	Tyr	Ser	Arg	Asp	Gly	Gln	Pro	Ile	Val	Leu	Ser		
			85					90					95				
Pro	Asn	His	Thr	Asp	His	Cys	His	Tyr	Gln	Gly	Cys	Val	Arg	Gly	Phe		
		100						105					110				
Arg	Glu	Ser	Trp	Val	Val	Leu	Ser	Thr	Cys	Ser	Gly	Met	Ser	Gly	Leu		
		115				120						125					
Ile	Val	Leu	Ser	Ser	Lys	Val	Ser	Tyr	Tyr	Leu	His	Pro	Trp	Met	Pro		
		130				135					140						
Gly	Asp	Thr	Lys	Asp	Phe	Pro	Thr	His	Lys	Ile	Phe	Arg	Val	Glu	Gln		
145					150					155				160			
Leu	Phe	Thr	Trp	Arg	Gly	Ala	Arg	Lys	Asp	Lys	Asn	Ser	Gln	Phe	Lys		
			165						170					175			
Ala	Gly	Met	Ala	Arg	Leu	Pro	His	Val	Pro	His	Arg	Arg	Met	Arg	Arg		
		180						185					190				
Glu	Ala	Arg	Arg	Ser	Pro	Lys	Tyr	Leu	Glu	Leu	Tyr	Ile	Val	Ala	Asp		
		195				200						205					
His	Ala	Leu	Phe	Leu	Leu	Gln	Arg	Gln	Asn	Leu	Asn	His	Thr	Arg	Gln		
		210				215						220					
Arg	Leu	Leu	Glu	Ile	Ala	Asn	Cys	Val	Asp	Gln	Ile	Leu	Arg	Thr	Leu		
225				230						235				240			
Asp	Ile	Gln	Leu	Val	Leu	Thr	Gly	Leu	Glu	Val	Trp	Thr	Glu	Gln	Asp		
			245						250					255			
His	Ser	Arg	Ile	Thr	Gln	Asp	Ala	Asn	Glu	Thr	Leu	Trp	Ala	Phe	Leu		

				260						265				270					
Gln	Trp	Arg	Arg	Gly	Leu	Trp	Val	Arg	Arg	Pro	His	Asp	Ser	Thr	Gln				
		275					280					285							
Leu	Leu	Thr	Gly	Arg	Thr	Phe	Gln	Gly	Thr	Thr	Val	Gly	Leu	Ala	Pro				
		290				295					300								
Val	Glu	Gly	Met	Cys	His	Ala	Glu	Ser	Ser	Gly	Gly	Val	Ser	Thr	Asp				
305				310						315					320				
His	Ser	Glu	Leu	Pro	Ile	Gly	Thr	Ala	Ala	Thr	Met	Ala	His	Glu	Ile				
			325						330					335					
Gly	His	Ser	Leu	Gly	Leu	His	His	Asp	Pro	Glu	Gly	Cys	Cys	Met	Glu				
			340					345					350						
Ala	Asp	Ala	Glu	Gln	Gly	Gly	Cys	Val	Met	Glu	Ala	Ala	Thr	Gly	His				
		355					360					365							
Pro	Phe	Pro	Arg	Val	Phe	Ser	Ala	Cys	Ser	Arg	Arg	Gln	Leu	Arg	Thr				
		370				375					380								
Phe	Phe	Arg	Lys	Gly	Gly	Gly	Ala	Cys	Leu	Ser	Asn	Val	Ser	Ala	Pro				
385				390						395					400				
Gly	Leu	Leu	Val	Leu	Pro	Ser	Arg	Cys	Gly	Asn	Gly	Phe	Val	Glu	Ala				
			405					410					415						
Glu	Glu	Glu	Cys	Asp	Cys	Gly	Ser	Gly	Gln	Lys	Arg	Pro	Asp	Pro	Cys				
			420					425					430						
Cys	Phe	Ala	His	Asn	Cys	Ser	Leu	Arg	Ala	Gly	Ala	Gln	Cys	Ala	Gln				
		435					440				445								
Gly	Asp	Cys	Cys	Ala	Arg	Cys	Leu	Leu	Lys	Pro	Ala	Gly	Thr	Pro	Cys				
		450				455					460								
Arg	Pro	Ala	Ala	Asn	Asp	Cys	Asp	Leu	Pro	Glu	Phe	Cys	Thr	Gly	Thr				
465				470						475					480				
Ser	Pro	His	Cys	Pro	Ala	Asp	Val	Tyr	Leu	Leu	Asp	Gly	Ser	Pro	Cys				
			485					490					495						
Ala	Glu	Gly	Arg	Gly	Tyr	Cys	Leu	Asp	Gly	Trp	Cys	Pro	Thr	Leu	Glu				
			500				505					510							
Lys	Gln	Cys	Gln	Gln	Leu	Trp	Gly	Pro	Gly	Ser	Gln	Pro	Ala	Pro	Glu				
		515					520					525							
Pro	Cys	Phe	Gln	Gln	Met	Asn	Ser	Val	Gly	Asn	Ser	Gln	Gly	Asn	Cys				
		530				535					540								
Gly	Gln	Asp	Ser	Lys	Gly	Ser	Phe	Leu	Pro	Cys	Thr	Gln	Arg	Asp	Ala				
545				550															

Gln Gln Pro Gly Arg Cys Cys Arg Arg Asp Ala Leu Cys Asn Arg Asp
 725 730 735
 Gln Pro Leu Gly Ser Val His Pro Val Glu Phe Gly Ser Ile Ile Thr
 740 745 750
 Gly Glu Pro Ser Pro Pro Asn Pro Glu Glu Ser Glu Leu Thr
 755 760 765

<210> 498
 <211> 609
 <212> PRT
 <213> Rat

<400> 498
 Met Trp Ile Thr Ala Leu Leu Leu Leu Val Leu Leu Leu Val Val Val
 1 5 10 15
 His Arg Val Tyr Val Gly Leu Phe Thr Gly Ser Ser Pro Asn Pro Phe
 20 25 30
 Ala Glu Asp Val Lys Arg Pro Pro Glu Pro Leu Val Thr Asp Lys Glu
 35 40 45
 Ala Arg Lys Lys Val Leu Lys Gln Ala Phe Ser Val Ser Arg Val Pro
 50 55 60
 Glu Lys Leu Asp Ala Val Val Ile Gly Ser Gly Ile Gly Gly Leu Ala
 65 70 75 80
 Ser Ala Ala Ile Leu Ala Lys Ala Gly Lys Arg Val Leu Val Leu Glu
 85 90 95
 Gln His Thr Lys Ala Gly Gly Cys Cys His Thr Phe Gly Glu Asn Gly
 100 105 110
 Leu Glu Phe Asp Thr Gly Ile His Tyr Ile Gly Arg Met Arg Glu Gly
 115 120 125
 Asn Ile Gly Arg Phe Ile Leu Asp Gln Ile Thr Glu Gly Gln Leu Asp
 130 135 140
 Trp Ala Pro Met Ala Ser Pro Phe Asp Leu Met Ile Leu Glu Gly Pro
 145 150 155 160
 Asn Gly Arg Lys Glu Phe Pro Met Tyr Ser Gly Arg Lys Glu Tyr Ile
 165 170 175
 Gln Gly Leu Lys Glu Lys Phe Pro Lys Glu Glu Ala Val Ile Asp Lys
 180 185 190
 Tyr Met Glu Leu Val Lys Val Val Ala His Gly Val Ser His Ala Ile
 195 200 205
 Leu Leu Lys Phe Leu Pro Leu Pro Leu Thr Gln Leu Leu Asn Lys Phe
 210 215 220
 Gly Leu Leu Thr Arg Phe Ser Pro Phe Cys Arg Ala Ser Thr Gln Ser
 225 230 235 240
 Leu Ala Glu Val Leu Lys Gln Leu Gly Ala Ser Pro Glu Leu Gln Ala
 245 250 255
 Val Leu Ser Tyr Ile Phe Pro Thr Tyr Gly Val Thr Pro Ser His Thr
 260 265 270
 Thr Phe Ser Leu His Ala Leu Leu Val Asp His Tyr Ile Gln Gly Ala
 275 280 285
 Tyr Tyr Pro Arg Gly Gly Ser Ser Glu Ile Ala Phe His Thr Ile Pro
 290 295 300
 Leu Ile Gln Arg Ala Gly Gly Ala Val Leu Thr Arg Ala Thr Val Gln
 305 310 315 320
 Ser Val Leu Leu Asp Ser Ala Gly Arg Ala Cys Gly Val Ser Val Lys
 325 330 335
 Lys Gly Gln Glu Leu Val Asn Ile Tyr Cys Pro Val Val Ile Ser Asn
 340 345 350

Ala Gly Met Phe Asn Thr Tyr Gln His Leu Leu Pro Glu Ser Val Arg
 355 360 365
 Tyr Leu Pro Asp Val Lys Lys Gln Leu Thr Met Val Lys Pro Gly Leu
 370 375 380
 Ser Met Leu Ser Ile Phe Ile Cys Leu Lys Gly Thr Lys Glu Glu Leu
 385 390 395 400
 Lys Leu Gln Ser Thr Asn Tyr Tyr Val Tyr Phe Asp Thr Asp Met Asp
 405 410 415
 Lys Ala Met Glu Arg Tyr Val Ser Met Pro Lys Glu Lys Ala Pro Glu
 420 425 430
 His Ile Pro Leu Leu Phe Ile Ala Phe Pro Ser Ser Lys Asp Pro Thr
 435 440 445
 Trp Glu Asp Arg Phe Pro Asp Arg Ser Thr Met Thr Val Leu Val Pro
 450 455 460
 Thr Ala Phe Glu Trp Phe Glu Glu Trp Gln Glu Glu Pro Lys Gly Lys
 465 470 475 480
 Arg Gly Val Asp Tyr Glu Thr Leu Lys Asn Thr Phe Leu Glu Ala Ser
 485 490 495
 Met Ser Val Ile Met Lys Leu Phe Pro Gln Leu Glu Gly Lys Val Glu
 500 505 510
 Ser Val Thr Gly Gly Ser Pro Leu Thr Asn Gln Tyr Tyr Leu Ala Ala
 515 520 525
 His Arg Gly Ala Thr Tyr Gly Ala Asp His Asp Leu Ala Arg Leu His
 530 535 540
 Pro His Ala Met Ala Ser Leu Arg Ala Gln Thr Pro Ile Pro Asn Leu
 545 550 555 560
 Tyr Leu Thr Gly Gln Asp Ile Phe Thr Cys Gly Leu Met Gly Ala Leu
 565 570 575
 Gln Gly Ala Leu Leu Cys Ser Ser Ala Ile Leu Lys Arg Asn Leu Tyr
 580 585 590
 Ser Asp Leu Gln Ala Leu Gly Ser Lys Val Arg Ala Gln Lys Lys Lys
 595 600 605
 Lys

<210> 499

<211> 559

<212> PRT

<213> Rat

<400> 499

Phe Gly Arg Glu Asn Phe Tyr Glu Val Gln Val Pro Glu Asp Thr Pro
 1 5 10 15
 Ile Gly Ser Ser Ile Ile Thr Ile Ser Ala Lys Asp Leu Asp Met Gly
 20 25 30
 Asn Tyr Gly Lys Ile Ser Tyr Ser Phe Leu His Ala Thr Glu Asp Val
 35 40 45
 Arg Lys Thr Phe Glu Ile Asn Pro Thr Ser Gly Glu Val Asn Leu Arg
 50 55 60
 Ser Leu Leu Asp Phe Glu Val Ile Gln Ser Tyr Ser Val Thr Ile Gln
 65 70 75 80
 Ala Thr Asp Gly Gly Gly Leu Ser Ala Lys Cys Thr Leu Ser Val Lys
 85 90 95
 Val Leu Asp Ile Asn Asp Asn Ala Pro Glu Val Ile Ile Ser Ser Val
 100 105 110
 Thr Lys Thr Ile Pro Glu Asn Ala Ser Glu Thr Leu Ile Thr Leu Phe
 115 120 125

Ser Val Arg Asp Gln Asp Ser Gly Asp Asn Gly Arg Ile Leu Cys Ser
 130 135 140
 Ile Pro Asp Asp Leu Pro Phe Ile Leu Lys Pro Thr Phe Lys Asn Phe
 145 150 155 160
 Phe Thr Leu Leu Ser Glu Lys Ala Leu Asp Arg Glu Ser Arg Ala Glu
 165 170 175
 Tyr Asn Ile Thr Ile Thr Val Ser Asp Leu Gly Thr Pro Arg Leu Thr
 180 185 190
 Thr Gln His Thr Ile Thr Val Gln Val Ser Asp Ile Asn Asp Asn Ala
 195 200 205
 Pro Ala Phe Thr Gln Thr Ser Tyr Thr Met Phe Val His Glu Asn Asn
 210 215 220
 Ser Pro Ala Leu His Ile Gly Thr Ile Ser Ala Thr Asp Ser Asp Ser
 225 230 235 240
 Gly Ser Asn Ala His Ile Thr Tyr Ser Leu Met Pro Pro Arg Asp Pro
 245 250 255
 Gln Leu Ala Leu Asp Ser Leu Ile Ser Ile Asn Ala Asp Asn Gly Gln
 260 265 270
 Leu Phe Ala Leu Arg Ala Leu Asp Tyr Glu Val Leu Gln Ala Phe Glu
 275 280 285
 Phe Arg Val Gly Ala Thr Asp Arg Gly Ser Pro Ala Leu Ser Ser Gln
 290 295 300
 Ala Leu Val Arg Val Val Val Leu Asp Asp Asn Asp Asn Ala Pro Phe
 305 310 315 320
 Val Leu Tyr Pro Leu Gln Asn Ala Ser Ala Pro Tyr Thr Glu Leu Leu
 325 330 335
 Pro Arg Ala Ala Glu Pro Gly Tyr Leu Val Thr Lys Val Val Ala Val
 340 345 350
 Asp Arg Asp Ser Gly Gln Asn Ala Trp Leu Ser Phe Gln Leu Leu Lys
 355 360 365
 Ala Thr Glu Pro Gly Leu Phe Ser Val Trp Ala His Asn Gly Glu Val
 370 375 380
 Arg Thr Ser Arg Leu Leu Ser Glu Arg Asp Ala Pro Lys His Lys Leu
 385 390 395 400
 Leu Leu Met Val Lys Asp Asn Gly Asp Pro Pro Arg Ser Ala Ser Val
 405 410 415
 Met Leu His Val Leu Val Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro
 420 425 430
 Leu Pro Glu Val Ala His Asn Pro Ala His Asp Glu Asp Thr Leu Thr
 435 440 445
 Leu Tyr Leu Val Ile Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Leu
 450 455 460
 Ser Val Leu Leu Phe Val Gly Val Arg Leu Cys Lys Lys Ala Arg Ala
 465 470 475 480
 Ala Ser Leu Gly Gly Cys Ser Val Pro Glu Gly His Phe Pro Gly His
 485 490 495
 Leu Val Asp Val Thr Gly Thr Gly Thr Leu Ser Gln Asn Tyr Gln Tyr
 500 505 510
 Glu Val Cys Leu Thr Gly Ser Thr Gly Thr Asn Glu Phe Lys Phe Leu
 515 520 525
 Lys Pro Val Met Pro Ser Leu Gln Leu Gln Asp Pro Asp Ser Asn Met
 530 535 540
 Leu Val Lys Glu Asn Phe Arg Asn Ser Leu Gly Phe Asn Ile Gln
 545 550 555

<210> 500

<211> 545

<212> PRT
<213> Mouse

<400> 500

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Ser Leu His Phe Glu Pro Ser Lys Ile Asn Ile Phe His Lys Asp Cys
 1          5          10 \          15
Lys Arg Asn Gly Arg Asp Ala Thr Cys Leu Ala Ala Phe Leu Cys Phe
          20          25          30
Gly Pro Ile Phe Leu Ala Pro His Phe His Thr Ala Thr Val Gly Ile
          35          40          45
Arg Tyr Asn Ala Thr Met Asp Glu Arg Arg Tyr Met Pro Arg Ala His
          50          55          60
Leu Asp Glu Gly Ala Asp Gln Phe Thr Asn Arg Ala Val Leu Leu Ser
65          70          75          80
Ser Gly Gln Glu His Cys Gln Arg Ile Asn Phe His Val Leu Asp Thr
          85          90          95
Ala Asp Tyr Val Lys Pro Val Ala Phe Ser Val Glu Tyr Ser Leu Glu
          100          105          110
Asp Pro Asp His Gly Pro Met Leu Asp Asn Gly Trp Pro Thr Thr Leu
          115          120          125
Arg Val Ser Val Pro Phe Trp Asn Gly Cys Asn Glu Asp Glu His Cys
          130          135          140
Val Pro Asp Leu Val Leu Asp Ala Arg Ser Asp Leu Pro Thr Ala Met
145          150          155          160
Glu Tyr Cys Gln Gln Val Leu Arg Arg Pro Ala Gln Asp Cys Ser Ser
          165          170          175
Tyr Thr Leu Ser Phe Asp Thr Thr Val Phe Ile Ile Glu Ser Thr Arg
          180          185          190
Arg Arg Val Ala Val Glu Ala Thr Leu Glu Asn Arg Gly Glu Asn Ala
          195          200          205
Tyr Ser Ala Val Leu Asn Ile Ser Gln Ser Glu Asn Leu Gln Phe Ala
          210          215          220
Ser Leu Ile Gln Lys Asp Asp Ser Asp Asn Ser Ile Glu Cys Val Asn
225          230          235          240
Glu Glu Arg Arg Leu His Lys Lys Val Cys Asn Val Ser Tyr Pro Phe
          245          250          255
Phe Arg Ala Lys Ala Lys Val Ala Phe Arg Leu Asp Phe Glu Phe Ser
          260          265          270
Lys Ser Val Phe Leu His His Leu Gln Ile His Leu Gly Ala Gly Ser
          275          280          285
Asp Ser His Glu Gln Asp Ser Thr Ala Asp Asp Asn Thr Ala Leu Leu
          290          295          300
Arg Phe His Leu Lys Tyr Glu Ala Asp Val Leu Phe Thr Arg Ser Ser
305          310          315          320
Ser Leu Ser His Phe Glu Val Lys Ala Asn Ser Ser Leu Glu Ser Tyr
          325          330          335
Asp Gly Ile Gly Pro Pro Phe Asn Cys Val Phe Lys Val Gln Asn Leu
          340          345          350
Gly Phe Phe Pro Ile His Gly Val Met Met Lys Ile Thr Val Pro Ile
          355          360          365
Ala Thr Arg Gly Gly Asn Arg Leu Leu Met Leu Lys Asp Phe Phe Thr
          370          375          380
Asp Gln Val Asn Thr Ser Cys Asn Ile Trp Gly Asn Ser Thr Glu Tyr
385          390          395          400
Arg Ser Thr Pro Thr Glu Glu Asp Leu Ser His Ala Pro Gln Arg Asn
          405          410          415
His Ser Asn Ser Asp Val Val Ser Ile Ile Cys Asn Val Arg Leu Ala

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          420          425          430
Pro Asn Gln Glu Thr Ser Phe Tyr Leu Val Gly Asn Leu Trp Leu Met
          435          440          445
Ser Leu Lys Ala Leu Lys Tyr Arg Ser Met Lys Ile Thr Val Asn Ala
          450          455          460
Ala Leu Gln Arg Gln Phe His Ser Pro Phe Ile Phe Arg Glu Glu Asp
          465          470          475          480
Pro Ser Arg Gln Val Thr Phe Glu Ile Ser Lys Gln Glu Asp Trp Gln
          485          490          495
Val Pro Ile Trp Ile Ile Val Gly Ser Ser Leu Gly Gly Leu Leu Leu
          500          505          510
Leu Ala Leu Leu Val Leu Ala Leu Trp Lys Leu Gly Phe Phe Lys Ser
          515          520          525
Ala Lys Arg Lys Arg Glu Pro Ser Leu Gly Pro Val Pro Lys Glu Leu
          530          535          540
Glu
545

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<210> 501
<211> 696
<212> PRT
<213> Rat

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          <400> 501
Gly Ala Pro Met Tyr Phe Ser Glu Gly Arg Glu Arg Gly Lys Val Tyr
1          5          10          15
Val Tyr Asn Leu Arg Gln Asn Arg Phe Val Phe Asn Gly Thr Leu Lys
          20          25          30
Asp Ser His Ser Tyr Gln Asn Ala Arg Phe Gly Ser Cys Ile Ala Ser
          35          40          45
Val Gln Asp Leu Asn Gln Asp Ser Tyr Asn Asp Val Val Val Gly Ala
          50          55          60
Pro Leu Glu Asp Ser His Arg Gly Ala Ile Tyr Ile Phe His Gly Phe
65          70          75          80
Gln Thr Asn Ile Leu Lys Lys Pro Val Gln Arg Ile Ser Ala Ser Glu
          85          90          95
Leu Ala Pro Gly Leu Gln His Phe Gly Cys Ser Ile His Gly Gln Leu
          100          105          110
Asp Leu Asn Glu Asp Gly Leu Val Asp Leu Ala Val Gly Ala Leu Gly
          115          120          125
Asn Ala Val Val Leu Trp Ala Arg Pro Val Val Gln Ile Asn Ala Ser
          130          135          140
Leu His Phe Glu Pro Ser Lys Ile Asn Ile Phe His Lys Asp Cys Lys
145          150          155          160
Arg Asn Gly Arg Asp Ala Thr Cys Leu Ala Ala Phe Leu Cys Phe Gly
          165          170          175
Pro Ile Phe Leu Ala Pro His Phe His Thr Ala Thr Val Gly Ile Arg
          180          185          190
Tyr Asn Ala Thr Met Asp Glu Arg Arg Tyr Met Pro Arg Ala His Leu
          195          200          205
Asp Glu Gly Ala Asp Gln Phe Thr Asn Arg Ala Val Leu Leu Ser Ser
          210          215          220
Gly Gln Glu His Cys Gln Arg Ile Asn Phe His Val Leu Asp Thr Ala
225          230          235          240
Asp Tyr Val Lys Pro Val Ala Phe Ser Val Glu Tyr Ser Leu Glu Asp
          245          250          255
Pro Asp His Gly Pro Met Leu Asp Asn Gly Trp Pro Thr Thr Leu Arg

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Val	Ser	Val	Pro	Phe	Trp	Asn	Gly	Cys	Asn	Glu	Asp	Glu	His	Cys	Val
		275					280					285			
Pro	Asp	Leu	Val	Leu	Asp	Ala	Arg	Ser	Asp	Leu	Pro	Thr	Ala	Met	Glu
		290					295					300			
Tyr	Cys	Gln	Gln	Val	Leu	Arg	Arg	Pro	Ala	Gln	Asp	Cys	Ser	Ser	Tyr
305					310					315					320
Thr	Leu	Ser	Phe	Asp	Thr	Thr	Val	Phe	Ile	Ile	Glu	Ser	Thr	Arg	Arg
				325					330					335	
Arg	Val	Ala	Val	Glu	Ala	Thr	Leu	Glu	Asn	Arg	Gly	Glu	Asn	Ala	Tyr
			340					345					350		
Ser	Ala	Val	Leu	Asn	Ile	Ser	Gln	Ser	Glu	Asn	Leu	Gln	Phe	Ala	Ser
		355					360					365			
Leu	Ile	Gln	Lys	Asp	Asp	Ser	Asp	Asn	Ser	Ile	Glu	Cys	Val	Asn	Glu
		370				375					380				
Glu	Arg	Arg	Leu	His	Lys	Lys	Val	Cys	Asn	Val	Ser	Tyr	Pro	Phe	Phe
385					390					395					400
Arg	Ala	Lys	Ala	Lys	Val	Ala	Phe	Arg	Leu	Asp	Phe	Glu	Phe	Ser	Lys
			405					410						415	
Ser	Val	Phe	Leu	His	His	Leu	Gln	Ile	His	Leu	Gly	Ala	Gly	Ser	Asp
			420					425					430		
Ser	His	Glu	Gln	Asp	Ser	Thr	Ala	Asp	Asp	Asn	Thr	Ala	Leu	Leu	Arg
		435				440					445				
Phe	His	Leu	Lys	Tyr	Glu	Ala	Asp	Val	Leu	Phe	Thr	Arg	Ser	Ser	Ser
		450				455					460				
Leu	Ser	His	Phe	Glu	Val	Lys	Ala	Asn	Ser	Ser	Leu	Glu	Ser	Tyr	Asp
465					470					475					480
Gly	Ile	Gly	Pro	Pro	Phe	Asn	Cys	Val	Phe	Lys	Val	Gln	Asn	Leu	Gly
				485					490				495		
Phe	Phe	Pro	Ile	His	Gly	Val	Met	Met	Lys	Ile	Thr	Val	Pro	Ile	Ala
		500						505					510		
Thr	Arg	Gly	Gly	Asn	Arg	Leu	Leu	Met	Leu	Lys	Asp	Phe	Phe	Thr	Asp
		515					520					525			
Gln	Val	Asn	Thr	Ser	Cys	Asn	Ile	Trp	Gly	Asn	Ser	Thr	Glu	Tyr	Arg
		530				535					540				
Ser	Thr	Pro	Thr	Glu	Glu	Asp	Leu	Ser	His	Ala	Pro	Gln	Arg	Asn	His
545					550					555					560
Ser	Asn	Ser	Asp	Val	Val	Ser	Ile	Ile	Cys	Asn	Val	Arg	Leu	Ala	Pro
			565						570				575		
Asn	Gln	Glu	Thr	Ser	Phe	Tyr	Leu	Val	Gly	Asn	Leu	Trp	Leu	Met	Ser
		580						585					590		
Leu	Lys	Ala	Leu	Lys	Tyr	Arg	Ser	Met	Lys	Ile	Thr	Val	Asn	Ala	Ala
		595					600					605			
Leu	Gln	Arg	Gln	Phe	His	Ser	Pro	Phe	Ile	Phe	Arg	Glu	Glu	Asp	Pro
		610				615					620				
Ser	Arg	Gln	Val	Thr	Phe	Glu	Ile	Ser	Lys	Gln	Glu	Asp	Trp	Gln	Val
625					630					635					640
Pro	Ile	Trp	Ile	Ile	Val	Gly	Ser	Ser	Leu	Gly	Gly	Leu	Leu	Leu	Leu
			645						650				655		
Ala	Leu	Leu	Val	Leu	Ala	Leu	Gly	Ser	Leu	Val	Ser	Leu	Lys	Val	Pro
		660						665					670		
Ser	Ala	Arg	Gly	Ser	Pro	Ala	Trp	Ala	Pro	Ser	Pro	Lys	Ser	Trp	Ser
		675					680					685			
Glu	Asp	Pro	Glu	Glu	Ala	Ser	Ser								
		690				695									

<210> 502

<211> 242

<212> PRT

<213> Rat

<400> 502

Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys Gly Gln
 1 5 10 15
 Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ser Ser His Leu Val
 20 25 30
 Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Thr Gly Pro Glu Glu
 35 40 45
 Ser His Cys Leu Gln Cys Arg Lys Gly Trp Ala Leu His His Leu Lys
 50 55 60
 Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gln Ala Thr Cys Gly Ala
 65 70 75 80
 Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg Asp Cys
 85 90 95
 Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg Cys Lys
 100 105 110
 Lys Cys Ser Arg Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu Asp Val
 115 120 125
 Asp Glu Cys Glu Thr Val Val Cys Pro Gly Glu Asn Glu Gln Cys Glu
 130 135 140
 Asn Thr Glu Gly Ser Tyr Arg Cys Val Cys Ala Glu Gly Phe Arg Gln
 145 150 155 160
 Glu Asp Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala Gly Phe
 165 170 175
 Phe Ala Glu Met Thr Glu Asp Glu Met Val Val Leu Gln Gln Met Phe
 180 185 190
 Phe Gly Val Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys Gly Asp
 195 200 205
 Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met Thr Gly
 210 215 220
 Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe Ile Lys
 225 230 235 240
 Gly Arg

<210> 503

<211> 819

<212> PRT

<213> Rat

<400> 503

Lys Ser Trp Thr Ile Ile Gln Glu Arg Leu Gln Met Asp Ser Met Val
 1 5 10 15
 Ile Lys Gly Leu Asp Pro Asp Thr Asn Tyr Gln Phe Ala Val Arg Ala
 20 25 30
 Met Asn Ala Tyr Gly Phe Ser Leu Arg Ser Gln Pro Ser Asn Thr Ile
 35 40 45
 Arg Thr Leu Gly Pro Gly Glu Ala Gly Ser Gly Arg Tyr Gly Pro Gly
 50 55 60
 Tyr Ile Thr Asp Thr Gly Val Ser Glu Asp Asp Ala Ser Glu Asp
 65 70 75 80
 Glu Leu Asp Leu Asp Val Ser Phe Glu Glu Val Lys Pro Leu Pro Ala
 85 90 95
 Thr Lys Val Gly Asn Lys Lys Ser Lys Lys Thr Ser Val Ser Asn Ser

233

Ile Leu His Pro Phe Ser Gly Ser Ile Gln Lys Ile Ile Leu Asn Asp
 565 570 575
 Arg Thr Ile His Val Arg His Asp Phe Thr Ser Gly Val Asn Val Glu
 580 585 590
 Asn Ala Ala His Pro Cys Val Gly Ala Pro Cys Ala His Gly Gly Ser
 595 600 605
 Cys Arg Pro Arg Lys Glu Gly Tyr Glu Cys Asp Cys Pro Leu Gly Phe
 610 615 620
 Glu Gly Leu Asn Cys Gln Lys Ala Ile Thr Glu Ala Ile Glu Ile Pro
 625 630 635 640
 Gln Phe Ile Gly Arg Ser Tyr Leu Thr Tyr Asp Asn Pro Asn Ile Leu
 645 650 655
 Lys Arg Val Ser Gly Ser Arg Ser Asn Ala Phe Met Arg Phe Lys Thr
 660 665 670
 Thr Ala Lys Asp Gly Leu Leu Leu Trp Arg Gly Asp Ser Pro Met Arg
 675 680 685
 Pro Asn Ser Asp Phe Ile Ser Leu Gly Leu Arg Asp Gly Ala Leu Val
 690 695 700
 Phe Ser Tyr Asn Leu Gly Ser Gly Val Ala Ser Ile Met Val Asn Gly
 705 710 715 720
 Ser Phe Ser Asp Gly Arg Trp His Arg Val Lys Ala Val Arg Asp Gly
 725 730 735
 Gln Ser Gly Lys Ile Thr Val Asp Asp Tyr Gly Ala Arg Thr Gly Lys
 740 745 750
 Ser Pro Gly Met Met Arg Gln Leu Asn Ile Asn Gly Ala Leu Tyr Val
 755 760 765
 Gly Gly Met Lys Glu Ile Ala Leu His Thr Asn Arg Gln Tyr Met Arg
 770 775 780
 Gly Leu Val Gly Cys Ile Ser His Phe Thr Leu Ser Thr Asp Tyr His
 785 790 795 800
 Ile Ser Leu Val Glu Asp Ala Val Asp Gly Lys Asn Ile Asn Thr Cys
 805 810 815
 Gly Ala Lys

<210> 504

<211> 127

<212> PRT

<213> Rat

<400> 504

Gly Glu Arg Gly Pro Lys Gly Glu Lys Gly Glu Arg Gly Glu Arg Ala
 1 5 10 15
 Ala Gly Asp Met Asp Phe Thr Met Ile Arg Leu Val Asn Gly Ser Gly
 20 25 30
 Pro His Gln Gly Arg Val Glu Val Phe His Asp Arg Arg Trp Gly Thr
 35 40 45
 Val Cys Asp Asp Gly Trp Asp Lys Lys Asp Gly Asp Val Val Cys Arg
 50 55 60
 Met Leu Gly Phe His Ser Val Glu Glu Val His Arg Thr Ala Arg Phe
 65 70 75 80
 Gly Gln Gly Thr Gly Arg Ile Trp Met Asp Asp Val Asn Cys Lys Gly
 85 90 95
 Thr Glu Ser Ser Ile Phe His Cys Gln Phe Ser Lys Trp Gly Val Thr
 100 105 110
 Asn Cys Gly His Ala Glu Asp Ala Gly Val Thr Cys Thr Ala Leu
 115 120 125

<210> 505
 <211> 125
 <212> PRT
 <213> Human

<400> 505
 Ser Leu His Ser Cys His Leu Glu Arg Ile Ser Arg Gly Ala Phe Gln
 1 5 10 15
 Glu Gln Gly His Leu Arg Ser Leu Val Leu Gly Asp Asn Cys Leu Ser
 20 25 30
 Glu Asn Tyr Glu Glu Thr Ala Ala Ala Leu His Ala Leu Pro Gly Leu
 35 40 45
 Arg Arg Leu Asp Leu Ser Gly Asn Ala Leu Thr Glu Asp Met Ala Ala
 50 55 60
 Leu Met Leu Gln Asn Leu Ser Ser Leu Arg Ser Val Ser Leu Ala Gly
 65 70 75 80
 Asn Thr Ile Met Arg Leu Asp Asp Ser Val Phe Glu Gly Leu Glu Arg
 85 90 95
 Leu Arg Glu Leu Asp Leu Gln Arg Asn Tyr Ile Phe Glu Ile Glu Gly
 100 105 110
 Gly Ala Phe Asp Gly Leu Ala Glu Leu Arg His Leu Asn
 115 120 125

<210> 506
 <211> 551
 <212> PRT
 <213> Rat

<400> 506
 Met Gln Pro Pro Trp Gly Leu Ala Leu Pro Leu Leu Leu Pro Trp Val
 1 5 10 15
 Ala Gly Gly Val Gly Thr Ser Pro Arg Asp Tyr Trp Leu Pro Ala Leu
 20 25 30
 Ala His Gln Pro Gly Val Cys His Tyr Gly Thr Lys Thr Ala Cys Cys
 35 40 45
 Tyr Gly Trp Lys Arg Asn Ser Lys Gly Val Cys Glu Ala Val Cys Glu
 50 55 60
 Pro Arg Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys
 65 70 75 80
 Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys
 85 90 95
 Ala Phe Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly
 100 105 110
 Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Leu Pro Asp Ala
 115 120 125
 Thr Cys Ser Asn Ser Arg Thr Cys Ala Arg Ile Asn Cys Gln Tyr Ser
 130 135 140
 Cys Glu Asp Thr Ala Glu Gly Pro Arg Cys Val Cys Pro Ser Ser Gly
 145 150 155 160
 Leu Arg Leu Gly Pro Asn Gly Arg Val Cys Leu Asp Ile Asp Glu Cys
 165 170 175
 Ala Ser Ser Lys Ala Val Cys Pro Ser Asn Arg Arg Cys Val Asn Thr
 180 185 190
 Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Lys Tyr
 195 200 205
 Ile Ser Arg Arg Tyr Asp Cys Val Asp Ile Asn Glu Cys Thr Leu Asn

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      210      215      220
Thr Arg Thr Cys Ser Pro His Ala Asn Cys Leu Asn Thr Gln Gly Ser
225      230      235      240
Phe Lys Cys Lys Cys Lys Gln Gly Tyr Arg Gly Asn Gly Leu Gln Cys
      245      250      255
Ser Val Ile Pro Glu His Ser Val Lys Glu Ile Leu Thr Ala Pro Gly
      260      265      270
Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys His Thr Met
      275      280      285
Lys Lys Lys Val Lys Leu Lys Asn Val Thr Pro Arg Pro Thr Ser Thr
      290      295      300
Arg Ala Pro Lys Val Asn Leu Pro Tyr Ser Ser Glu Glu Gly Val Ser
305      310      315      320
Arg Gly Arg Asn Ser Gly Gly Glu Gln Lys Arg Lys Glu Glu Arg Lys
      325      330      335
Arg Lys Arg Leu Glu Glu Glu Lys Ser Glu Lys Ala Leu Arg Asn Glu
      340      345      350
Val Glu Gln Glu Arg Pro Leu Arg Gly Asp Val Phe Ser Pro Lys Val
      355      360      365
Asn Glu Ala Glu Asp Leu Asp Leu Val Tyr Ile Gln Arg Lys Glu Leu
      370      375      380
Asn Ser Lys Gln Glu His Lys Ala Asp Leu Asn Ile Ser Val Asp Cys
385      390      395      400
Ser Phe Asp Leu Gly Val Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp
      405      410      415
Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Asp Val Gly Tyr Tyr Met
      420      425      430
Ala Val Pro Ala Leu Ala Gly His Lys Lys Asn Ile Gly Arg Leu Lys
      435      440      445
Leu Leu Leu Pro Asn Leu Thr Pro Gln Ser Asn Phe Cys Leu Leu Phe
      450      455      460
Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val
465      470      475      480
Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Glu Thr Lys Thr Glu Asp
      485      490      495
Gly Lys Trp Lys Thr Gly Lys Val Pro Leu Tyr Gln Gly Ile Asp Thr
      500      505      510
Thr Lys Ser Val Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly
      515      520      525
Glu Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp
      530      535      540
Asp Phe Leu Ser Glu Glu Gly
545      550

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<210> 507
<211> 244
<212> PRT
<213> Mouse

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      <400> 507
Tyr Ala Ser Ala Ser Glu Pro Thr Glu Ile Tyr Arg Thr Glu Leu Gln
1      5      10      15
Gly Leu Trp Ile Asn Asp Ile Val Pro Ile Gly Arg Ile Gln Glu Pro
      20      25      30
Ala His Leu Asp Phe Met Cys Leu Gln Asn Glu Val Tyr Lys Gln Thr
      35      40      45
Glu Gln Leu Ala Glu Leu Ser Lys Gly Val Gln Glu Val Val Leu Ser

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      50      55      60
Ser Ile Leu Ser Met Leu Tyr Glu Gly Asp Arg Lys Val Leu Tyr Asp
65      70      75      80
Leu Met Asn Met Leu Glu Leu Asn Gln Leu Gly His Met Asp Gly Pro
      85      90      95
Gly Gly Lys Ile Leu Asp Glu Leu Arg Lys Asp Ser Ser Asn Pro Cys
100      105      110
Val Asp Leu Lys Asp Leu Ile Leu Tyr Leu Leu Gln Ala Leu Met Val
115      120      125
Leu Ser Asp Ser Gln Leu Asn Leu Leu Ala Gln Ser Val Glu Met Gly
130      135      140
Ile Leu Pro His Gln Val Glu Leu Val Lys Ser Ile Leu Gln Pro Asn
145      150      155      160
Phe Lys Tyr Pro Trp Asn Ile Pro Phe Thr Val Gln Pro Gln Leu Leu
165      170      175
Ala Pro Leu Gln Gly Glu Gly Leu Ala Ile Thr Tyr Glu Leu Leu Glu
180      185      190
Glu Cys Gly Leu Lys Met Glu Leu Asn Asn Pro Arg Ser Thr Trp Asp
195      200      205
Leu Glu Ala Lys Met Pro Leu Ser Ala Leu Tyr Gly Ser Leu Ser Phe
210      215      220
Leu Gln Gln Leu Arg Lys Ala Asn Ser Ser Ser Lys Pro Ser Leu Arg
225      230      235      240
Pro Gly Tyr Ile

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<210> 508
<211> 248
<212> PRT
<213> Human

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      <400> 508
Val Ser Cys Arg Tyr Leu Lys Asn Ser Leu His Val Phe Val Ser Gly
1      5      10      15
Gly Ala Ile Gly Thr Ser Ser Pro Ala Leu Leu Glu Cys Gln Glu Gly
20      25      30
Val Gly Pro Ala Arg Pro Ser Leu Leu Val Pro Pro Pro Arg Pro
35      40      45
Arg Arg Leu Asp Leu Ala Arg Thr Leu Pro Ala Glu Arg Thr Asp Ser
50      55      60
Gln Ser Leu Tyr Ile Val Tyr Ile Ala Leu Pro Gly Arg Thr Pro Arg
65      70      75      80
Pro Ala Leu Ala Phe Ala Phe Leu Met Pro Ala Cys Cys Asn Arg Pro
85      90      95
Ser Pro Arg Pro Ser Pro Ala His Leu Thr Ala Ser Ser Val Leu Arg
100      105      110
Arg Gln Arg His Val Leu Ala Ala Ser Ala Ala Ser Pro Cys Gln Trp
115      120      125
Ser Gly Leu Arg Val Ala His Ser Leu Arg Gln Val Val Ser Leu Cys
130      135      140
Pro Arg Cys Thr Gly Ser Cys Pro Phe Ser Gly Ala Cys Ala Ser Ser
145      150      155      160
Leu Pro Ser Pro Leu Ser Cys Pro His Ser His Ser Gly Ser Trp Gly
165      170      175
Thr Trp Ser Gln Gly Arg Pro Cys Ser Ser Thr Glu Val Ala Gly Leu
180      185      190
Ala Leu Trp Pro Thr Asp Phe Leu Ser Cys Leu Leu Asp Ala Ser Glu

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          340          345          350
Asp Phe Gln Leu Val Ala Gly His Pro Asn Leu Cys Val Gln Val Ser
          355          360          365
Thr Trp Glu Lys Val Gln Leu Gln Ala Cys Leu Trp Ala Asp Ser Leu
          370          375          380
Gly Pro Phe Lys Asp Asp Met Leu Leu Val Glu Met Lys Thr Gly Leu
          385          390          395
Asn Asn Thr Ser Val Cys Ala Leu Glu Pro Ser Gly Cys Thr Pro Leu
          405          410          415
Pro Ser Met Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu Glu Leu Leu
          420          425          430
Gln Asp Phe Arg Ser His Gln Cys Met Gln Leu Trp Asn Asp Asp Asn
          435          440          445
Met Gly Ser Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His Arg Arg
          450          455          460
Trp Val Leu Val Trp Leu Ala Cys Leu Leu Leu Ala Ala Ala Leu Phe
          465          470          475
Phe Phe Leu Leu Leu Lys Lys Asp Arg Arg Lys Ala Ala Arg Gly Ser
          485          490          495
Arg Thr Ala Leu Leu Leu His Ser Ala Asp Gly Ala Gly Tyr Glu Arg
          500          505          510
Leu Val Gly Ala Leu Ala Ser Ala Leu Ser Gln Met Pro Leu Arg Val
          515          520          525
Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala His Gly Ala Leu
          530          535          540
Ala Trp Phe His His Gln Arg Arg Arg Ile Leu Gln Glu Gly Gly Val
          545          550          555
Val Ile Leu Leu Phe Ser Pro Ala Ala Val Ala Gln Cys Gln Gln Trp
          565          570          575
Leu Gln Leu Gln Thr Val Glu Pro Gly Pro His Asp Ala Leu Ala Ala
          580          585          590
Trp Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala Thr Gly
          595          600          605
Arg Tyr Val Gly Val Tyr Phe Asp Gly Leu Leu His Pro Asp Ser Val
          610          615          620
Pro Ser Pro Phe Arg Val Ala Pro Leu Phe Ser Leu Pro Ser Gln Leu
          625          630          635
Pro Ala Phe Leu Asp Ala Leu Gln Gly Gly Cys Ser Thr Ser Ala Gly
          645          650          655
Arg Pro Ala Asp Arg Val Glu Arg Val Thr Gln Ala Leu Arg Ser Ala
          660          665          670
Leu Asp Ser Cys Thr Ser Thr Ser Glu Ala Pro Gly Cys Cys Glu Glu
          675          680          685
Trp Asp Leu Gly Pro Cys Thr Thr Leu Glu
          690          695

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<210> 510
 <211> 1700
 <212> DNA
 <213> Rat

<400> 1
 ccttttgtgg cacacccagg gccagttac ttctcaggtt cgagtctaaa ctctcagccg
 tagacgttgt agacgtcggg gttccagctc catctttgca cacataatcc aggaagccgc
 tagctctcga tgtcttctgt caagttatgg ctcaatgggt cgtcatcgat ctctctcgtg
 ggctctgaag aactggagaa cctaggattt gtgggcaaag gcgggttcgg agccgtgttc
 cgggcacgcc acacagcatg gaaccttgat gttagcagtc agatcgtgaa ctccaagaag

atatccaggg	aggatgaaggc	tatgggtgaat	cttcgtcatg	agaacgtgct	gtcctgtctg	360
ggggctactg	agaacctcga	gtgggactac	gtgtacgggc	cggctctggt	gacaggattc	420
atggagaacg	gtccctcttc	agggctgctg	caaccttcat	gccctcggcc	ctggcctctc	480
ctctgtcgcc	tgctagagga	agtgggtgctg	gggatgtgct	acctacacag	cttgaacctc	540
tcgtactctg	accgggacct	caagccctcc	aatgttctgc	tggatccaga	gtccacgccc	600
aagttagcag	actttggcct	gtccacattt	caggagggtg	cacagtcagg	gtcagggtca	660
ggatcgagag	attctggggg	caccttagct	tacttggccc	cagagctgtt	ggataatgac	720
ggaaaggctt	ctaaagcaag	tgatgtttac	agttttgggg	tcctcgtgtg	gacagtgtctg	780
gctggaagag	aagctgaggt	ggtagacaag	acctcactaa	ttcgtggagc	agtgtgtaac	840
aggcagaggg	gacctccatt	gacagagctg	cctccggaca	gccctgagac	tcctggctta	900
gaaggactga	aggagttaat	gacgcattgc	tggagtctctg	agcctaaaga	caggccatcc	960
ttccaagact	gtgaatcaaa	aaccaataat	gtttacatcc	tggtagacga	caaggtagat	1020
gctgtgtgtc	ccaaggtaaa	gcattatctg	tctcagtaca	gaagcagtga	cacaaagtgtg	1080
ttctccagag	agtccagcca	aaaagggtaca	gaggtggatt	gccccaggga	aacctagttt	1140
tatgaaatgc	tggaaccgct	gcattctggag	gagccctctg	gatcagttcc	tgaaagactc	1200
acaagtctta	ctgagaggag	aggaaaggaa	gcattcattt	ggcatgccac	accagcaggg	1260
acatcatctg	acaccttggc	tggcactccc	caaattccac	atactttacc	ctccagaggc	1320
acaacacctt	ggccagcctt	tactgagact	ccaggtcctg	acccccaaag	gaatcaggga	1380
gatggaagaa	acagcaatcc	ttggtacacc	tggaaacgcac	caaatccaat	gacagggcta	1440
cagtctattg	tcttaaacaa	ctgttctgaa	gtgcagattg	gacaacacaa	ctgcatgtca	1500
gtacaaccga	gaactgcctt	tccaagaag	gagccagcac	agttcggcag	gggtaggggc	1560
tggtagcccg	tccacgtcca	cgagtagact	tcggagagga	cctgcaagtg	cctgaagcag	1620
gaaatacacc	attcaggcag	ccagtataaa	tagagtgaag	ataaaagcac	tttctaagca	1680
aaaaaaaaaa	aaaaaaaaaa					1700

<210> 511

<211> 2538

<212> DNA

<213> Rat

<400> 2

ctggagggga	aagtactttc	gtgccgggtg	gtagtagcgg	gtgggtgtag	cttgggtgtag	60
aagcttgagc	catgcgtctc	acagctgccc	gcgcctcct	cggggaagct	cgttctgccc	120
cgcccgcccc	gccctcctct	cttcacccca	cctcatagge	tcccaggcgc	ttctgcttgg	180
cttgagcgcc	gaacgtcgac	ttcccagcag	tcocgcgcgc	gtctccttgg	cgacgatgtt	240
aaacaaccac	accggtccaa	gctgtgagct	tcaggctgag	gcttggcagg	gcgccgccaa	300
ctggggacct	gtgaagtgtc	tttttagacat	gatctgtgga	gtcctcagga	ttctggcatc	360
aatcaacact	tcctgttcga	cttttggacc	gtcagctcgg	ctgcccgaact	gttgtttctg	420
tgagtgaaca	agccagtttt	tatcttgttt	ggagcaatgc	tgaaattcca	agagactgct	480
aagtgtggac	ccacagccat	tcctgtgtac	ccaccactg	tgattgcaag	aagatacgtt	540
ctccaacaga	agcttggcag	cgggagtttt	ggaactgtct	atctgggtgc	agacaagaaa	600
gccaagcatg	gagaggaact	aaaagtactg	aaggaaatct	ctgttggaga	attaaatcca	660
aatgaaagtg	tgcaaggccag	tatggaagcc	cagctcctgt	ccacgctaaa	ccatccggcc	720
atcgtcaggt	tccacgcaag	cttcatggag	cagggtacat	tttgcattat	cacggagtac	780
tgtgagggcc	gagatctgga	ctataaaatc	caggaatata	aagaagctgg	gaaaatcttt	840
cctgacaatc	agatagtgga	atggtttatc	cagttgtctg	ttggagtgtg	ttacatgcac	900
gagaggagga	tacttcatcg	agacttgaaa	tcaaagaata	tatttctgaa	aaataatcta	960
cccaaaattg	gggacttttg	agtttctcgg	ctgctgatgg	gttcatgtga	gctggctaca	1020
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gccaaagtctg	acatctggtc	actggcatgc	attttatacg	agatgtgttg	catggatcat	1140
gcgtttttctg	gtcccaattt	cttgtctgtg	gttttgaata	tcgttgaagg	caacacgcct	1200
tcactccctg	acagataccc	acgagaacta	aacatcatca	tgtcacgcac	gttgaacaag	1260
agtcctctcc	tgagaccgtc	ggctgcagag	attttaaaag	cccttctatg	ggaagagtgc	1320
cttcagcagc	tgatgtataa	acatccagag	gcgacactgg	aagacaagag	gaactcagcc	1380
tgtcagaagg	aggctgccc	tcaggttaac	gccataaaga	ttactgaagg	aagaagatat	1440
aaagaaaata	acaaaagggc	caaagaacta	agatcccaga	actttgggtc	tgtgagtgcc	1500
catgtgctcc	aggaattaga	tgaactgact	ctggagagcc	tgtctcaacc	tcagtccctt	1560

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cettgcctga acctcgatga acttgagccc agtttagaag gcaccattgt tgacctcgga 1620
cattatgaga tcccagaaga cccgcttggt gctgaacaat attatgctga tgtatttgat 1680
tcctgttctg aagacagtgg ggagcaggag gaagaaatgg cattttcaga agcaggggga 1740
gacatgagag aggagggatc cccacctaca tacagaacaa accaacaggt accccctccc 1800
gctctggcca gaagagatgt agctgtccgc ggtgctgaac ggattctgga ctcaggctaa 1860
gaaagcgcag agggagcgag cgggtcttgaa cctggagttg gggtcaggtt gctcaggact 1920
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gaactatgag actctgatca ggacctgtt tagaggggag gggctaggct agtcagtcca 2040
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gtaagtgcg aaagtctctc tcacaggcgg agtgggtttt ttgtttgttt gtttttttga 2160
tttttatcat tttccagcct ataatcagat ttgggtttgt tttaaaattt tgatgtaagt 2220
acagatttat aaagactgat tccattctgy agttaaaatt tggaaagtctg aatgttagga 2280
aatgttcttt atagctttgt gcagcctctg aggagctctc atcacatgct gcaactgggtc 2340
tctctgcata gatgctctag tcgtagaact tcttaattag aaagactgag ctagagtagg 2400
tctaataaga taagaaatgg ccctgctttg cccctttcct tttgattttt ggagttgaaa 2460
taaagtgtga tacaagcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2520
aaaaaaaaa aaaaaaaaaa 2538

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<210> 512

<211> 478

<212> PRT

<213> Rat

<400> 3

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Met Ser Ser Val Lys Leu Trp Leu Asn Gly Ala Ser Ser Ile Ser Leu
1 5 10 15
Val Gly Ser Glu Glu Leu Glu Asn Leu Gly Phe Val Gly Lys Gly Gly
20 25 30
Phe Gly Ala Val Phe Arg Ala Arg His Thr Ala Trp Asn Leu Asp Val
35 40 45
Ala Val Lys Ile Val Asn Ser Lys Lys Ile Ser Arg Glu Val Lys Ala
50 55 60
Met Val Asn Leu Arg His Glu Asn Val Leu Leu Leu Gly Val Thr
65 70 75 80
Glu Asn Leu Glu Trp Asp Tyr Val Tyr Gly Pro Ala Leu Val Thr Gly
85 90 95
Phe Met Glu Asn Gly Ser Leu Ser Gly Leu Leu Gln Pro Ser Cys Pro
100 105 110
Arg Pro Trp Pro Leu Leu Cys Arg Leu Leu Glu Glu Val Val Leu Gly
115 120 125
Met Cys Tyr Leu His Ser Leu Asn Pro Ser Leu Leu His Arg Asp Leu
130 135 140
Lys Pro Ser Asn Val Leu Leu Asp Pro Glu Leu His Ala Lys Leu Ala
145 150 155 160
Asp Phe Gly Leu Ser Thr Phe Gln Gly Gly Ser Gln Ser Gly Ser Gly
165 170 175
Ser Gly Ser Arg Asp Ser Gly Gly Thr Leu Ala Tyr Leu Ala Pro Glu
180 185 190
Leu Leu Asp Asn Asp Gly Lys Ala Ser Lys Ala Ser Asp Val Tyr Ser
195 200 205
Phe Gly Val Leu Val Trp Thr Val Leu Ala Gly Arg Glu Ala Glu Val
210 215 220
Val Asp Lys Thr Ser Leu Ile Arg Gly Ala Val Cys Asn Arg Gln Arg
225 230 235 240
Arg Pro Pro Leu Thr Glu Leu Pro Pro Asp Ser Pro Glu Thr Pro Gly
245 250 255
Leu Glu Gly Leu Lys Glu Leu Met Thr His Cys Trp Ser Ser Glu Pro

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260 265 270
 Lys Asp Arg Pro Ser Phe Gln Asp Cys Glu Ser Lys Thr Asn Asn Val
 275 280 285
 Tyr Ile Leu Val Gln Asp Lys Val Asp Ala Ala Val Ser Lys Val Lys
 290 295 300
 His Tyr Leu Ser Gln Tyr Arg Ser Ser Asp Thr Lys Leu Ser Ala Arg
 305 310 315 320
 Glu Ser Ser Gln Lys Gly Thr Glu Val Asp Cys Pro Arg Glu Thr Ile
 325 330 335
 Val Tyr Glu Met Leu Asp Arg Leu His Leu Glu Glu Pro Ser Gly Ser
 340 345 350
 Val Pro Glu Arg Leu Thr Ser Leu Thr Glu Arg Arg Gly Lys Glu Ala
 355 360 365
 Ser Phe Gly His Ala Thr Pro Ala Gly Thr Ser Ser Asp Thr Leu Ala
 370 375 380
 Gly Thr Pro Gln Ile Pro His Thr Leu Pro Ser Arg Gly Thr Thr Pro
 385 390 395 400
 Arg Pro Ala Phe Thr Glu Thr Pro Gly Pro Asp Pro Gln Arg Asn Gln
 405 410 415
 Gly Asp Gly Arg Asn Ser Asn Pro Trp Tyr Thr Trp Asn Ala Pro Asn
 420 425 430
 Pro Met Thr Gly Leu Gln Ser Ile Val Leu Asn Asn Cys Ser Glu Val
 435 440 445
 Gln Ile Gly Gln His Asn Cys Met Ser Val Gln Pro Arg Thr Ala Phe
 450 455 460
 Pro Lys Lys Glu Pro Ala Gln Phe Gly Arg Gly Arg Gly Trp
 465 470 475

<210> 513

<211> 467

<212> PRT

<213> Rat

<400> 4

Met Leu Lys Phe Gln Glu Thr Ala Lys Cys Gly Pro Thr Ala Ile Pro
 1 5 10 15
 Val Tyr Pro Pro Thr Val Ile Ala Arg Arg Tyr Val Leu Gln Gln Lys
 20 25 30
 Leu Gly Ser Gly Ser Phe Gly Thr Val Tyr Leu Val Ser Asp Lys Lys
 35 40 45
 Ala Lys His Gly Glu Glu Leu Lys Val Leu Lys Glu Ile Ser Val Gly
 50 55 60
 Glu Leu Asn Pro Asn Glu Ser Val Gln Ala Ser Met Glu Ala Gln Leu
 65 70 75 80
 Leu Ser Thr Leu Asn His Pro Ala Ile Val Arg Phe His Ala Ser Phe
 85 90 95
 Met Glu Gln Gly Thr Phe Cys Ile Ile Thr Glu Tyr Cys Glu Gly Arg
 100 105 110
 Asp Leu Asp Tyr Lys Ile Gln Glu Tyr Lys Glu Ala Gly Lys Ile Phe
 115 120 125
 Pro Asp Asn Gln Ile Val Glu Trp Phe Ile Gln Leu Leu Gly Val
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 Asp Tyr Met His Glu Arg Arg Ile Leu His Arg Asp Leu Lys Ser Lys
 145 150 155 160
 Asn Ile Phe Leu Lys Asn Asn Leu Pro Lys Ile Gly Asp Phe Gly Val
 165 170 175
 Ser Arg Leu Leu Met Gly Ser Cys Glu Leu Ala Thr Thr Leu Thr Gly

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Ala Lys Ser Asp Ile Trp Ser Leu Ala Cys Ile Leu Tyr Glu Met Cys
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Cys Met Asp His Ala Phe Ser Gly Ser Asn Phe Leu Ser Val Val Leu
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Asn Ile Val Glu Gly Asn Thr Pro Ser Leu Pro Asp Arg Tyr Pro Arg
      245      250      255
Glu Leu Asn Ile Ile Met Ser Arg Met Leu Asn Lys Ser Pro Ser Leu
      260      265      270
Arg Pro Ser Ala Ala Glu Ile Leu Lys Ala Pro Tyr Val Glu Glu Cys
      275      280      285
Leu Gln Gln Leu Met Tyr Lys His Pro Glu Ala Thr Leu Glu Asp Lys
      290      295      300
Arg Asn Ser Ala Cys Gln Lys Glu Ala Ala His Ala Val Asn Ala Ile
      305      310      315      320
Lys Ile Thr Glu Gly Arg Arg Tyr Lys Glu Asn Asn Lys Arg Ala Lys
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Glu Leu Arg Ser Gln Asn Phe Gly Ser Val Ser Ala His Val Leu Gln
      340      345      350
Glu Leu Asp Glu Leu Thr Leu Glu Ser Leu Ser Gln Pro Gln Ser Leu
      355      360      365
Pro Cys Leu Asn Leu Asp Glu Leu Glu Pro Ser Leu Glu Gly Thr Ile
      370      375      380
Val Asp Leu Gly His Tyr Glu Ile Pro Glu Asp Pro Leu Val Ala Glu
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Gln Tyr Tyr Ala Asp Val Phe Asp Ser Cys Ser Glu Asp Ser Gly Glu
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Gln Glu Glu Glu Met Ala Phe Ser Glu Ala Gly Gly Asp Met Arg Glu
      420      425      430
Glu Gly Ser Pro Pro Thr Tyr Arg Thr Asn Gln Gln Val Pro Pro
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<210> 514
 <211> 3380
 <212> DNA
 <213> Rat

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<210> 515

<211> 1183

<212> DNA

<213> Rat

<400> 515

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<210> 516
 <211> 1858
 <212> DNA
 <213> Rat

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<210> 517
 <211> 1376
 <212> DNA
 <213> Rat

<400> 517

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<210> 518

<211> 763

<212> DNA

<213> Rat

<400> 518

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<210> 519

<211> 1496

<212> DNA

<213> Rat

<400> 519

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 <211> 1243
 <212> DNA
 <213> Rat

<400> 520						
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<211> 1372

<212> DNA

<213> Rat

<400> 522

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<211> 1265

<212> DNA

<213> Rat

<400> 523

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<210> 524

<211> 980

<212> DNA

<213> Rat

<400> 524

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<210> 525

<211> 2929

<212> DNA

<213> Rat

<400> 525

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<211> 672

<212> DNA

<213> Rat

<400> 526

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<210> 527

<211> 690

<212> DNA

<213> Rat

<400> 527

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<210> 528

<211> 2597

<212> DNA

<213> Rat

<400> 528

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<211> 1081

<212> DNA

<213> Rat

<400> 529

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<210> 530

<211> 906

<212> DNA

<213> Rat

<400> 530

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<210> 531

<211> 2271

<212> DNA

<213> Rat

<400> 531

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<210> 532

<211> 642

<212> DNA

<213> Rat

<400> 532

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<210> 533

<211> 910

<212> DNA

<213> Rat

<400> 533

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<210> 534

<211> 2928

<212> DNA

<213> Rat

<400> 534

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<210> 535

<211> 924

<212> DNA

<213> Rat

<400> 535

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<211> 1744

<212> DNA

<213> Rat

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<210> 537

<211> 891

<212> DNA

<213> Rat

<400> 537

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<212> DNA

<213> Rat

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<213> Rat

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<211> 1178

<212> DNA

<213> Rat

<400> 552

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<210> 553

<211> 1600

<212> DNA

<213> Rat

<400> 553

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<210> 554

<211> 2401

<212> DNA

<213> Rat

<400> 554

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<211> 2729

<212> DNA

<213> Rat

<400> 555

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<211> 2494

<212> DNA

<213> Rat

<400> 556

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<211> 2198

<212> DNA

<213> Mouse

<400> 557

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2198

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<211> 1683

<212> DNA

<213> Mouse

<400> 558

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<211> 2559

<212> DNA

<213> Mouse

<400> 559

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<211> 1274

<212> DNA

<213> Mouse

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<210> 562

<211> 1847

<212> DNA

<213> Mouse

<400> 562

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 <211> 1972
 <212> DNA
 <213> Mouse

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 <212> DNA
 <213> Mouse

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<211> 1258

<212> DNA

<213> Mouse

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<211> 546

<212> DNA

<213> Mouse

<400> 566

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<212> DNA

<213> Mouse

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<211> 2167
 <212> DNA
 <213> Mouse

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 <212> DNA
 <213> Mouse

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<210> 570

<211> 926

<212> DNA

<213> Mouse

<400> 570

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<210> 571

<211> 1589

<212> DNA

<213> Mouse

<400> 571

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<210> 572

<211> 2920

<212> DNA

<213> Mouse

<400> 572

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 <211> 1859
 <212> DNA
 <213> Mouse

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 <211> 2305
 <212> DNA
 <213> Mouse

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 <211> 1930
 <212> DNA
 <213> Mouse

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<210> 576

<211> 2618

<212> DNA

<213> Mouse

<400> 576

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<210> 577

<211> 1480

<212> DNA

<213> Mouse

<400> 577

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<210> 578

<211> 802

<212> DNA

<213> Mouse

<400> 578

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<210> 579

<211> 2112

<212> DNA

<213> Mouse

<400> 579

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<210> 580
 <211> 919
 <212> DNA
 <213> Mouse

<400> 580	
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 <212> DNA
 <213> Mouse

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<210> 582
 <211> 1288
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 <211> 999
 <212> DNA
 <213> Mouse

<400> 583
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<210> 584
 <211> 2123
 <212> DNA
 <213> Mouse

<400> 584

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<210> 585

<211> 1864

<212> DNA

<213> Mouse

<400> 585

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<210> 586

<211> 1391

<212> DNA

<213> Mouse

<400> 586

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<210> 587

<211> 2324

<212> DNA

<213> Mouse

<400> 587

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<210> 588

<211> 1859

<212> DNA

<213> Mouse

<400> 588

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<210> 589

<211> 724

<212> DNA

<213> Mouse

<400> 589

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<211> 2395

<212> DNA

<213> Mouse

<400> 590

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<210> 591

<211> 909

<212> DNA

<213> Mouse

<400> 591

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<210> 592

<211> 881

<212> DNA
<213> Mouse

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<210> 593
<211> 556
<212> DNA
<213> Mouse

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<210> 594
<211> 750
<212> DNA
<213> Mouse

<400> 594
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<210> 595
 <211> 1896
 <212> DNA
 <213> Mouse

<400> 595
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 <211> 1854
 <212> DNA
 <213> Mouse

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<210> 597

<211> 1318

<212> DNA

<213> Mouse

<400> 597

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<211> 2866

<212> DNA

<213> Mouse

<400> 598

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<211> 1515

<212> DNA

<213> Mouse

<400> 610

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 <211> 1817
 <212> DNA
 <213> Mouse

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 <212> DNA

<213> Mouse

<400> 612

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<210> 613

<211> 509

<212> DNA

<213> Mouse

<400> 613

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<210> 614

<211> 948

<212> DNA

<213> Mouse

<400> 614

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<210> 615

<211> 505

<212> DNA

<213> Mouse

<400> 615

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<211> 1251

<212> DNA

<213> Mouse

<400> 616

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<210> 617

<211> 502

<212> DNA

<213> Mouse

<400> 617

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<210> 618

<211> 528

<212> DNA

<213> Human

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<210> 619
<211> 2013
<212> DNA
<213> Mouse

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<210> 620
<211> 1002
<212> DNA
<213> Mouse

<400> 620

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<210> 621

<211> 1843

<212> DNA

<213> Mouse

<400> 621

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gatatccccc	tgcccttagg	ctgcttcggg	tacagccccc	atctgggtga	agagcgttgt	1800
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<210> 622
 <211> 2368
 <212> DNA
 <213> Mouse

<400> 622
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 tacaggagtc gcaacctctc cgctccagc ccgcagcttc tactgccacc caagtgcgag 240
 atgttgcatg tggctatcgt gtgtgcggga tacaactcca gccgagagat tattacccta 300
 acgaagtcctc tgctattcta caggaaaaat ccgctgcacc tccacctgat aactgatgcc 360
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<210> 623
 <211> 2275
 <212> DNA
 <213> Mouse

<400> 623
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 gtgggtgtcg gaatttgaac tcaggacctt cagaagagca gtcagtgtctc ttaaccctga 180

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atcgagctg caaggaaaga ggctccattc ctatgtggca cagttacgta cgtttgtaat 360
cctggctgtt taggaggctg agggagaaga aggatttaag accatgaatt ccacatcagt 420
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tgtgttatga gaaaacagac atccgggaag atagttcagt ggtagagtgc ttgcctactg 600
cacatgaggt cctcggttca attctcagt tctcaagtta ccagcaaaat gaacaaataa 660
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cagaaccagg caaactatgc cagagactag ccacccctaa agagctaata ccagacttct 780
gcaagcccac gcctccaacc aaccacagaa gaacatacac tcaactgagc cttaccatg 840
gcagcacaca gtggaagct atggagatcg tgcaggacat aggatgtgcc cgagcacaca 900
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<210> 624

<211> 688

<212> PRT

<213> Rat

<400> 624

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Gly Ala Pro Met Tyr Phe Ser Glu Gly Arg Glu Arg Gly Lys Val Tyr
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Val Tyr Asn Leu Arg Gln Asn Arg Phe Val Phe Asn Gly Thr Leu Lys
20          25          30
Asp Ser His Ser Tyr Gln Asn Ala Arg Phe Gly Ser Cys Ile Ala Ser
35          40          45
Val Gln Asp Leu Asn Gln Asp Ser Tyr Asn Asp Val Val Val Gly Ala
50          55          60
Pro Leu Glu Asp Ser His Arg Gly Ala Ile Tyr Ile Phe His Gly Phe
65          70          75          80
Gln Thr Asn Ile Leu Lys Lys Pro Val Gln Arg Ile Ser Ala Ser Glu
85          90          95
Leu Ala Pro Gly Leu Gln His Phe Gly Cys Ser Ile His Gly Gln Leu
100         105         110
Asp Leu Asn Glu Asp Gly Leu Val Asp Leu Ala Val Gly Ala Leu Gly

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			115					120				125				
Asn	Ala	Val	Val	Leu	Trp	Ala	Arg	Pro	Val	Val	Gln	Ile	Asn	Ala	Ser	
	130					135					140					
Leu	His	Phe	Glu	Pro	Ser	Lys	Ile	Asn	Ile	Phe	Lys	Asp	Cys	Lys		
145					150					155					160	
Arg	Asn	Gly	Arg	Asp	Ala	Thr	Cys	Leu	Ala	Ala	Phe	Leu	Cys	Phe	Gly	
				165					170					175		
Pro	Ile	Phe	Leu	Ala	Pro	His	Phe	His	Thr	Ala	Thr	Val	Gly	Ile	Arg	
			180				185					190				
Tyr	Asn	Ala	Thr	Met	Asp	Glu	Arg	Arg	Tyr	Met	Pro	Arg	Ala	His	Leu	
	195					200					205					
Asp	Glu	Gly	Ala	Asp	Gln	Phe	Thr	Asn	Arg	Ala	Val	Leu	Leu	Ser	Ser	
	210					215					220					
Gly	Gln	Glu	His	Cys	Gln	Arg	Ile	Asn	Phe	His	Val	Leu	Asp	Thr	Ala	
225				230					235						240	
Asp	Tyr	Val	Lys	Pro	Val	Ala	Phe	Ser	Val	Glu	Tyr	Ser	Leu	Glu	Asp	
			245					250					255			
Pro	Asp	His	Gly	Pro	Met	Leu	Asp	Asn	Gly	Trp	Pro	Thr	Thr	Leu	Arg	
			260				265					270				
Val	Ser	Val	Pro	Phe	Trp	Asn	Gly	Cys	Asn	Glu	Asp	Glu	His	Cys	Val	
	275					280					285					
Pro	Asp	Leu	Val	Leu	Asp	Ala	Arg	Ser	Asp	Leu	Pro	Thr	Ala	Met	Glu	
	290				295					300						
Tyr	Cys	Gln	Gln	Val	Leu	Arg	Arg	Pro	Ala	Gln	Asp	Cys	Ser	Ser	Tyr	
305				310					315						320	
Thr	Leu	Ser	Phe	Asp	Thr	Thr	Val	Phe	Ile	Ile	Glu	Ser	Thr	Arg	Arg	
			325					330						335		
Arg	Val	Ala	Val	Glu	Ala	Thr	Leu	Glu	Asn	Arg	Gly	Glu	Asn	Ala	Tyr	
			340				345					350				
Ser	Ala	Val	Leu	Asn	Ile	Ser	Gln	Ser	Glu	Asn	Leu	Gln	Phe	Ala	Ser	
	355					360					365					
Leu	Ile	Gln	Lys	Asp	Asp	Ser	Asp	Asn	Ser	Ile	Glu	Cys	Val	Asn	Glu	
	370				375					380						
Glu	Arg	Arg	Leu	His	Lys	Lys	Val	Cys	Asn	Val	Ser	Tyr	Pro	Phe	Phe	
385				390					395						400	
Arg	Ala	Lys	Ala	Lys	Val	Ala	Phe	Arg	Leu	Asp	Phe	Glu	Phe	Ser	Lys	
			405					410						415		
Ser	Val	Phe	Leu	His	His	Leu	Gln	Ile	His	Leu	Gly	Ala	Gly	Ser	Asp	
			420				425				430					
Ser	His	Glu	Gln	Asp	Ser	Thr	Ala	Asp	Asp	Asn	Thr	Ala	Leu	Leu	Arg	
	435					440					445					
Phe	His	Leu	Lys	Tyr	Glu	Ala	Asp	Val	Leu	Phe	Thr	Arg	Ser	Ser	Ser	
	450															

```

Asn Gln Glu Thr Ser Phe Tyr Leu Val Gly Asn Leu Trp Leu Met Ser
      580      585      590
Leu Lys Ala Leu Lys Tyr Arg Ser Met Lys Ile Thr Val Asn Ala Ala
      595      600      605
Leu Gln Arg Gln Phe His Ser Pro Phe Ile Phe Arg Glu Glu Asp Pro
      610      615      620
Ser Arg Gln Val Thr Phe Glu Ile Ser Lys Gln Glu Asp Trp Gln Val
      625      630      635      640
Pro Ile Trp Ile Ile Val Gly Ser Ser Leu Gly Gly Leu Leu Leu Leu
      645      650      655
Ala Leu Leu Val Leu Ala Leu Trp Lys Leu Gly Phe Phe Lys Ser Ala
      660      665      670
Lys Arg Lys Arg Glu Pro Ser Leu Gly Pro Val Pro Lys Glu Leu Glu
      675      680      685

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<210> 625

<211> 242

<212> PRT

<213> Rat

<400> 625

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Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys Gly Gln
  1      5      10      15
Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ser Ser His Leu Val
      20      25      30
Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Thr Gly Pro Glu Glu
      35      40      45
Ser His Cys Leu Gln Cys Arg Lys Gly Trp Ala Leu His His Leu Lys
      50      55      60
Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gln Ala Thr Cys Gly Ala
      65      70      75      80
Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg Asp Cys
      85      90      95
Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg Cys Lys
      100      105      110
Lys Cys Ser Arg Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu Asp Val
      115      120      125
Asp Glu Cys Glu Thr Val Val Cys Pro Gly Glu Asn Glu Gln Cys Glu
      130      135      140
Asn Thr Glu Gly Ser Tyr Arg Cys Val Cys Ala Glu Gly Phe Arg Gln
      145      150      155      160
Glu Asp Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala Gly Phe
      165      170      175
Phe Ala Glu Met Thr Glu Asp Glu Met Val Val Leu Gln Gln Met Phe
      180      185      190
Phe Gly Val Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys Gly Asp
      195      200      205
Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met Thr Gly
      210      215      220
Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe Ile Lys
      225      230      235      240
Gly Arg

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<210> 626

<211> 576

<212> PRT

<213> Rat

<400> 626

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Met Pro Phe Arg Leu Ile Pro Leu Gly Leu Val Cys Val Leu Leu
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Pro Leu His His Gly Ala Pro Gly Pro Glu Gly Thr Ala Pro Asp Pro
20      25      30
Ala His Tyr Arg Glu Arg Val Lys Ala Met Phe Tyr His Ala Tyr Asp
35      40      45
Ser Tyr Leu Glu Asn Ala Phe Pro Tyr Asp Glu Leu Arg Pro Leu Thr
50      55      60
Cys Asp Gly His Asp Thr Trp Gly Ser Phe Ser Leu Thr Leu Ile Asp
65      70      75      80
Ala Leu Asp Thr Leu Leu Ile Leu Gly Asn Thr Ser Glu Phe Gln Arg
85      90      95
Val Val Glu Val Leu Gln Asp Asn Val Asp Phe Asp Ile Asp Val Asn
100     105     110
Ala Ser Val Phe Glu Thr Asn Ile Arg Val Val Gly Gly Leu Leu Ser
115     120     125
Ala His Leu Leu Ser Lys Lys Ala Gly Val Glu Val Glu Ala Gly Trp
130     135     140
Pro Cys Ser Gly Pro Leu Leu Arg Met Ala Glu Glu Ala Ala Arg Lys
145     150     155     160
Leu Leu Pro Ala Phe Gln Thr Pro Thr Gly Met Pro Tyr Gly Thr Val
165     170     175
Asn Leu Leu His Gly Val Asn Pro Gly Glu Thr Pro Val Thr Cys Thr
180     185     190
Ala Gly Ile Gly Thr Phe Ile Val Glu Phe Ala Thr Leu Ser Ser Leu
195     200     205
Thr Gly Asp Pro Val Phe Glu Asp Val Ala Arg Val Ala Leu Met Arg
210     215     220
Leu Trp Glu Ser Arg Ser Asp Ile Gly Leu Val Gly Asn His Ile Asp
225     230     235     240
Val Leu Thr Gly Lys Trp Val Ala Gln Asp Ala Gly Ile Gly Ala Gly
245     250     255
Val Asp Ser Tyr Phe Glu Tyr Leu Val Lys Gly Ala Ile Leu Leu Gln
260     265     270
Asp Lys Lys Leu Met Ala Met Phe Leu Glu Tyr Asn Lys Ala Ile Arg
275     280     285
Asn Tyr Thr His Phe Asp Asp Trp Tyr Leu Trp Val Gln Met Tyr Lys
290     295     300
Gly Thr Val Ser Met Pro Val Phe Gln Ser Leu Glu Ala Tyr Trp Pro
305     310     315     320
Gly Leu Gln Ser Leu Ile Gly Asp Ile Asp Asn Ala Met Arg Thr Phe
325     330     335
Leu Asn Tyr Tyr Thr Val Trp Lys Gln Phe Gly Gly Leu Pro Glu Phe
340     345     350
Tyr Asn Ile Pro Gln Gly Tyr Thr Val Glu Lys Arg Glu Gly Tyr Pro
355     360     365
Leu Arg Pro Glu Leu Ile Glu Ser Ala Met Tyr Leu Tyr Arg Ala Thr
370     375     380
Gly Asp Pro Thr Leu Leu Glu Leu Gly Arg Asp Ala Val Glu Ser Ile
385     390     395     400
Glu Lys Ile Ser Lys Val Glu Cys Gly Phe Ala Thr Ile Lys Asp Leu
405     410     415
Arg Asp His Lys Leu Asp Asn Arg Met Glu Ser Phe Phe Leu Ala Glu
420     425     430

```

Thr Val Lys Tyr Leu Tyr Leu Leu Phe His Pro Asn Asn Phe Ile His
 435 440 445
 Asn Asn Gly Ser Thr Phe Asp Ser Val Met Thr Pro His Gly Glu Cys
 450 455 460
 Ile Leu Gly Ala Gly Gly Tyr Ile Phe Asn Thr Glu Ala His Pro Ile
 465 470 475 480
 Asp Pro Ala Ala Leu His Cys Cys Arg Arg Leu Lys Glu Glu Gln Trp
 485 490 495
 Glu Val Glu Asp Leu Ile Lys Glu Phe Tyr Ser Leu Arg Gln Ser Arg
 500 505 510
 Ser Arg Ala Gln Arg Lys Thr Val Ser Ser Gly Pro Trp Glu Pro Pro
 515 520 525
 Ala Gly Pro Gly Thr Leu Ser Ser Pro Glu Asn Gln Pro Arg Glu Lys
 530 535 540
 Gln Pro Ala Arg Gln Arg Ala Pro Leu Leu Ser Cys Pro Ser Gln Pro
 545 550 555 560
 Phe Thr Ser Lys Leu Ala Leu Leu Gly Gln Val Phe Leu Asp Ser Ser
 565 570 575

<210> 627
 <211> 226
 <212> PRT
 <213> Rat

<400> 627
 Arg Lys Ile Lys Asn Lys Ile Ser Ala Gln Glu Ser Arg Arg Lys Lys
 1 5 10 15
 Lys Glu Tyr Val Glu Cys Leu Glu Lys Lys Val Glu Thr Tyr Thr Ser
 20 25 30
 Glu Asn Asn Glu Leu Trp Lys Lys Val Glu Thr Leu Glu Thr Ala Asn
 35 40 45
 Arg Thr Leu Leu Gln Gln Leu Gln Lys Leu Gln Thr Leu Val Thr Ser
 50 55 60
 Lys Ile Ser Arg Pro Tyr Lys Met Ala Ala Thr Gln Thr Gly Thr Cys
 65 70 75 80
 Leu Met Val Ala Ala Leu Cys Phe Val Leu Val Leu Gly Ser Leu Ala
 85 90 95
 Pro Cys Leu Pro Ala Phe Ser Ser Gly Ser Lys Thr Val Lys Glu Asp
 100 105 110
 Pro Val Ala Ala Asp Ser Val Tyr Ala Ala Ser Gln Met Pro Ser Arg
 115 120 125
 Ser Leu Leu Phe Tyr Asp Asp Gly Ala Gly Ser Trp Glu Asp Gly His
 130 135 140
 Arg Gly Ala Leu Leu Pro Val Glu Pro Pro Glu Gly Trp Glu Leu Lys
 145 150 155 160
 Pro Gly Gly Pro Ala Glu Pro Arg Pro Gln Asp His Leu Arg His Asp
 165 170 175
 His Ala Asp Ser Ile His Glu Thr Thr Lys Tyr Leu Arg Glu Thr Trp
 180 185 190
 Pro Glu Asp Thr Glu Asp Asn Gly Ala Ser Pro Asn Phe Ser His Pro
 195 200 205
 Lys Glu Trp Phe His Asp Arg Asp Leu Gly Pro Asn Thr Thr Ile Lys
 210 215 220
 Leu Ser
 225

<210> 628

<211> 82
 <212> PRT
 <213> Rat

<400> 628

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Pro Ile Thr Leu Ser Cys Gln Ser Gly Asn Ala Ala Ser Leu Gln Pro
1          5          10          15
Leu His Phe Pro Pro Val Pro Pro Glu Ala Cys Pro Cys Ala Phe Arg
20          25          30
Leu Arg Pro Phe Cys Leu His Thr Gly Cys Ala Gly Cys Ser Leu Arg
35          40          45
Ala Ala Thr Glu Gln Cys Ala Val Ala Leu Ala Pro Gln Leu Pro Ser
50          55          60
Ala Ser Arg Ala Phe Pro Pro Leu Thr Leu Cys Asn Pro Cys Val Leu
65          70          75          80
Thr Arg

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<210> 629
 <211> 242
 <212> PRT
 <213> Rat

<400> 629

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Met Ala Gly Ala Gly Pro Val Leu Ser Ile Leu Gly Leu Leu Leu Val
1          5          10          15
Ser Ala Leu Phe Gly Val Leu Gly Glu Arg Pro Asn Pro Asp Leu Gly
20          25          30
Ala His Pro Glu Arg Arg Ser Gln Val Gly Pro Gly Ala Thr Glu Pro
35          40          45
Arg Arg Gln Pro Pro Pro Lys Asp Gln Arg Glu Arg Ala Arg Ala Gly
50          55          60
Ser Leu Ser Leu Gly Ala Leu Tyr Thr Ala Ala Ile Val Ala Phe Val
65          70          75          80
Leu Phe Lys Cys Leu Gln Gln Gly Pro Asp Glu Ala Ala Val Pro Arg
85          90          95
Glu Glu Lys Asn Lys Lys Lys Ser Ser Gln Ser Glu Gln Gln Leu Val
100          105          110
Gln Leu Thr Gln Gln Leu Ala Gln Thr Glu Glu His Leu Asn Asn Leu
115          120          125
Met Thr Gln Leu Asp Pro Leu Phe Glu Arg Val Thr Thr Leu Val Gly
130          135          140
Thr Gln Arg Glu Leu Leu Asn Ala Lys Leu Lys Thr Ile His His Leu
145          150          155          160
Leu Gln Asp Cys Lys Pro Gly Ile Gly Val Glu Ala Pro Glu Pro Glu
165          170          175
Ala Pro Ile His Phe Pro Glu Asp Leu Gly Lys Glu Asp Gln Glu Asp
180          185          190
Ala Gly Asn Ser Gln Ala Trp Glu Glu Pro Ile Asn Trp Ser Ser Glu
195          200          205
Thr Trp Asn Leu Ala Pro Ser Trp Glu Val Glu Gln Gly Leu Arg Arg
210          215          220
Arg Trp His Lys Thr Lys Gly Pro Ala Val Asn Gly Gly Gln Ala Leu
225          230          235          240
Lys Val

```

<210> 630
 <211> 289
 <212> PRT
 <213> Rat

<400> 630

```

Met Ile Val Leu Leu Tyr Val Thr Ser Leu Ala Ile Cys Ala Ser Gly
 1           5           10           15
Gln Pro Arg Gly Asn Gln Ala Lys Gly Glu Ser Tyr Ser Pro Arg Tyr
 20           25           30
Ile Cys Ser Ile Pro Gly Leu Pro Gly Pro Pro Gly Pro Pro Gly Ala
 35           40           45
Asn Gly Ser Pro Gly Pro His Gly Arg Ile Gly Leu Pro Gly Arg Asp
 50           55           60
Gly Arg Asp Gly Arg Lys Gly Glu Lys Gly Glu Lys Gly Thr Ala Gly
 65           70           75           80
Leu Lys Gly Lys Thr Gly Pro Leu Gly Leu Ala Gly Glu Lys Gly Asp
 85           90           95
Gln Gly Glu Thr Gly Lys Lys Gly Pro Ile Gly Pro Glu Gly Glu Lys
100           105           110
Gly Glu Val Gly Pro Ala Gly Pro Pro Gly Pro Lys Gly Asp Arg Gly
115           120           125
Asp Gln Gly Asp Pro Gly Leu Pro Gly Val Cys Arg Cys Gly Ser Ile
130           135           140
Val Leu Lys Ser Ala Phe Ser Val Gly Ile Thr Thr Ser Tyr Pro Glu
145           150           155           160
Glu Arg Leu Pro Ile Ile Phe Asn Lys Val Leu Phe Asn Glu Gly Glu
165           170           175
His Tyr Asn Pro Ala Thr Gly Lys Phe Ile Cys Ala Phe Pro Gly Ile
180           185           190
Tyr Tyr Phe Ser Tyr Asp Ile Thr Leu Ala Asn Lys His Leu Ala Ile
195           200           205
Gly Leu Val His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp Ala Asn
210           215           220
Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr Val Ile Tyr Leu Gln
225           230           235           240
Pro Glu Asp Glu Val Trp Leu Glu Ile Phe Phe Asn Asp Gln Asn Gly
245           250           255
Leu Phe Ser Asp Pro Gly Trp Ala Asp Ser Leu Phe Ser Gly Phe Leu
260           265           270
Leu Tyr Val Asp Thr Asp Tyr Leu Asp Ser Ile Ser Glu Asp Asp Glu
275           280           285
Leu

```

<210> 631
 <211> 213
 <212> PRT
 <213> Rat

<400> 631

```

Met Val Leu Gly Gly Cys Pro Val Ser Tyr Leu Leu Leu Cys Gly Gln
 1           5           10           15
Ala Ala Leu Leu Gly Asn Leu Leu Leu His Cys Val Ser Arg
 20           25           30
Ser His Ser Phe Asn Ala Thr Ala Glu Leu Asp Leu Thr Pro Ser Gly
 35           40           45

```


Ala Ala His Leu Glu Gly Pro Ala Ala Ser Ser Trp Glu Tyr Ser Asp
 50 55 60
 Pro Asn Ser Pro Val Ile Leu Cys Ser Tyr Leu Pro Asp Glu Phe Val
 65 70 75 80
 Asp Cys Asp Ala Pro Val Asp His Val Gly Asn Ala Thr Ala Tyr Gln
 85 90 95
 Glu Leu Gly Tyr Gly Cys Leu Lys Phe Gly Gly Gln Ala Tyr Ser Asp
 100 105 110
 Val Glu His Thr Ala Val Gln Cys Arg Ala Leu Glu Gly Ile Glu Cys
 115 120 125
 Ala Ser Pro Arg Thr Phe Leu Arg Lys Asn Lys Pro Cys Ile Lys Tyr
 130 135 140
 Thr Gly His Tyr Phe Ile Thr Thr Leu Leu Tyr Ser Phe Phe Leu Gly
 145 150 155 160
 Cys Phe Gly Val Asp Arg Phe Cys Leu Gly His Thr Gly Thr Ala Val
 165 170 175
 Gly Lys Leu Leu Thr Leu Gly Gly Leu Gly Ile Trp Trp Phe Val Asp
 180 185 190
 Leu Ile Leu Leu Ile Thr Gly Gly Leu Met Pro Ser Asp Gly Ser Asn
 195 200 205
 Trp Cys Thr Val Tyr
 210

<210> 632

<211> 167

<212> PRT

<213> Rat

<400> 632

Met Ala Ser Pro Arg Thr Ile Thr Ile Val Ala Leu Ser Val Ala Leu
 1 5 10 15
 Gly Leu Phe Phe Val Phe Met Gly Thr Ile Lys Leu Thr Pro Arg Leu
 20 25 30
 Ser Lys Asp Ala Tyr Ser Glu Met Lys Arg Ala Tyr Lys Ser Tyr Val
 35 40 45
 Arg Ala Leu Pro Leu Leu Lys Lys Met Gly Ile Asn Ser Ile Leu Leu
 50 55 60
 Arg Lys Ser Ile Gly Ala Leu Glu Val Ala Cys Gly Ile Val Met Thr
 65 70 75 80
 Leu Val Pro Gly Arg Pro Lys Asp Val Ala Asn Phe Phe Leu Leu Leu
 85 90 95
 Leu Val Leu Ala Val Leu Phe Phe His Gln Leu Val Gly Asp Pro Leu
 100 105 110
 Lys Arg Tyr Ala His Ala Leu Val Phe Gly Ile Leu Leu Thr Cys Arg
 115 120 125
 Leu Leu Ile Ala Arg Lys Pro Glu Asp Arg Ser Phe Glu Lys Lys Ala
 130 135 140
 Leu Pro Glu Ser Ala Glu Glu Gln Pro Ser Leu Tyr Glu Lys Ala Pro
 145 150 155 160
 Gln Gly Lys Val Lys Val Ser
 165

<210> 633

<211> 138

<212> PRT

<213> Rat

<400> 633

```

Phe Ile Arg Gly Met Leu Lys Leu Ile Leu Leu Leu Leu Phe Ser Gly
 1           5           10           15
Ala Thr Leu Ser Ser Thr Trp Phe Thr Leu Thr Cys Leu Asn Ser Val
 20           25           30
Thr His Leu Pro Leu Thr Thr Val Thr Leu Tyr Ala Ser Cys Ile Leu
 35           40           45
Leu Gly Val Phe Leu Asn Ser Ser Val Pro Ile Phe Phe Glu Leu Phe
 50           55           60
Val Glu Thr Val Tyr Pro Val Pro Glu Gly Ile Thr Cys Gly Val Val
 65           70           75           80
Thr Phe Leu Ser Asn Met Phe Met Gly Val Leu Leu Phe Phe Val Thr
 85           90           95
Phe Tyr His Thr Glu Leu Ser Trp Phe Asn Trp Cys Leu Pro Gly Ser
100          105          110
Cys Leu Leu Ser Leu Leu Leu Ile Leu Cys Phe Arg Glu Ser Tyr Asp
115          120          125
Arg Leu Tyr Leu Asp Val Val Val Ser Val
130          135

```

<210> 634

<211> 75

<212> PRT

<213> Rat

<400> 634

```

Met Ile Gly Asp Ile Leu Leu Phe Gly Thr Leu Leu Met Asn Ala Gly
 1           5           10           15
Ala Val Leu Asn Phe Lys Leu Lys Lys Lys Asp Thr Gln Gly Phe Gly
 20           25           30
Glu Glu Ser Arg Glu Pro Ser Thr Gly Asp Asn Ile Arg Glu Phe Leu
 35           40           45
Leu Ser Leu Arg Tyr Phe Arg Ile Phe Ile Ala Leu Trp Asn Val Phe
 50           55           60
Met Met Leu Cys Met Ile Val Leu Phe Gly Ser
 65           70           75

```

<210> 635

<211> 186

<212> PRT

<213> Rat

<400> 635

```

Met Val Ala Ala Val Ala Thr Ala Trp Leu Leu Leu Trp Ala Ala Ala
 1           5           10           15
Cys Thr Gln Ser Glu Gln Asp Phe Tyr Asp Phe Lys Ala Val Asn Ile
 20           25           30
Arg Gly Lys Leu Val Ser Leu Glu Lys Tyr Arg Gly Ser Val Ser Leu
 35           40           45
Val Val Asn Val Ala Ser Glu Cys Gly Phe Thr Asp Gln Asn Tyr Arg
 50           55           60
Ala Leu Gln Gln Leu Gln Arg Asp Leu Gly Pro Tyr His Phe Asn Val
 65           70           75           80
Leu Ala Phe Pro Cys Asn Gln Phe Gly Gln Gln Glu Pro Asp Ser Asn
 85           90           95
Arg Glu Ile Glu Asn Phe Ala Arg Arg Thr Tyr Ser Val Ser Phe Pro
100          105          110

```

Met Phe Ser Lys Ile Ala Val Thr Gly Thr Gly Ala His Pro Ala Phe
 115 120 125
 Lys Tyr Leu Thr Gln Thr Ser Gly Lys Glu Pro Thr Trp Asn Phe Trp
 130 135 140
 Lys Tyr Leu Val Ala Pro Asp Gly Lys Val Val Gly Ala Trp Asp Pro
 145 150 155 160
 Thr Val Pro Val Glu Glu Ile Lys Pro Arg Ile Thr Glu Gln Val Met
 165 170 175
 Lys Leu Ile Leu Gln Lys Arg Glu Asp Leu
 180 185

<210> 636

<211> 930

<212> PRT

<213> Rat

<400> 636

Met Pro Ser Leu Leu Ser Leu Val Leu Thr Phe Leu Ala Val Ser Ser
 1 5 10 15
 Pro Ser Cys Cys Gln Asn Ser Asp Thr Ala Ser Pro Lys Ala Ser Asn
 20 25 30
 Gly Ala Ser Phe Leu Trp Asn Asn Met Arg Leu Pro Glu Tyr Ile Thr
 35 40 45
 Pro Ile His Tyr Asp Leu Met Ile His Ala Asn Leu Ser Thr Leu Thr
 50 55 60
 Phe Trp Gly Lys Thr Glu Val Glu Ile Thr Val Ser Gln Pro Thr Ser
 65 70 75 80
 Thr Ile Ile Met His Ser His Gln Leu Gln Ile Ser Lys Ala Thr Leu
 85 90 95
 Arg Arg Gly Ala Glu Glu Met Leu Pro Glu Glu Pro Leu Lys Leu Met
 100 105 110
 Glu Tyr Ser Ala His Glu Gln Val Ala Leu Leu Thr Ala Gln Pro Leu
 115 120 125
 Leu Ala Gly Ser Val Tyr Thr Val Ile Ile Thr Tyr Ala Ala Asn Leu
 130 135 140
 Ser Glu Asn Phe His Gly Phe Tyr Lys Ser Thr Tyr Arg Thr Gln Glu
 145 150 155 160
 Gly Glu Arg Arg Ile Leu Ala Ala Thr Gln Phe Glu Pro Thr Ala Ala
 165 170 175
 Arg Met Ala Phe Pro Cys Phe Asp Glu Pro Ala Leu Lys Ala Ser Phe
 180 185 190
 Ser Ile Lys Ile Lys Arg Asp Pro Arg His Leu Ala Ile Ser Asn Met
 195 200 205
 Pro Leu Val Lys Ser Val Thr Val Ala Glu Gly Leu Ile Glu Asp His
 210 215 220
 Phe Asp Ile Thr Val Lys Met Ser Thr Tyr Leu Val Ala Phe Ile Ile
 225 230 235 240
 Ser Asp Phe Lys Ser Val Ser Lys Met Thr Lys Ser Gly Val Lys Val
 245 250 255
 Ser Val Tyr Ala Val Pro Asp Lys Ile Asn Gln Ala Asp Tyr Ala Leu
 260 265 270
 Asp Ala Ala Val Thr Leu Leu Glu Phe Tyr Glu Asp Tyr Phe Ser Ile
 275 280 285
 Pro Tyr Pro Leu Pro Lys Gln Asp Leu Ala Ala Ile Pro Asp Phe Gln
 290 295 300
 Ser Gly Ala Met Glu Asn Trp Gly Leu Thr Thr Tyr Arg Glu Ser Ala
 305 310 315 320

Leu Leu Tyr Asp Lys Glu Lys Ser Ser Ala Ser Ser Lys Leu Gly Ile
 325 330 335
 Thr Met Thr Val Ser His Glu Leu Ala His Gln Trp Phe Gly Asn Leu
 340 345 350
 Val Thr Met Glu Trp Trp Asn Asp Leu Trp Leu Asn Glu Gly Phe Ala
 355 360 365
 Lys Phe Met Glu Phe Val Ser Val Thr Val Thr His Pro Glu Leu Lys
 370 375 380
 Val Glu Glu Tyr Phe Phe Gly Lys Cys Val Asn Ala Met Glu Val Asp
 385 390 395 400
 Ala Leu Asn Ser Ser His Pro Val Ser Thr Pro Val Glu Asn Pro Ala
 405 410 415
 Gln Ile Arg Glu Met Phe Asp Glu Val Ser Tyr Glu Lys Gly Ala Cys
 420 425 430
 Ile Leu Asn Met Leu Arg Asp Tyr Leu Ser Ala Asp Thr Phe Lys Arg
 435 440 445
 Gly Ile Val Gln Tyr Leu Gln Lys Tyr Ser Tyr Lys Asn Thr Lys Asn
 450 455 460
 Glu Asp Leu Trp Asn Ser Met Met His Ile Cys Pro Thr Asp Gly Thr
 465 470 475 480
 Gln Thr Met Asp Gly Phe Cys Ser Arg Asn Gln His Ser Ser Ser Thr
 485 490 495
 Ser His Trp Arg Gln Glu Val Ile Asp Ile Lys Ser Met Met Asn Thr
 500 505 510
 Trp Thr Leu Gln Lys Gly Phe Pro Leu Ile Thr Ile Thr Val Arg Gly
 515 520 525
 Arg Asn Val His Leu Lys Gln Glu His Tyr Met Lys Gly Ser Glu Cys
 530 535 540
 Phe Pro Glu Thr Gly Ser Leu Trp His Val Pro Leu Thr Phe Ile Thr
 545 550 555 560
 Ser Lys Ser Asp Ser Val Gln Arg Phe Leu Leu Lys Thr Lys Thr Asp
 565 570 575
 Val Ile Ile Leu Pro Glu Ala Val Glu Trp Ile Lys Phe Asn Val Gly
 580 585 590
 Met Asn Gly Tyr Tyr Ile Val His Tyr Gly Asp Asp Gly Trp Ala Ser
 595 600 605
 Leu Asn Gly Leu Leu Lys Glu Ala His Thr Thr Ile Ser Ser Asn Asp
 610 615 620
 Arg Ala Ser Leu Ile Asn Asn Ala Phe Gln Leu Val Ser Ile Gly Lys
 625 630 635 640
 Leu Ser Ile Glu Lys Ala Leu Asp Leu Ile Leu Tyr Leu Lys Asn Glu
 645 650 655
 Thr Glu Ile Met Pro Ile Phe Gln Gly Leu Asn Glu Leu Ile Pro Met
 660 665 670
 Tyr Lys Leu Met Glu Lys Arg Asp Met Val Glu Val Glu Thr Gln Phe
 675 680 685
 Lys Asp Phe Leu Leu Arg Leu Leu Lys Asp Leu Ile Asn Lys Gln Thr
 690 695 700
 Trp Thr Asp Glu Gly Ser Val Ser Glu Arg Met Leu Arg Ser Gln Leu
 705 710 715 720
 Leu Leu Leu Ala Cys Val His Arg Tyr Gln Leu Cys Val Gln Arg Ala
 725 730 735
 Glu Arg Tyr Phe Arg Glu Trp Lys Ala Ser Asn Gly Asn Met Ser Leu
 740 745 750
 Pro Ile Asp Val Thr Leu Ala Val Phe Ala Val Gly Ala Gln Asn Thr
 755 760 765
 Glu Gly Trp Asp Phe Leu Tyr Ser Lys Tyr Gln Ser Ser Leu Ser Ser

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      770              775              780
Thr Glu Lys Ser Gln Ile Glu Phe Ser Leu Cys Ile Ser Gln Asp Pro
785              790              795              800
Glu Lys Leu Gln Trp Leu Leu Asp Gln Ser Phe Lys Gly Glu Ile Ile
      805              810              815
Lys Thr Gln Glu Phe Pro His Ile Leu Thr Leu Ile Gly Arg Asn Pro
      820              825              830
Val Gly Tyr Pro Leu Ala Trp Lys Phe Leu Lys Glu Asn Trp Asn Lys
      835              840              845
Ile Val Gln Lys Phe Glu Leu Gly Ser Ser Ser Ile Ala His Met Val
      850              855              860
Met Gly Thr Thr Asn Gln Phe Ser Thr Arg Ala Arg Leu Glu Glu Val
865              870              875              880
Lys Gly Phe Phe Ser Ser Leu Lys Lys Asn Gly Ser Gln Leu Arg Cys
      885              890              895
Val Gln Gln Thr Ile Glu Thr Ile Glu Glu Asn Ile Arg Trp Met Asp
      900              905              910
Lys Asn Phe Asp Lys Ile Arg Leu Trp Leu Gln Lys Glu Arg Gln Glu
      915              920              925
Leu Leu
      930

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<210> 637
 <211> 161
 <212> PRT
 <213> Rat

```

<400> 637
Met Ala Tyr His Ser Gly Tyr Gly Val His Ala Met Ala Phe Ile Thr
1              5              10              15
Tyr Val Leu Leu Ala Gly Met Ala Leu Gly Ile Gln Gln Arg Phe Ser
      20              25              30
Pro Glu Val Leu Gly Leu Cys Ala Ser Thr Ala Leu Val Trp Val Leu
      35              40              45
Met Glu Val Leu Ala Leu Leu Leu Gly Leu Tyr Leu Ala Thr Val Arg
      50              55              60
Ser Glu Leu Gly Thr Phe His Leu Leu Ala Tyr Ser Gly Tyr Lys Tyr
65              70              75              80
Val Gly Met Ile Leu Ser Val Leu Thr Gly Leu Leu Phe Gly Ser Asp
      85              90              95
Gly Tyr Tyr Val Ala Leu Ala Trp Thr Ser Ser Ala Leu Met Tyr Phe
      100              105              110
Thr Val Arg Ser Leu Arg Thr Ala Ala Ser Gly Pro Asp Ser Met Gly
      115              120              125
Gly Pro Thr Pro Arg Gln His Leu Gln Leu Tyr Leu Thr Leu Gly Ala
      130              135              140
Ala Ala Phe Gln Pro Leu Ile Ile Tyr Trp Leu Thr Phe His Leu Val
145              150              155              160
Arg

```

<210> 638
 <211> 165
 <212> PRT
 <213> Rat

<400> 638

```

Met Ala Arg Ala Ala Gly Ile Thr Ala Ala Ile Thr Leu Ala Leu Leu
 1           5           10           15
Gly Val Leu Ala Leu Gly Ala Gly Asp Gly Asp Phe Arg Leu Asp Asp
          20           25           30
Ala Leu Glu Asp Thr Asp Lys Lys Pro Thr Pro Lys Pro Pro Thr Pro
      35           40           45
Lys Lys Pro Ser Ser Gly Asp Phe Asp Leu Glu Glu Ala Leu Thr Gly
      50           55           60
Gly Ala Asp Glu Asp Pro Arg Arg Pro Gly Ser Arg Pro Lys Pro Asp
      65           70           75           80
Pro Lys Pro Pro Gly Pro Pro Arg Asp Ser Gly Gly Ile Ser Asp Arg
          85           90           95
Asp Leu Glu Asp Val Ala Gly His Gly Gly Arg Gly Gly Ala Gly
      100           105           110
Asp Arg Gly Thr Asp Gly Ala Glu Ser Glu Gly Gln Pro Gln Gly Leu
      115           120           125
Ile Pro Gly Val Val Ala Ala Val Leu Ala Ala Leu Ala Gly Ala Val
      130           135           140
Ser Ser Phe Val Ala Tyr Gln Lys Arg Arg Leu Cys Phe Arg Glu Gly
      145           150           155           160
Gly Ser Ala Pro Val
          165

```

<210> 639

<211> 61

<212> PRT

<213> Rat

<400> 639

```

Met His Ile Tyr Lys Tyr Val His Ile Asn Tyr Tyr Leu His Leu His
 1           5           10           15
Ile Cys Ile Tyr Val Tyr Thr His Ile Ser Val Gly Met Cys Ile Arg
          20           25           30
Ile Cys Leu Pro Ser Ser Ser His Trp Lys Lys Glu Ser Ile Arg Ser
      35           40           45
Gly Gly Ser Lys Asn Ala His Tyr Pro Gly Ser Gly Ile
      50           55           60

```

<210> 640

<211> 73

<212> PRT

<213> Rat

<400> 640

```

Met Cys Phe Ser Leu Cys Ser Val Glu Val Phe Phe Leu Lys Gln Asn
 1           5           10           15
Ser Asn Leu Leu Pro Ala His Ile Phe Ile Arg Ala Ser Pro Ile Cys
          20           25           30
Ile Ile Gly Asn Glu Tyr Glu Tyr Ile Phe Met Tyr Val Cys Asn His
      35           40           45
Arg Ser His Leu Tyr Leu Gly Phe Ala Ala Ala Asp Tyr Phe Phe Pro
      50           55           60
His His Gly Thr Gly Asn Cys Phe Gln
      65           70

```

<210> 641

<211> 442

<212> PRT

<213> Rat

<400> 641

```

Met Pro Val Leu Trp Leu Leu Leu Leu Leu Pro Leu Leu Pro Leu Leu
 1          5          10          15
Ala Met Leu Cys Gln Gln Arg Ser Pro Gly Ala Arg Pro Cys Trp Leu
 20          25          30
Ile Ser Leu Gln His Arg Val Ala Cys Val Val Leu Ser Trp Ala Ala
 35          40          45
Ala Trp Gln Arg Arg Lys Leu Glu Gln Ser Thr Leu Asn Val Ser Gln
 50          55          60
Ser Gln Gln Gln Ala Leu Met Gly Cys Leu Lys Glu Ala Gln Gly Ser
 65          70          75          80
Cys Cys Leu Pro Arg Glu Asn Thr Asp Met Thr Thr Phe Arg Asn Leu
 85          90          95
Pro Leu Thr Lys Thr Ser His Thr Gln Gln Lys Glu Ser Glu Glu Lys
100          105          110
Leu Leu Pro Pro Thr Leu Pro Gln Tyr His Gly Asp Ala Ser Leu Gln
115          120          125
Val Thr Leu Leu Gly Leu Met Thr Leu Asn Lys Ala Tyr Pro Glu Val
130          135          140
Leu Ala Pro Gly Ser Thr Ala Cys Val Thr Pro Thr Ser Pro Trp Pro
145          150          155          160
Tyr Ser Val Pro Trp Leu Gly His Ala Leu Gly Arg Val Ser Pro Ile
165          170          175
Gly Ala Lys Asp Ala Arg Thr Leu Leu Leu Glu Ala Leu Ile Ser Pro
180          185          190
Gly Leu Arg Val Leu Glu Ala Arg Thr Ala Val Glu Leu Leu Asp Val
195          200          205
Phe Val Gly Leu Glu Ala Asp Gly Glu Glu Leu Ala Glu Val Ile Ala
210          215          220
Ser Gly Ser Leu Gly Lys Leu Pro Arg Arg Ala Ala Glu Leu Gln Glu
225          230          235          240
Ala Leu Glu Gln Gly Pro Arg Gly Leu Ala Leu Arg Leu Trp Pro Lys
245          250          255
Leu Gln Val Val Val Thr Leu Asp Ala Gly Gly Gln Ala Glu Ala Val
260          265          270
Ala Ala Leu Arg Val Leu Trp Cys Gln Gly Leu Ala Phe Phe Ser Pro
275          280          285
Ala Tyr Ala Ala Ser Gly Gly Val Met Ala Ile Asn Leu Trp Pro Glu
290          295          300
Gln Pro Gln Gly Ser Tyr Leu Leu Ser Pro Gly Val Pro Phe Ile Glu
305          310          315          320
Leu Leu Pro Ile Lys Glu Gly Thr Gln Glu Glu Ala Ala Ser Thr Leu
325          330          335
Leu Leu Thr Asp Val Arg Arg Glu Glu Lys Tyr Glu Leu Val Leu Thr
340          345          350
Asp Ser Thr Ser Leu Thr Arg Cys Arg Leu Gly Asp Val Val Gln Val
355          360          365
Ile Gly Thr Tyr Asn Gln Cys Pro Val Val Arg Phe Thr Cys Arg Leu
370          375          380
Gly Gln Thr Leu Ser Val Arg Gly Glu Val Thr Asp Glu Asn Val Phe
385          390          395          400
Ser Val Ala Leu Ala Gln Ala Val Gly Gln Cys Gln Gly Pro Ser Cys
405          410          415

```

Trp Thr Met Ser Val Trp Arg Ala Thr Phe Trp Thr Pro Met Arg Asp
 420 425 430
 Pro Pro His Thr Thr Lys Cys Leu Trp Ser
 435 440

<210> 642
 <211> 65
 <212> PRT
 <213> Rat

<400> 642
 Met Thr Val Cys Thr Leu Leu Val Ala Lys Ser Thr Leu Leu Leu Ser
 1 5 10 15
 Leu Ser Cys Leu Leu Leu Cys Ser Leu Phe Leu Tyr Ser Val Ser Gly
 20 25 30
 Ser Tyr Ser Arg Cys Pro Val Arg Trp Leu Val Cys Leu Ser Ser Gln
 35 40 45
 Leu Pro Trp Ala Thr Ser Gln Ser Leu Leu Lys Arg Lys Leu Ser Met
 50 55 60
 Asn
 65

<210> 643
 <211> 197
 <212> PRT
 <213> Rat

<400> 643
 Pro Arg Pro Gly Arg Ala Arg Thr Leu Arg Ser Pro Ser Gly Ser Arg
 1 5 10 15
 Val Val Gln Arg Pro Arg Asn Asp Gly Val Ala Ala Leu Thr Gly Ala
 20 25 30
 Gly Gly Cys Arg Ala Pro Arg Ala Gly Met Ala Gly Gln Phe Arg Ser
 35 40 45
 Tyr Val Trp Asp Pro Leu Leu Ile Leu Ser Gln Ile Val Leu Met Gln
 50 55 60
 Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu Ala Leu Val Asp Ala
 65 70 75 80
 Leu Val Arg Ser Asn Pro Ser Leu Asp Gln Met Phe Asp Ala Glu Ile
 85 90 95
 Leu Gly Phe Ser Thr Pro Pro Gly Arg Leu Ser Met Met Ser Phe Val
 100 105 110
 Leu Asn Ala Leu Thr Cys Ala Leu Gly Leu Leu Tyr Phe Ile Arg Arg
 115 120 125
 Gly Lys Gln Cys Leu Asp Phe Thr Val Thr Val His Phe Phe His Leu
 130 135 140
 Leu Gly Cys Trp Leu Tyr Ser Ser Arg Phe Pro Ser Ala Leu Thr Trp
 145 150 155 160
 Trp Leu Val Gln Ala Val Cys Ile Ala Leu Met Ala Val Ile Gly Glu
 165 170 175
 Tyr Leu Cys Met Arg Thr Glu Leu Lys Glu Ile Pro Leu Ser Ser Ala
 180 185 190
 Pro Lys Ser Asn Val
 195

<210> 644
 <211> 930

<212> PRT

<213> Rat

<400> 644

```

Met Pro Ser Leu Leu Ser Leu Val Leu Thr Phe Leu Ala Val Ser Ser
 1          5          10          15
Pro Ser Cys Cys Gln Asn Ser Asp Thr Ala Ser Pro Lys Ala Ser Asn
 20          25          30
Gly Ala Ser Phe Leu Trp Asn Asn Met Arg Leu Pro Glu Tyr Ile Thr
 35          40          45
Pro Ile His Tyr Asp Leu Met Ile His Ala Asn Leu Ser Thr Leu Thr
 50          55          60
Phe Trp Gly Lys Thr Glu Val Glu Ile Thr Val Ser Gln Pro Thr Ser
 65          70          75          80
Thr Ile Ile Met His Ser His Gln Leu Gln Ile Ser Lys Ala Thr Leu
 85          90          95
Arg Arg Gly Ala Glu Glu Met Leu Pro Glu Glu Pro Leu Lys Leu Met
100          105          110
Glu Tyr Ser Ala His Glu Gln Val Ala Leu Leu Thr Ala Gln Pro Leu
115          120          125
Leu Ala Gly Ser Val Tyr Thr Val Ile Ile Thr Tyr Ala Ala Asn Leu
130          135          140
Ser Glu Asn Phe His Gly Phe Tyr Lys Ser Thr Tyr Arg Thr Gln Glu
145          150          155          160
Gly Glu Arg Arg Ile Leu Ala Ala Thr Gln Phe Glu Pro Thr Ala Ala
165          170          175
Arg Met Ala Phe Pro Cys Phe Asp Glu Pro Ala Leu Lys Ala Ser Phe
180          185          190
Ser Ile Lys Ile Lys Arg Asp Pro Arg His Leu Ala Ile Ser Asn Met
195          200          205
Pro Leu Val Lys Ser Val Thr Val Ala Glu Gly Leu Ile Glu Asp His
210          215          220
Phe Asp Ile Thr Val Lys Met Ser Thr Tyr Leu Val Ala Phe Ile Ile
225          230          235          240
Ser Asp Phe Lys Ser Val Ser Lys Met Thr Lys Ser Gly Val Lys Val
245          250          255
Ser Val Tyr Ala Val Pro Asp Lys Ile Asn Gln Ala Asp Tyr Ala Leu
260          265          270
Asp Ala Ala Val Thr Leu Leu Glu Phe Tyr Glu Asp Tyr Phe Ser Ile
275          280          285
Pro Tyr Pro Leu Pro Lys Gln Asp Leu Ala Ala Ile Pro Asp Phe Gln
290          295          300
Ser Gly Ala Met Glu Asn Trp Gly Leu Thr Thr Tyr Arg Glu Ser Ala
305          310          315          320
Leu Leu Tyr Asp Lys Glu Lys Ser Ser Ala Ser Ser Lys Leu Gly Ile
325          330          335
Thr Met Thr Val Ser His Glu Leu Ala His Gln Trp Phe Gly Asn Leu
340          345          350
Val Thr Met Glu Trp Trp Asn Asp Leu Trp Leu Asn Glu Gly Phe Ala
355          360          365
Lys Phe Met Glu Phe Val Ser Val Thr Val Thr His Pro Glu Leu Lys
370          375          380
Val Glu Glu Tyr Phe Phe Gly Lys Cys Phe Asn Ala Met Glu Val Asp
385          390          395          400
Ala Leu Asn Ser Ser His Pro Val Ser Thr Pro Val Glu Asn Pro Ala
405          410          415
Gln Ile Arg Glu Met Phe Asp Glu Val Ser Tyr Glu Lys Gly Ala Cys

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Ile	Leu	Asn	Met	Leu	Arg	Asp	Tyr	Leu	Ser	Ala	Asp	Thr	Phe	Lys	Arg
		435					440					445			
Gly	Ile	Val	Gln	Tyr	Arg	Gln	Lys	Tyr	Ser	Tyr	Lys	Asn	Thr	Lys	Asn
		450					455					460			
Glu	Asp	Leu	Trp	Asn	Ser	Met	Met	His	Ile	Cys	Pro	Thr	Asp	Gly	Thr
465						470				475					480
Gln	Thr	Met	Asp	Gly	Phe	Cys	Ser	Arg	Asn	Gln	His	Ser	Ser	Ser	Thr
				485					490						495
Ser	His	Trp	Arg	Gln	Glu	Val	Ile	Asp	Ile	Lys	Ser	Met	Met	Asn	Thr
				500				505						510	
Trp	Thr	Leu	Gln	Lys	Gly	Phe	Pro	Leu	Ile	Thr	Ile	Thr	Val	Arg	Gly
		515					520					525			
Arg	Asn	Val	His	Leu	Lys	Gln	Glu	His	Tyr	Met	Lys	Gly	Ser	Glu	Cys
		530				535					540				
Phe	Pro	Glu	Thr	Gly	Ser	Leu	Trp	His	Val	Pro	Leu	Thr	Phe	Ile	Thr
545					550					555					560
Ser	Lys	Ser	Asp	Ser	Val	Gln	Arg	Phe	Leu	Leu	Lys	Thr	Lys	Thr	Asp
				565					570						575
Val	Ile	Ile	Leu	Pro	Glu	Ala	Val	Glu	Trp	Ile	Lys	Phe	Asn	Val	Gly
				580				585						590	
Met	Asn	Gly	Tyr	Tyr	Ile	Val	His	Tyr	Gly	Asp	Asp	Gly	Trp	Ala	Ser
		595					600					605			
Leu	Asn	Gly	Leu	Leu	Lys	Glu	Ala	His	Thr	Thr	Ile	Ser	Ser	Asn	Asp
		610				615					620				
Arg	Ala	Ser	Leu	Ile	Asn	Asn	Ala	Phe	Gln	Leu	Val	Ser	Ile	Gly	Lys
625					630					635					640
Leu	Ser	Ile	Glu	Lys	Ala	Leu	Asp	Leu	Ile	Leu	Tyr	Leu	Lys	Asn	Glu
				645					650					655	
Thr	Glu	Ile	Met	Pro	Ile	Phe	Gln	Gly	Leu	Asn	Glu	Leu	Ile	Pro	Met
			660					665					670		
Tyr	Lys	Leu	Met	Glu	Lys	Arg	Asp	Met	Val	Glu	Val	Glu	Thr	Gln	Phe
		675					680					685			
Lys	Asp	Phe	Leu	Leu	Arg	Leu	Leu	Lys	Asp	Leu	Ile	Asn	Lys	Gln	Thr
		690				695					700				
Trp	Thr	Asp	Glu	Gly	Ser	Val	Ser	Glu	Arg	Met	Leu	Arg	Ser	Gln	Leu
705					710					715					720
Leu	Leu	Leu	Ala	Cys	Val	His	Arg	Tyr	Gln	Leu	Cys	Val	Gln	Arg	Ala
				725					730					735	
Glu	Arg	Tyr	Phe	Arg	Glu	Trp	Lys	Ala	Ser	Asn	Gly	Asn	Met	Ser	Leu
				740				745					750		
Pro	Ile	Asp	Val	Thr	Leu	Ala	Val	Phe	Ala	Val	Gly	Ala	Gln	Asn	Thr
		755					760				765				
Glu	Gly	Trp	Asp	P											

Lys Gly Phe Phe Ser Ser Leu Lys Lys Asn Gly Phe Gln Leu Arg Cys
 885 890 895
 Val Gln Gln Thr Ile Glu Thr Ile Glu Lys Asn Ile Arg Trp Met Asp
 900 905 910
 Lys Asn Phe Asp Lys Ile Arg Leu Trp Leu Gln Lys Lys Arg Gln Glu
 915 920 925
 Leu Leu
 930

<210> 645

<211> 179

<212> PRT

<213> Rat

<400> 645

Met Leu His Asn Val Ser Lys Gly Val Val Tyr Ser Ala Thr Val Val
 1 5 10 15
 Leu Gly Leu Leu Ala Tyr Val Ala Phe Lys Cys Trp Arg Ser Arg Lys
 20 25 30
 Gln Arg Gln Gln Leu Ala Lys Ala Arg Thr Val Glu Leu Gly Asp Pro
 35 40 45
 Asp Arg Asp Gln Arg His Gly Asp Ser Ser Ile Phe Val Asp Ser Pro
 50 55 60
 His Gly Leu Glu Pro Cys Ile Pro Ser Gln Gly Pro His Ala Asp Leu
 65 70 75 80
 Gly Cys Arg Leu Tyr Leu His Ile Pro Gln Gln Gln Gln Glu Glu Val
 85 90 95
 Gln Arg Leu Leu Ile Leu Gly Glu Pro Ala Lys Gly Trp Gln Gly Leu
 100 105 110
 Ala Gly Gln Leu Gly Tyr Gln Ala Glu Ala Val Glu Thr Met Ala Cys
 115 120 125
 Asp Gln Asp Pro Ala Tyr Ala Leu Leu Arg Asp Trp Ala Ala Gln Glu
 130 135 140
 Gly Ser Gly Ala Thr Leu Arg Val Leu Glu Asp Ala Leu Thr Ala Ile
 145 150 155 160
 Gly Arg Glu Asp Val Val Gln Val Leu Ser Ser Pro Ala Glu Gly Cys
 165 170 175
 Ser Val Val

<210> 646

<211> 298

<212> PRT

<213> Rat

<400> 646

Met Lys Tyr Leu Leu Asp Leu Ile Leu Leu Leu Pro Leu Leu Ile Val
 1 5 10 15
 Phe Cys Ile Glu Ser Phe Ile Lys Arg Leu Ile Pro Lys Lys Lys Lys
 20 25 30
 Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
 35 40 45
 Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Asn Thr Lys Leu Val
 50 55 60
 Leu Trp Asp Ile Asn Lys Asn Gly Ile Glu Glu Thr Ala Ala Lys Cys
 65 70 75 80
 Arg Lys Leu Gly Ala Gln Val His Pro Phe Val Val Asp Cys Ser Gln

```

      85      90      95
Arg Glu Glu Ile Tyr Ser Ala Val Arg Lys Val Lys Glu Glu Val Gly
      100      105      110
Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ala Asp
      115      120      125
Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn
      130      135      140
Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Met
      145      150      155      160
Lys Asn Asn His Gly His Val Val Thr Val Ala Ser Ala Ala Gly His
      165      170      175
Thr Val Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala
      180      185      190
Val Gly Phe His Arg Ala Leu Thr Asp Glu Leu Ala Ala Leu Gly Cys
      195      200      205
Thr Gly Val Arg Thr Ser Cys Leu Cys Pro Asn Phe Ile Asn Thr Gly
      210      215      220
Phe Ile Lys Asn Pro Ser Thr Asn Leu Gly Pro Thr Leu Glu Pro Glu
      225      230      235      240
Glu Val Val Glu His Leu Met His Gly Ile Leu Thr Asn Gln Lys Met
      245      250      255
Ile Phe Val Pro Gly Ser Ile Ala Leu Leu Thr Val Leu Glu Arg Val
      260      265      270
Phe Pro Glu Arg Phe Leu Asp Val Leu Lys His Arg Ile Asn Val Lys
      275      280      285
Phe Asp Ala Val Val Gly Tyr Lys Asp Lys
      290      295

```

<210> 647

<211> 59

<212> PRT

<213> Rat

<400> 647

```

Met Asn Ser Val Pro Thr Gln Leu Ile Leu Val Leu Thr Ser Leu Leu
  1      5      10      15
Leu Ile Leu Pro Gly Val Glu Ala Val Glu Ala Gly Asp Ala Ile Ala
  20      25      30
Leu Leu Leu Gly Val Val Leu Ser Val Thr Gly Ile Cys Ala Cys Leu
  35      40      45
Gly Ile Tyr Ala Arg Lys Arg Asn Gly Gln Ile
  50      55

```

<210> 648

<211> 281

<212> PRT

<213> Rat

<400> 648

```

Val Leu Ser Thr Ala Pro Pro Thr Met Arg Pro Ala Pro Gln Pro Gln
  1      5      10      15
Asp Cys Pro Ala Ser Ile Cys Leu Asn Gly Gly Ser Cys Arg Val Gly
  20      25      30
Ala Lys His His Leu Glu Cys Leu Cys Pro Glu Gly Phe Ile Gly Leu
  35      40      45
Tyr Cys Glu Ser Pro Val Glu Gln Arg Thr Lys Pro Ser Ser Ile Pro
  50      55      60

```

```

Asp Thr Pro Arg Pro Pro Arg Leu Leu Pro Leu Arg Ile Glu Pro Val
65          70          75          80
Ser Pro Thr Ser Leu Arg Val Glu Leu Gln Arg Tyr Leu Gln Gly Asn
      85          90          95
Thr Val Gln Leu Arg Ser Leu Arg Leu Thr Tyr Arg Asn Leu Ser Gly
      100         105         110
Pro Asp Lys Arg Leu Val Thr Leu Arg Leu Pro Ala Ser Leu Ala Glu
      115         120         125
Tyr Thr Val Thr Gln Leu Arg Pro Asn Ala Thr Tyr Ser Ile Cys Val
      130         135         140
Thr Ala Leu Gly Ala Gly Arg Thr Pro Glu Gly Glu Glu Ala Cys Gly
      145         150         155         160
Glu Ala Asn Thr Pro Gln Ala Val Arg Ser Asn His Ala Pro Val Thr
      165         170         175
Gln Ala Arg Glu Gly Asn Leu Pro Leu Leu Ile Ala Pro Ala Leu Ala
      180         185         190
Ala Val Leu Leu Ala Val Leu Ala Ala Ser Gly Ala Val Tyr Cys Val
      195         200         205
Arg Arg Ala Arg Ala Ser Ser Thr Ala Gln Asp Lys Gly Gln Val Gly
      210         215         220
Pro Gly Thr Gly Pro Leu Glu Leu Glu Gly Val Lys Val Pro Leu Glu
      225         230         235         240
Pro Gly Ser Lys Ala Ser Glu Gly Gly Gly Glu Ala Leu Ser Gly Gly
      245         250         255
Pro Glu Cys Glu Val Pro Leu Met Gly Tyr Pro Gly Pro Ser Leu Gln
      260         265         270
Gly Val Leu Pro Ala Gln Pro Tyr Ile
      275         280

```

<210> 649

<211> 88

<212> PRT

<213> Rat

<400> 649

```

Leu Gly Ser Val Ser Val Thr Thr Ile Glu Pro Cys Val Gln Val Gly
1          5          10          15
Ser Pro Ala Arg His Ser Leu His Pro Pro Leu Cys Ile Ser Ile Gly
      20          25          30
Ala Thr Val Pro Tyr Phe Ala Glu Gly Ser Gly Gly Pro Val Pro Thr
      35          40          45
Thr Ser Ala Leu Ile Leu Pro Pro Glu Tyr Ser Ser Trp Gly Tyr Pro
      50          55          60
Tyr Glu Ala Pro Pro Ser Tyr Glu Gln Ser Cys Gly Ala Gly Gly Thr
      65          70          75          80
Asp Val Gly Leu Ile Pro Gly Ser
      85

```

<210> 650

<211> 290

<212> PRT

<213> Rat

<400> 650

```

Glu Val Asp Pro Asp Leu Lys Cys Ala Leu Cys His Lys Val Leu Glu
1          5          10          15
Asp Pro Leu Thr Thr Pro Cys Gly His Val Phe Cys Ala Gly Cys Val

```

```

                20                25                30
Leu Pro Trp Val Val Gln Glu Gly Ser Cys Pro Ser Arg Cys Arg Gly
                35                40                45
Arg Leu Ser Ala Lys Glu Leu Asn His Val Leu Pro Leu Lys Arg Leu
                50                55                60
Ile Leu Lys Leu Asp Ile Lys Cys Ala His Ala Ala Arg Gly Cys Gly
65                70                75                80
Arg Val Val Lys Leu Gln Asp Leu Pro Glu His Leu Glu Arg Cys Asp
                85                90                95
Phe Ala Pro Ala Arg Cys Arg His Ala Gly Cys Gly Gln Leu Leu Leu
                100                105                110
Arg Arg Asp Val Glu Ala His Met Arg Asp Ala Cys Asp Ala Arg Pro
                115                120                125
Val Gly Arg Cys Gln Glu Gly Cys Gly Leu Pro Leu Thr His Gly Glu
                130                135                140
Gln Arg Ala Gly Gly His Cys Cys Ala Arg Ala Leu Arg Ala His Asn
145                150                155                160
Gly Ala Leu Gln Ala Arg Leu Gly Ala Leu His Lys Ala Leu Lys Lys
                165                170                175
Glu Ala Leu Arg Ala Gly Lys Arg Glu Lys Ser Leu Val Ala Gln Leu
                180                185                190
Ala Ala Ala Gln Leu Glu Leu Gln Met Thr Ala Leu Arg Tyr Gln Lys
                195                200                205
Lys Phe Thr Glu Tyr Ser Ala Arg Leu Asp Ser Leu Ser Arg Cys Val
                210                215                220
Ala Ala Pro Pro Gly Gly Lys Gly Glu Glu Thr Lys Ser Val Thr Leu
225                230                235                240
Val Leu His Arg Asp Ser Gly Ser Leu Gly Phe Asn Ile Ile Gly Gly
                245                250                255
Arg Pro Cys Val Asp Asn Gln Asp Gly Ser Ser Ser Glu Gly Ile Phe
                260                265                270
Val Ser Lys Ile Val Asp Ser Gly Pro Ala Ala Lys Lys Arg Pro Ala
                275                280                285
Asn Ser
                290

```

<210> 651
 <211> 202
 <212> PRT
 <213> Rat

```

<400> 651
Met Ala Arg Pro Arg Pro Arg Glu Tyr Lys Ala Gly Asp Leu Val Phe
 1                5                10                15
Ala Lys Met Lys Gly Tyr Pro His Trp Pro Ala Arg Ile Asp Glu Leu
                20                25                30
Pro Glu Gly Ala Val Lys Pro Pro Ala Asn Lys Tyr Pro Ile Phe Phe
                35                40                45
Phe Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro
                50                55                60
Tyr Lys Glu Tyr Lys Asp Lys Phe Gly Lys Ser Asn Lys Arg Lys Gly
65                70                75                80
Phe Asn Glu Gly Leu Trp Glu Ile Glu Asn Asn Pro Gly Val Lys Phe
                85                90                95
Thr Gly Tyr Gln Thr Ile Gln Gln Gln Ser Ser Ser Glu Thr Glu Gly
                100                105                110
Glu Gly Gly Asn Thr Ala Asp Ala Ser Ser Glu Glu Glu Gly Asp Arg

```

```

      115      120      125
Val Glu Asp Gly Lys Gly Lys Arg Lys Asn Glu Lys Gly Gly Ser Lys
      130      135      140
Arg Lys Lys Ser Tyr Thr Ser Lys Lys Ser Ser Lys Gln Ser Arg Lys
145      150      155      160
Ser Pro Gly Asp Glu Asp Asp Lys Asp Cys Lys Glu Glu Glu Asn Lys
      165      170      175
Ser Ser Ser Glu Gly Gly Asp Ala Gly Asn Asp Thr Arg Asn Thr Thr
      180      185      190
Ser Asp Leu Gln Lys Ala Gly Glu Gly Thr
      195      200

```

<210> 652
 <211> 79
 <212> PRT
 <213> Rat

```

<400> 652
Met Pro Val Ala Val Gly Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe
 1      5      10      15
Asp Arg Val Lys Met Gly Phe Val Met Gly Cys Ala Val Gly Met Ala
      20      25      30
Ala Gly Ala Leu Phe Gly Thr Phe Ser Cys Leu Arg Ile Gly Met Arg
      35      40      45
Gly Arg Glu Leu Met Gly Gly Ile Gly Lys Thr Met Met Gln Ser Gly
      50      55      60
Gly Thr Phe Gly Thr Phe Met Ala Ile Gly Met Gly Ile Arg Cys
      65      70      75

```

<210> 653
 <211> 555
 <212> PRT
 <213> Rat

```

<400> 653
Met Pro Val Asn Leu Gly Gln Ala Leu Gly Leu Leu Pro Phe Leu Ala
 1      5      10      15
Lys Ala Glu Asp Ala Thr Phe Ser Gly Ser Asp Val Ile Gln Gln Arg
      20      25      30
Glu Leu Ala Asn Pro Glu Thr Ala Arg Gln Leu Phe Arg Gln Phe Arg
      35      40      45
Tyr Gln Val Met Ser Gly Pro Gln Glu Thr Leu Arg Gln Leu Arg Lys
      50      55      60
Leu Cys Phe Gln Trp Leu Arg Pro Glu Val His Thr Lys Glu Gln Ile
      65      70      75      80
Leu Glu Ile Leu Met Leu Glu Gln Phe Leu Thr Ile Leu Pro Gly Glu
      85      90      95
Ile Gln Met Trp Val Arg Lys Gln Cys Pro Gly Ser Gly Glu Glu Ala
      100      105      110
Val Thr Leu Val Glu Ser Leu Lys Gly Asp Pro Gln Lys Leu Trp Gln
      115      120      125
Trp Ile Ser Ile Gln Val Leu Gly Gln Glu Ile Pro Phe Glu Lys Glu
      130      135      140
Asn Ser Ala Arg Cys Arg Gly Asp Lys Val Glu Pro Ala Leu Glu Ala
      145      150      155      160
Glu Pro Thr Val Glu Val Val Pro Gln Asp Leu Pro Leu Gln Asn Thr
      165      170      175

```

Ser Ser Ala Pro Gly Glu Leu Leu Ser His Gly Val Lys Glu Glu Ser
 180 185 190
 Asp Met Glu Pro Glu Leu Ala Leu Ala Ala Ser Gln Leu Pro Ala Arg
 195 200 205
 Ser Glu Glu Arg Pro Thr Arg Asp Gln Glu Val Gly Thr Ala Leu Leu
 210 215 220
 Pro Ser Leu Gln Glu Glu Gln Trp Arg His Leu Asp Ser Thr Gln Lys
 225 230 235 240
 Glu Gln Tyr Trp Asp Leu Met Leu Glu Thr Tyr Gly Lys Met Val Ser
 245 250 255
 Gly Ala Gly Ile Ser Asn Ser Lys Pro Asp Leu Thr Asn Met Ala Glu
 260 265 270
 Tyr Gly Glu Glu Leu Val Gly Leu His Leu His Ser Ala Glu Lys Met
 275 280 285
 Ala Arg Ala Pro Cys Lys Glu Asp Arg Gln Glu Asn Asp Lys Glu Asn
 290 295 300
 Leu Asn Leu Glu Asn His Arg Asp Gln Gly Cys Leu Asp Val Phe Asp
 305 310 315 320
 Gln Ala Pro Gly Glu Ala Pro Pro Gln Thr Ala Leu Ser Asp Phe Phe
 325 330 335
 Gly Glu Ser Glu Pro His His Phe Gly Glu Ser Val Pro Glu Ala
 340 345 350
 Leu Glu Asn Leu Gln Gly Glu Gly Thr Gly Ala His Leu Phe Pro His
 355 360 365
 Glu Arg Gly Ser Gly Lys Gln Leu Gly Gln His Ile Gln Ser Ser Ser
 370 375 380
 Ser Gly Glu Leu Ser Ala Leu Trp Leu Glu Glu Lys Arg Glu Ala Ser
 385 390 395 400
 Gln Lys Gly Gln Ala Arg Ala Pro Met Ala Gln Lys Leu Pro Thr Cys
 405 410 415
 Arg Glu Cys Gly Lys Thr Phe Tyr Arg Asn Ser Gln Leu Val Phe His
 420 425 430
 Gln Arg Thr His Thr Gly Glu Thr Tyr Phe His Cys Arg Ile Cys Lys
 435 440 445
 Lys Ala Phe Leu Arg Ser Ser Asp Phe Val Lys His Gln Arg Thr His
 450 455 460
 Thr Gly Glu Lys Pro Cys Lys Cys Asp Tyr Cys Gly Lys Gly Phe Ser
 465 470 475 480
 Asp Phe Ser Gly Leu Arg His His Glu Lys Ile His Thr Gly Glu Lys
 485 490 495
 Pro Tyr Lys Cys Pro Ile Cys Glu Lys Ser Phe Ile Gln Arg Ser Asn
 500 505 510
 Phe Asn Arg His Gln Arg Val His Thr Gly Glu Lys Pro Tyr Lys Cys
 515 520 525
 Thr His Cys Gly Lys Arg Phe Ser Trp Ser Ser Leu Asp Lys His
 530 535 540
 Gln Arg Ser His Leu Gly Lys Lys Pro Cys Pro
 545 550 555

<210> 654

<211> 244

<212> PRT

<213> Rat

<400> 654

Leu Ala Tyr Tyr Asn Pro Phe Tyr Phe Leu Ser Ala Ala Ala Pro Gly
 1 5 10 15


```

Pro Gly Ala Ala Thr Ser Ala Gly Ala Thr Pro Thr Ala Val Ala Gly
      20      25      30
Leu Thr Ala Arg Ala Pro His Val Gln Ala Ser Ala Arg Ala Val Pro
      35      40      45
Val Thr Arg Val Gly Ser Ala Ala Pro Ala Arg Thr Ala Ser Asp Thr
      50      55      60
Gly Arg Gln Ala Gly Arg Glu Tyr Val Ile Pro Ser Leu Ala His Arg
      65      70      75      80
Phe Met Ala Glu Met Val Asp Phe Phe Ile Leu Phe Phe Ile Lys Ala
      85      90      95
Thr Ile Val Leu Ser Ile Met His Leu Ser Gly Ile Lys Asp Ile Ser
      100      105      110
Lys Phe Ala Met His Tyr Ile Ile Glu Glu Ile Asp Glu Asp Thr Ser
      115      120      125
Met Glu Asp Leu Gln Lys Met Met Ile Val Ala Leu Ile Tyr Arg Leu
      130      135      140
Leu Val Cys Phe Tyr Glu Ile Ile Cys Ile Trp Gly Ala Gly Gly Ala
      145      150      155      160
Thr Pro Gly Lys Phe Leu Leu Gly Leu Arg Val Val Thr Cys Asp Thr
      165      170      175
Ser Val Leu Ile Ala Pro Ser Arg Val Leu Val Ile Pro Ser Ser Asn
      180      185      190
Val Ser Ile Thr Thr Ser Thr Ile Arg Ala Leu Ile Lys Asn Phe Ser
      195      200      205
Ile Ala Ser Phe Phe Pro Ala Phe Ile Thr Leu Leu Phe Phe Gln His
      210      215      220
Asn Arg Thr Ala Tyr Asp Ile Val Ala Gly Thr Ile Val Val Lys Arg
      225      230      235      240
Asn Gly Val Arg

```

<210> 655
 <211> 265
 <212> PRT
 <213> Rat

```

<400> 655
Met Gly Leu Leu Phe Leu Val Leu Leu Ser Pro Leu Ser Cys Val Leu
  1      5      10
Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Gly Leu His Gly
      20      25      30
Arg Thr Leu Gly Asn Gly Tyr Gly Glu Gly Leu Phe Asn Gly Val Lys
      35      40      45
Leu Val Val Glu Thr Thr Glu Glu Ser Leu Phe Ser His Gln Gly Ala
      50      55      60
Ser Val Thr Leu Pro Cys His Tyr His Tyr Glu Pro Ala Leu Ala Ser
      65      70      75      80
Pro Arg His Val Arg Ile Lys Trp Trp Lys Leu Ser Glu Asn Gly Thr
      85      90      95
Pro Glu Gln Asp Val Leu Val Ala Ile Gly Gln Arg His Arg Ser Phe
      100      105      110
Gly Asp Tyr Gln Gly Arg Val Gln Leu Arg Gln Asp Lys Glu Gln Glu
      115      120      125
Val Ser Leu Glu Leu Arg Asp Leu Arg Leu Glu Asp Ser Gly Arg Tyr
      130      135      140
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu
      145      150      155      160

```

```

Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Pro Arg Glu Gly Arg
      165      170      175
Tyr Gln Leu Asn Phe His Glu Ala Gln Gln Val Cys Gln Glu Gln Asp
      180      185      190
Ala Val Val Ala Thr Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly
      195      200      205
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Ser Ser Cys Arg
      210      215      220
Phe Gly Thr Ser Ser Cys Arg Ile Arg His Glu Ala Cys Arg Arg Pro
      225      230      235      240
Leu Trp Cys Gly Asp Pro Arg Val Asn Pro Pro Thr Pro Cys Leu Thr
      245      250      255
Arg Arg Gln Asn Leu Gln Leu Arg Thr
      260      265

```

<210> 656

<211> 343

<212> PRT

<213> Rat

<400> 656

```

Met Ala Val Cys Pro Tyr Gly Ala Ala Ala Val Val Met Ala Leu Leu
  1      5      10      15
Ser Ala Ala Ile Ala Phe His Trp Ser Pro Leu Leu Ala Val Leu Gln
      20      25      30
Arg Ala Leu Ser Leu His Thr Ala His Ala Thr Lys Asp Met Asp Asn
      35      40      45
Leu Phe Gln Leu Val Arg Asn Ile Val Pro Ala Leu Thr Ser Lys Lys
      50      55      60
His Lys Gly Gln Asp Gly Arg Ile Gly Ile Val Gly Gly Cys Gln Glu
      65      70      75      80
Tyr Thr Gly Ala Pro Tyr Phe Ala Gly Ile Ser Ala Leu Lys Val Gly
      85      90      95
Ala Asp Leu Thr His Val Phe Cys Ala Arg Glu Ala Ala Pro Val Ile
      100      105      110
Lys Ser Tyr Ser Pro Glu Leu Ile Val His Pro Val Leu Asp Ser Ser
      115      120      125
Asp Ala Val Glu Glu Val Lys Lys Trp Leu Pro Arg Leu His Ala Leu
      130      135      140
Val Val Gly Pro Gly Leu Gly Arg Asp Asp Leu Leu Leu Asn Asn Val
      145      150      155      160
Arg Gly Ile Leu Glu Ser Thr Lys Ala Arg Asp Ile Pro Val Val Ile
      165      170      175
Asp Ala Asp Gly Leu Trp Leu Ile Ala Gln Arg Pro Ala Leu Val His
      180      185      190
Gly Tyr Gln Lys Ala Val Leu Thr Pro Asn His Val Glu Phe Ser Arg
      195      200      205
Leu Trp Asp Ala Val Leu Ser Ser Pro Met Asp Thr Ser Asn His Ser
      210      215      220
Gly Ser Val Leu Lys Leu Ser Gln Ala Leu Gly Asn Ile Thr Ile Val
      225      230      235      240
Gln Lys Gly Glu Gln Asp Leu Ile Ser Asn Gly Gln Gln Val Leu Val
      245      250      255
Cys Asn Gln Glu Gly Ser Ser Arg Arg Cys Gly Gly Gln Gly Asp Leu
      260      265      270
Leu Ser Gly Ser Leu Gly Val Met Ala His Trp Ala Leu Arg Ala Gly
      275      280      285

```

Pro Glu Lys Thr Asn Gly Ser Ser Pro Leu Leu Val Ala Ala Trp Gly
 290 295 300
 Ala Cys Thr Leu Thr Arg Glu Cys Asn His Leu Ala Phe Gln Lys Tyr
 305 310 315 320
 Gly Arg Ser Thr Thr Thr Asp Met Ile Ala Glu Val Gly Ala Ala
 325 330 335
 Phe Ser Lys Leu Phe Thr Thr
 340

<210> 657

<211> 61

<212> PRT

<213> Rat

<400> 657

Met Pro Cys Trp Ser Leu Tyr Gln Leu Met Val Leu Tyr Gln Ile Ile
 1 5 10 15
 Ile Leu Phe Phe Leu Phe Lys Gln Val Ser Val Arg Thr Cys Tyr Leu
 20 25 30
 Ser Thr Glu Gly Lys Pro Cys Gly Ser Val Leu Phe Ala Cys Lys Ser
 35 40 45
 Leu Gln Gln Cys Leu Leu Thr Val Leu Val Thr Pro Val
 50 55 60

<210> 658

<211> 1172

<212> PRT

<213> Rat

<400> 658

Met Leu Trp Ala Leu Ala Leu Leu Ala Leu Gly Ile Gly Pro Arg Ala
 1 5 10 15
 Tyr Ala Gly Asp His Gly Glu Asp Thr Ala Phe Asp Leu Phe Ser Ile
 20 25 30
 Ser Asn Ile Asn Arg Lys Thr Ile Gly Ala Lys Gln Phe Arg Gly Pro
 35 40 45
 Asp Pro Gly Val Pro Ala Tyr Arg Phe Val Arg Phe Asp Tyr Val Pro
 50 55 60
 Pro Val Asn Thr Asp Asp Leu Asn Arg Ile Val Lys Leu Ala Arg Arg
 65 70 75 80
 Lys Glu Gly Phe Phe Leu Thr Ala Gln Leu Lys Gln Asp Arg Lys Ser
 85 90 95
 Arg Gly Thr Leu Leu Val Leu Glu Gly Pro Gly Thr Ser Gln Arg Gln
 100 105 110
 Phe Glu Ile Val Ser Asn Gly Pro Gly Asp Thr Leu Asp Leu Asn Tyr
 115 120 125
 Trp Val Glu Gly His Gln His Thr Asn Phe Leu Glu Asp-Val Gly Leu
 130 135 140
 Ala Asp Ser Gln Trp Lys Asn Val Thr Val Gln Val Ala Ser Asp Thr
 145 150 155 160
 Tyr Ser Leu Tyr Val Gly Cys Asp Leu Ile Asp Ser Val Thr Leu Glu
 165 170 175
 Glu Pro Phe Tyr Glu Gln Leu Glu Ala Asp Lys Ser Arg Met Tyr Val
 180 185 190
 Ala Lys Gly Ala Ser Arg Glu Ser His Phe Arg Gly Leu Leu Gln Asn
 195 200 205
 Val His Leu Val Phe Ala Asp Ser Val Glu Asp Ile Leu Ser Lys Lys

210		215		220
Gly Cys Gln His Ser	Gln Gly Ala Glu Val	Asn Thr Ile Ser Glu His		
225	230	235	240	
Thr Glu Thr Leu His	Leu Ser Pro His Ile	Thr Thr Asp Leu Val Val		
	245	250	255	
Gln Gly Val Glu Lys	Ala Gln Glu Val Cys	Thr His Ser Cys Glu Glu		
	260	265	270	
Leu Ser Asn Met Met	Asn Glu Leu Ser Gly	Leu His Val Met Val Asn		
	275	280	285	
Gln Leu Ser Lys Asn	Leu Glu Arg Val Ser	Ser Asp Asn Gln Phe Leu		
	290	295	300	
Leu Glu Leu Ile Gly	Gly Pro Leu Lys Thr	Arg Asn Met Ser Ala Cys		
305	310	315	320	
Val Gln Glu Gly Arg	Ile Phe Ala Glu Asn	Glu Thr Trp Val Val Asp		
	325	330	335	
Ser Cys Thr Thr Cys	Thr Cys Lys Lys Phe	Lys Thr Val Cys Asn Gln		
	340	345	350	
Ile Thr Cys Ser Pro	Ala Thr Cys Ala Asn	Pro Ser Leu Val Glu Gly		
	355	360	365	
Glu Cys Cys Pro Ser	Cys Ser His Ser Ala	Asp Asn Asp Glu Gly Trp		
	370	375	380	
Ser Pro Trp Ala Glu	Trp Thr Glu Cys Ser	Val Thr Cys Gly Ser Gly		
385	390	395	400	
Thr Gln Gln Arg Gly	Arg Ser Cys Asp Val	Thr Ser Asn Thr Cys Leu		
	405	410	415	
Gly Pro Ser Ile Gln	Thr Arg Thr Cys Ser	Leu Gly Lys Cys Asp Thr		
	420	425	430	
Arg Ile Arg Gln Asn	Gly Gly Trp Ser His	Trp Ser Pro Trp Ser Ser		
	435	440	445	
Cys Ser Val Thr Cys	Gly Val Gly Asn Val	Thr Arg Ile Arg Leu Cys		
	450	455	460	
Asn Ser Pro Val Pro	Gln Met Gly Gly Lys	Asn Cys Lys Gly Ser Gly		
	465	470	475	
Arg Glu Thr Lys Ala	Cys Gln Arg Ala Pro	Cys Pro Ile Asp Gly Arg		
	485	490	495	
Trp Ser Pro Trp Ser	Pro Trp Ser Ala Cys	Thr Val Thr Cys Ala Gly		
	500	505	510	
Gly Ile Arg Glu Arg	Thr Arg Val Cys Asn	Ser Pro Glu Pro Gln Tyr		
	515	520	525	
Gly Gly Lys Asp Cys	Val Gly Asp Val Thr	Glu His Gln Met Cys Asn		
	530	535	540	
Lys Arg Ser Cys Pro	Ile Asp Gly Cys Leu	Ser Asn Pro Cys Phe Pro		
	545	550	555	
Gly Ala Lys Cys Asn	Ser Phe Pro Asp Gly	Ser Trp Ser Cys Gly Ser		
	565	570	575	
Cys Pro Val Gly Phe	Leu Gly Asn Gly Thr	His Cys Glu Asp Leu Asp		
	580	585	590	
Glu Cys Ala Val Val	Ala Asp Ile Cys Phe	Ser Ile Asn Lys Ala Ser		
	595	600	605	
Arg Cys Val Asn Thr	Asn Pro Gly Phe His	Cys Leu Pro Cys Pro Pro		
	610	615	620	
Arg Tyr Lys Gly Thr	Gln Pro Phe Gly Ile	Gly Leu Glu Asp Ala Lys		
	625	630	635	
Thr Glu Lys Gln Val	Cys Glu Pro Glu Asn	Pro Cys Lys Asp Lys Thr		
	645	650	655	
His Asn Cys His Lys	His Ala Glu Cys Ile	Tyr Leu Gly His Phe Ser		
	660	665	670	

Asp Pro Met Tyr Lys Cys Glu Cys Gln Thr Gly Tyr Ala Gly Asp Gly
 675 680 685
 Leu Ile Cys Gly Glu Asp Ser Asp Leu Asp Gly Trp Pro Asn Ser Asn
 690 695 700
 Leu Val Cys Ala Thr Asn Ala Thr Tyr His Cys Val Lys Asp Asn Cys
 705 710 715 720
 Pro Lys Leu Pro Asn Ser Gly Gln Glu Asp Phe Asp Lys Asp Gly Ile
 725 730 735
 Gly Asp Ala Cys Asp Glu Asp Asp Asp Gly Val Ser Asp Glu
 740 745 750
 Lys Asp Asn Cys Pro Leu Leu Phe Asn Pro Arg Gln Leu Asp Tyr Asp
 755 760 765
 Lys Asp Glu Val Gly Asp Arg Cys Asp Asn Cys Pro Tyr Val His Asn
 770 775 780
 Gln Ala Gln Ile Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ser
 785 790 795 800
 Val Asp Ile Asp Gly Asp Asp Val Phe Asn Glu Arg Asp Asn Cys Pro
 805 810 815
 Tyr Val Tyr Asn Thr Asp Gln Arg Asp Thr Asp Gly Asp Gly Val Gly
 820 825 830
 Asp His Cys Asp Asn Cys Pro Leu Met His Asn Pro Asp Gln Met Asp
 835 840 845
 Gln Asp Asn Asp Leu Val Gly Asp Gln Cys Asp Asn Asn Glu Asp Ile
 850 855 860
 Asp Asp Asp Gly His Gln Asn Asn Gln Asp Asn Cys Pro Tyr Ile Ser
 865 870 875 880
 Asn Ser Asn Gln Ala Asp His Asp Asn Asp Gly Lys Gly Asp Ala Cys
 885 890 895
 Asp Ser Asp Asp Asp Asn Asp Gly Val Pro Asp Asp Arg Asp Asn Cys
 900 905 910
 Arg Leu Val Phe Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg
 915 920 925
 Gly Asp Ile Cys Lys Asp Asp Phe Asp Asn Asp Asn Val Pro Asp Ile
 930 935 940
 Asp Asp Val Cys Pro Glu Asn Asn Ala Ile Thr Glu Thr Asp Phe Arg
 945 950 955 960
 Asn Phe Gln Met Val Pro Leu Asp Pro Lys Gly Thr Thr Gln Ile Asp
 965 970 975
 Pro Asn Trp Val Ile Arg His Gln Gly Lys Glu Leu Val Gln Thr Ala
 980 985 990
 Asn Ser Asp Pro Gly Ile Ala Val Gly Phe Asp Glu Phe Gly Ser Val
 995 1000 1005
 Asp Phe Ser Gly Thr Phe Tyr Val Asn Thr Asp Arg Asp Asp Asp Tyr
 1010 1015 1020
 Ala Gly Phe Val Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val
 1025 1030 1035 1040
 Met Trp Lys Gln Val Thr Gln Thr Tyr Trp Glu Asp Lys Pro Ser Arg
 1045 1050 1055
 Ala Tyr Gly Tyr Ser Gly Val Ser Leu Lys Val Val Asn Ser Thr Thr
 1060 1065 1070
 Gly Thr Gly Glu His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr
 1075 1080 1085
 Glu Gly Gln Val Arg Thr Leu Trp His Asp Pro Lys Asn Ile Gly Trp
 1090 1095 1100
 Lys Asp Tyr Thr Ala Tyr Arg Trp His Leu Ile His Arg Pro Lys Thr
 1105 1110 1115 1120
 Gly Tyr Met Arg Val Leu Val His Glu Gly Lys Gln Val Met Ala Asp

```

                1125      1130      1135
Ser Gly Pro Ile Tyr Asp Gln Thr Tyr Ala Gly Gly Arg Leu Gly Leu
                1140      1145      1150
Phe Val Phe Ser Gln Glu Met Val Tyr Phe Ser Asp Leu Lys Tyr Glu
                1155      1160      1165
Cys Arg Asp Ala
                1170

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<210> 659

<211> 442

<212> PRT

<213> Rat

<400> 659

```

Met Glu Leu Leu Ser Arg Val Leu Leu Trp Lys Leu Val Leu Leu Gln
 1      5      10      15
Ser Ser Ala Val Leu Ser Ser Gly Ser Pro Gly Thr Ala Ala Ser
 20      25      30
Ser Ser Val Val Ser Glu Ser Ala Val Ser Trp Ala Ala Gly Thr Gln
 35      40      45
Ala Val Leu Arg Cys Gln Ser Pro Arg Met Val Trp Thr Gln Asp Arg
 50      55      60
Leu His Asp Arg Gln Arg Val Val His Trp Asp Leu Ser Gly Gly Pro
 65      70      75      80
Gly Ser Gln Gly Arg Arg Leu Val Asp Met Tyr Ser Ala Gly Glu Gln
 85      90      95
Arg Val Tyr Gln Pro Arg Asp Arg Asp Arg Leu Leu Leu Ser Pro Ser
 100     105     110
Ala Phe His Asp Gly Asn Phe Ser Leu Leu Ile Arg Ala Val Glu Arg
 115     120     125
Gly Asp Glu Gly Val Tyr Thr Cys Asn Leu His His His Tyr Cys His
 130     135     140
Leu Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Asp Pro Leu
 145     150     155     160
Leu Ser Arg Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Val Val Ala
 165     170     175
Leu Gly Ala Pro Ala Leu Met Thr Cys Val Asn Arg Glu His Leu Trp
 180     185     190
Thr Asp Arg His Leu Glu Glu Ala Gln Gln Val Val His Trp Asp Arg
 195     200     205
Gln Leu Pro Gly Val Pro His Asp Arg Ala Asp Arg Leu Leu Asp Leu
 210     215     220
Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro Pro Phe Leu Arg Asp
 225     230     235     240
Arg Val Ser Val Asn Thr Asn Ala Phe Ala Arg Gly Asp Phe Ser Leu
 245     250     255
Arg Ile Asp Asp Leu Glu Pro Ala Asp Glu Gly Ile Tyr Ser Cys His
 260     265     270
Leu His His His Tyr Cys Gly Leu His Glu Arg Arg Val Phe His Leu
 275     280     285
Arg Val Thr Glu Pro Val Phe Glu Pro Pro Ala Arg Ala Ser Pro Gly
 290     295     300
Asn Gly Ser Gly His Asn Ser Val Pro Ser Pro Asp Pro Thr Met Ala
 305     310     315     320
Arg Gly His Ser Ile Ile Asn Val Ile Val Pro Glu Asp His Thr His
 325     330     335
Phe Phe Gln Gln Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile

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          340          345          350
Leu Leu Leu Ile Thr Val Val Leu Ala Thr Arg His Arg His Ser Gly
          355          360          365
Gly Cys Lys Thr Ser Asp Arg Lys Ala Gly Lys Ser Lys Gly Lys Asp
          370          375          380
Val Asn Met Met Glu Phe Ala Ile Ala Thr Arg Asp Gln Ala Pro Tyr
385          390          395          400
Arg Thr Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu
          405          410          415
Arg Ala Gly Leu Ala His Ser Pro Leu Pro Ala Lys Asp Val Asp Leu
          420          425          430
Asp Lys Glu Phe Arg Lys Glu Tyr Cys Lys
          435          440

```

<210> 660

<211> 218

<212> PRT

<213> Rat

<400> 660

```

Gln Leu Ser Pro Leu Asp Phe Pro His Leu Pro His Gln Ser Glu Leu
1          5          10          15
Ser Ser Thr Ala Arg Ala Arg Pro Pro Asn Ala Ala Ile Asp Arg Arg
          20          25          30
Gln Gly Gln Leu Leu Phe Ser Cys Pro Trp Ser Cys Ile Thr Ser Thr
          35          40          45
His Thr Phe Ile Ala Ser Ser Thr Val Leu Pro Gly Lys Val Gln Ala
          50          55          60
Pro Phe Ser Arg Val Leu Gln Leu Val Arg Gly Arg Ala Ser Ser Pro
65          70          75          80
Lys Leu Met Thr Leu Trp Gly Ala Phe Pro Pro Ala Arg Gly Asp Glu
          85          90          95
Val Leu Gly Arg Gly Trp Asn Ile Thr Ser Val Pro Leu Pro Ser His
          100          105          110
Ser Arg Gln Val Ala Gly Ser Ala Ser His Thr His Thr Leu Gly Ala
          115          120          125
Ala Ser Pro Thr Pro Leu Ser Pro Gly Pro Ala Pro Leu Cys Ser Thr
          130          135          140
Met Leu Pro Gly Gln Gly Thr Gly Pro Thr Leu Pro Ser Ala Gly Thr
145          150          155          160
Val Pro Ala Leu Pro Ser Ala Ala Thr Gly Glu Gly Trp Gly Gln Val
          165          170          175
Ser Arg Gly Pro His Pro Val Arg Asp Gly Val Val His Ile Pro Trp
          180          185          190
Thr Cys Thr Trp Cys Leu Met Ala Ala Pro Thr Arg Asn Thr Pro Met
          195          200          205
Ser Ser Ile Gly Asn Met Ser His Gly His
          210          215

```

<210> 661

<211> 108

<212> PRT

<213> Rat

<400> 661

```

Met Ser Leu Ile Gln Ala Ile Val Tyr Lys Val His Ser Phe Ser Cys
1          5          10          15

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Asp Leu Glu Tyr Ile Tyr Asn Leu Asp Gly Ile Gln Val Arg Asn Lys
    20                25                30
Ala Ile Gly Cys Pro Gln Arg His Gln Leu Pro Ala Leu Gln Glu Ala
    35                40                45
Thr Ala Phe Ala Gly Val His Arg Pro Leu Gln Ile His Pro Leu Gly
    50                55                60
Arg Gly Leu Arg Pro Trp Glu Gln Gln Gln Gln Arg His Cys Gly His
    65                70                75                80
Ile Trp Pro Gly Trp Glu Pro Leu Arg Ser Asp Ser Leu Ala Leu Gly
    85                90                95
Thr Ala Ser Cys Glu Thr Asn Arg Asn Ser Pro Leu
    100                105

```

<210> 662

<211> 516

<212> PRT

<213> Rat

<400> 662

```

Asn Gln Gly Arg Arg Gly Arg Ser Ser Lys Pro Ser Ile Lys Thr Pro
  1          5          10          15
Glu Pro Ile Val Pro Thr Gly Pro Glu Leu Gln Pro Leu Thr Ser Ala
    20                25                30
Glu Gln Pro Val Thr Pro Asn Leu Thr Ser Arg Ala Ser Arg Gly Arg
    35                40                45
Ser Asn Lys Ser Ile Arg Thr Pro Glu Pro Val Val Gln Thr Gly Pro
    50                55                60
Glu Phe His Pro Ser Thr Ser Ser Glu Gln Ser Asp Thr Pro Glu Pro
    65                70                75                80
Ser Ser Gln Gly Arg Thr Arg Arg Ser Val Arg Thr Pro Glu Ala Ser
    85                90                95
Val Ser Thr Thr Pro Ala Leu Gln Pro Ser Thr Ser Lys Lys Gln Pro
    100                105                110
Thr Pro Lys Pro Thr Ala Leu Val Thr Arg Gly Arg Thr His Lys Pro
    115                120                125
Ser Thr Glu Gly Leu Glu Ser Val Gly Pro Val Ala Pro Asp Phe Glu
    130                135                140
Pro Pro Thr Ser Thr Asp His Leu Ala Thr Ser Lys Val Thr Gly Gln
    145                150                155                160
Ser Leu Thr Leu Gln Ser Ser Pro Val Ser Ala Ser Pro Val Ser Thr
    165                170                175
Thr Pro Glu Leu Lys Pro Pro Val Pro Ile Ala Gln Pro Leu Thr Leu
    180                185                190
Glu Pro Val Pro Gln Thr Ser His Gln Arg Arg Arg Arg Ala Thr Gly
    195                200                205
Lys Gln Gly Ser Arg Thr Ala Pro Val Gly Pro Lys Ser Tyr Ser Thr
    210                215                220
Pro Ala Glu Pro Glu Pro Gln Ser Ser Ala Ser Gln Ser Ser Gly Ala
    225                230                235                240
Ser Glu Ala Asp Ser Pro His Gln Lys Arg Pro Arg Arg Gln Val Thr
    245                250                255
Gln Lys Thr Val Val Val Lys Glu Glu Asp Pro Gly Glu Ile Gln Val
    260                265                270
Lys Glu Glu Pro Gln Glu Thr Ala Ile Ser Thr Pro Gly Lys Arg Lys
    275                280                285
Arg Asp Pro Ala Glu Gly Glu Thr Gln Gly Asn Pro Thr Arg Ser Arg
    290                295                300

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Arg Thr Lys Pro Asn Gln Glu Ala Ala Ala Pro Lys Val Leu Phe Thr
 305 310 315 320
 Gly Val Val Asp Ser Arg Gly Glu Arg Ala Val Leu Ala Leu Gly Gly
 325 330 335
 Ser Leu Ala Ser Ser Val Asn Glu Ala Ser His Leu Val Thr Asp Arg
 340 345 350
 Ile Arg Arg Thr Val Lys Phe Leu Cys Ala Val Gly Lys Gly Ile Pro
 355 360 365
 Ile Leu Ser Leu Asn Trp Leu Tyr Gln Ser Arg Lys Ala Gly Cys Phe
 370 375 380
 Leu Pro Pro Asp Asp Tyr Leu Val Thr Asp Pro Glu Gln Glu Lys Asn
 385 390 395 400
 Phe Ser Phe Ser Leu Arg Asp Ser Leu Ser Arg Ala Arg Glu Arg Arg
 405 410 415
 Leu Leu Glu Asp Tyr Glu Ile His Val Thr Pro Gly Val Gln Pro Pro
 420 425 430
 Pro Pro Gln Met Gly Glu Ile Ile Ser Cys Cys Gly Gly Thr Val Leu
 435 440 445
 Pro Ser Met Pro His Ser Tyr Lys Leu His Arg Val Val Ile Thr Cys
 450 455 460
 Thr Glu Asp Leu Pro Arg Cys Ala Ile Ala Ser Arg Leu Gly Leu Pro
 465 470 475 480
 Leu Leu Ser Pro Glu Phe Leu Leu Thr Gly Val Leu Lys Gln Glu Ala
 485 490 495
 Thr Pro Glu Ala Trp Ser Ser Pro Ile Trp Lys Cys Ser Leu Pro Lys
 500 505 510
 Lys Lys Lys Lys
 515

<210> 663

<211> 747

<212> PRT

<213> Rat

<400> 663

Glu Ala Thr Val Ile Thr Thr Glu Lys Arg Glu Arg Pro Ala Pro Pro
 1 5 10 15
 Arg Glu Leu Leu Val Pro Gln Ala Glu Val Thr Ala Arg Ser Leu Arg
 20 25 30
 Leu Gln Trp Val Pro Gly Ser Asp Gly Ala Ser Pro Ile Arg Tyr Phe
 35 40 45
 Thr Val Gln Val Arg Glu Leu Pro Gly Gly Glu Trp Gln Thr Tyr Ser
 50 55 60
 Ser Ser Ile Ser His Glu Ala Thr Leu Cys Ala Val Glu Arg Leu Arg
 65 70 75 80
 Pro Phe Thr Ser Tyr Lys Leu Arg Leu Lys Ala Thr Asn Asp Ile Gly
 85 90 95
 Asp Ser Asp Phe Ser Ala Glu Thr Glu Ala Val Thr Thr Leu Gln Asp
 100 105 110
 Val Pro Gly Glu Pro Pro Gly Ser Val Ser Ala Thr Pro His Thr Thr
 115 120 125
 Ser Ser Val Leu Ile Gln Trp Gln Pro Pro Arg Asp Glu Ser Leu Asn
 130 135 140
 Gly Leu Leu Gln Gly Tyr Arg Ile Tyr Tyr Arg Glu Leu Glu Ser Glu
 145 150 155 160
 Thr Gly Leu Ser Pro Glu Pro Lys Thr Leu Lys Ser Pro Ser Ala Leu
 165 170 175

Arg Ala Glu Leu Thr Ala Gln Ser Ser Phe Lys Thr Val Asn Ser Ser
 180 185 190
 Ser Thr Leu Thr Thr Tyr Glu Leu Thr His Leu Lys Lys Tyr Arg Arg
 195 200 205
 Tyr Glu Val Ile Met Thr Ala Tyr Asn Ile Ile Gly Glu Ser Pro Ala
 210 215 220
 Ser Val Pro Val Glu Val Phe Val Gly Glu Ala Ala Pro Ala Met Ala
 225 230 235 240
 Pro Gln Asn Ile Gln Val Thr Pro Leu Thr Ala Ser Gln Leu Glu Val
 245 250 255
 Thr Trp Asp Pro Pro Pro Pro Glu Ser Gln Asn Gly Asn Ile Gln Gly
 260 265 270
 Tyr Lys Val Tyr Tyr Trp Glu Ala Asp Ser Arg Asn Glu Thr Glu Lys
 275 280 285
 Met Lys Val Leu Phe Leu Pro Glu Pro Val Val Lys Ile Lys Asp Leu
 290 295 300
 Thr Ser His Thr Lys Tyr Leu Val Ser Ile Ser Ala Phe Asn Ala Ala
 305 310 315 320
 Gly Asp Gly Pro Arg Ser Asp Pro Cys Gln Gly Arg Thr His Gln Ala
 325 330 335
 Ala Pro Gly Pro Pro Ser Phe Leu Glu Phe Ser Glu Ile Thr Ser Thr
 340 345 350
 Thr Leu Asn Val Ser Trp Gly Glu Pro Ser Ala Ala Asn Gly Ile Leu
 355 360 365
 Gln Gly Tyr Arg Val Val Tyr Glu Pro Leu Ala Pro Val Gln Gly Val
 370 375 380
 Ser Lys Val Val Thr Val Asp Val Lys Gly Asn Trp Gln Arg Trp Leu
 385 390 395 400
 Lys Val Arg Asp Leu Thr Lys Gly Val Thr Tyr Phe Phe Arg Val Gln
 405 410 415
 Ala Arg Thr Ile Ala Tyr Gly Pro Glu Leu Gln Ala Asn Val Thr Ala
 420 425 430
 Gly Pro Ala Glu Gly Ser Pro Gly Ser Pro Arg Asn Val Leu Val Thr
 435 440 445
 Lys Ser Ala Ser Glu Leu Thr Leu Gln Trp Thr Glu Gly Asn Thr Gly
 450 455 460
 Asn Thr Pro Thr Thr Gly Tyr Val Ile Glu Ala Arg Pro Ser Asp Glu
 465 470 475 480
 Gly Leu Trp Asp Met Phe Ala Lys Asp Ile Pro Arg Ser Ala Thr Ser
 485 490 495
 Tyr Thr Val Gly Leu Asp Lys Leu Arg Gln Gly Val Thr Tyr Glu Phe
 500 505 510
 Arg Val Val Ala Val Asn Lys Ala Gly Phe Gly Glu Pro Ser Arg Pro
 515 520 525
 Ser Ile Ala Val Ser Ala Gln Ala Glu Ala Pro Phe Tyr Glu Glu Trp
 530 535 540
 Trp Phe Leu Leu Val Ile Ala Leu Ser Ser Leu Leu Leu Val Leu Leu
 545 550 555 560
 Val Val Phe Val Leu Val Leu His Gly Gln Ser Lys Lys Tyr Lys Asn
 565 570 575
 Cys Gly Ser Gly Lys Gly Ile Ser Asn Met Glu Glu Thr Val Thr Leu
 580 585 590
 Asp Asn Gly Gly Phe Ala Ala Leu Glu Leu Asn Ser Arg His Leu Asn
 595 600 605
 Val Lys Ser Thr Phe Ser Lys Lys Asn Gly Thr Arg Ser Pro Pro Arg
 610 615 620
 Pro Ser Pro Gly Gly Leu His Tyr Ser Asp Glu Asp Ile Cys Asn Lys

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625          630          635          640
Tyr Asn Gly Ala Val Leu Thr Glu Ser Val Asn Leu Lys Glu Lys Ser
645          650          655
Val Asp Gly Ser Glu Ser Glu Ala Ser Asp Ser Asp Tyr Glu Glu Ala
660          665          670
Leu Pro Lys His Ser Phe Val Asn His Tyr Met Ser Asp Pro Thr Tyr
675          680          685
Tyr Asn Phe Trp Lys Arg Arg Pro Pro Ala Ala Pro His Arg Tyr
690          695          700
Glu Ala Val Ala Gly Ala Glu Ala Gly Pro His Leu His Thr Val Ile
705          710          715          720
Thr Thr Gln Ser Ala Gly Gly Val Tyr Thr Pro Ala Gly Pro Gly Ala
725          730          735
Arg Ala Pro Leu Thr Gly Phe Ser Ser Phe Val
740          745

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<210> 664

<211> 307

<212> PRT

<213> Rat

<400> 664

```

Met Gln Leu Asn Arg Phe Phe Ser Gly Pro Gly Leu Phe Leu Leu Leu
1          5          10          15
Phe Cys Ser Leu Cys Val Glu Ala Glu Val Lys Glu Val Asn Ala Met
20          25          30
Val Gly Ser Asp Val Glu Leu Arg Cys Val Tyr Pro Arg Arg Ser His
35          40          45
Phe Ser Leu Asp Asp Leu Tyr Val Tyr Trp Gln Ile Val Asp Glu Ala
50          55          60
Lys Thr Val Val Thr Tyr Tyr Leu Pro Ser Ala Asn Glu Ser Ser Thr
65          70          75          80
Ile His Val Ser Asn Ser Tyr Lys Asn Arg Ala His Leu Ser Pro Asp
85          90          95
Leu Met Lys Glu Gly Asp Phe Ser Leu His Leu Gln Asn Val Thr Pro
100          105          110
Gln Asp Thr Gln Glu Phe Lys Cys Leu Val Phe Arg Met Ser Thr Val
115          120          125
Leu Gly Lys Ala Leu Glu Glu Val Val Arg Leu Arg Val Ala Ala Asn
130          135          140
Phe Ser Thr Pro Val Ile Ser Thr Ser Gly Ser Ser Asp Pro Gly Gln
145          150          155          160
Glu Arg Thr Phe Thr Cys Met Ser Lys Asn Gly Tyr Pro Glu Pro Asn
165          170          175
Leu Tyr Trp Ile Asn Arg Thr Asp Asn Thr Leu Ile Asp Glu Thr Leu
180          185          190
Gln Asn Asn Thr Val Tyr Leu Asn Glu Leu Gly Leu Tyr Asp Val Val
195          200          205
Ser Thr Leu Arg Ile Pro Trp Thr Pro His Val Asp Val Ile Cys Cys
210          215          220
Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile Ser Arg Ala
225          230          235          240
Asp Ser Phe Thr Gly Ser Met Asn Thr Glu Arg Pro Gln Glu Ile His
245          250          255
Arg Glu Ala Thr Lys Val Leu Phe Tyr Ala Leu Ala Ala Leu Leu Ala
260          265          270
Val Val Val Val Ile Phe Ile Ile Val Leu Tyr Arg Cys Arg Arg Arg

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275 280 285
 Pro Cys Gln Ser Tyr Thr Gly Pro Arg Ala Val Gln Leu Glu Leu Thr
 290 295 300
 Asp His Ser
 305

<210> 665
 <211> 143
 <212> PRT
 <213> Rat

<400> 665
 Lys Lys Tyr Asp Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Val
 1 5 10 15
 Val Leu Phe Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Thr Gly Val
 20 25 30
 Thr Val Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg
 35 40 45
 His Thr Gly Met His Asn Ser Ala Phe Ser Gly Phe Met Leu Gly Pro
 50 55 60
 Phe Phe Trp Leu Leu Phe Lys Ser Pro Gln Leu Ala Ala Gln Pro Ser
 65 70 75 80
 Thr Tyr Leu Ala Val Ala Glu Glu Leu Glu Ser Val Ser Gly Lys Tyr
 85 90 95
 Phe Asp Gly Leu Arg Glu Lys Ala Pro Ser Pro Glu Ala Glu Asp Glu
 100 105 110
 Glu Val Ala Arg Arg Leu Trp Thr Glu Ser Ala His Leu Val Gly Leu
 115 120 125
 Asp Met Ala His Gly Ser Ser Gly Arg Gly His Ser Ile Ser Arg
 130 135 140

<210> 666
 <211> 298
 <212> PRT
 <213> Mouse

<400> 666
 Met Glu Ser Ala Asn Thr Leu Cys Pro Gly Arg Lys Cys Lys Gly Gly
 1 5 10 15
 Val Leu Ala His Leu Glu Arg Leu Glu Ala Gln Thr Asn Ile Ser Asn
 20 25 30
 Arg Lys Ser Glu Glu Pro Ala Val Arg Lys Lys Glu Ser Ser Leu Arg
 35 40 45
 Thr Lys Ile Arg Glu Leu Arg Gln Gln Arg Asp Lys Leu Arg Ala Glu
 50 55 60
 Val Lys Gln Trp Gly Ala Arg Val Lys Glu Pro Ala Lys Glu Asp
 65 70 75 80
 Pro Ser Arg Thr Val Ile Ser Glu Gln Glu Val Leu Glu Arg Glu Trp
 85 90 95
 Arg Asn Val Asp Ala Ile Leu Glu Ala Tyr Arg Phe Thr Gly Leu Ser
 100 105 110
 Gly Lys Leu Thr Ser Arg Gly Val Cys Met Cys Ile Ser Thr Ala Phe
 115 120 125
 Glu Gly Asn Leu Leu Asp Ser Tyr Phe Val Asp Leu Val Ile Glu Lys
 130 135 140
 Pro Leu Arg Ile His His His Ser Val Pro Val Phe Ile Pro Leu Glu
 145 150 155 160

Lys Ile Ala Ala Ala His Leu Gln Thr Asp Val Gln Arg Phe Leu Phe
 165 170 175
 Arg Leu Trp Glu Tyr Leu Asn Ala Tyr Ala Gly Arg Lys Tyr Gln Ala
 180 185 190
 Asp Gln Leu Glu Ser Asp Phe Cys Asp Val Leu Thr Gly Pro Leu Gln
 195 200 205
 Arg Asn Ala Leu Cys Asn Leu Leu Ser Phe Thr Tyr Lys Val Glu Gln
 210 215 220
 Arg Cys Gln Thr Phe Ser Phe Ser Ala Arg Leu Leu Tyr Glu Asp Pro
 225 230 235 240
 Thr Ala Ala Leu Pro Thr Asn Val Thr Val Thr Arg Pro Gly Val Glu
 245 250 255
 Ala Ser Ser Pro Pro Trp Glu Glu His Arg Ala Ser His Gln Met Leu
 260 265 270
 Phe Arg Thr Lys Pro Leu His Lys Val Phe Ala Ser Phe Ser Lys Glu
 275 280 285
 Thr Glu Lys Leu His Leu Asn Leu Val Ser
 290 295

<210> 667

<211> 226

<212> PRT.

<213> Mouse

<400> 667

Met Glu Ala Glu Leu Gly Gly Ser Phe Ile Lys Leu Arg Gln Ala Leu
 1 5 10 15
 Phe Gln Leu Asn Ser Val Asp Ser Ser Leu Leu Phe Thr Ala Gln Ala
 20 25 30
 Leu Leu Arg Trp His Asp Gly His Gln Phe Cys Ser Lys Ser Gly Gln
 35 40 45
 Pro Thr Gln Lys Asn Val Ala Gly Ser Lys Arg Val Cys Pro Ser Ser
 50 55 60
 Lys Ile Ile Tyr Tyr Pro Gln Met Ala Pro Val Val Ile Thr Leu Val
 65 70 75 80
 Ser Asp Gly Ala Arg Cys Leu Leu Ala Arg Gln Ser Ser Phe Pro Lys
 85 90 95
 Gly Leu Tyr Ser Ala Leu Ala Gly Phe Cys Asp Ile Gly Glu Ser Val
 100 105 110
 Glu Glu Thr Val His Arg Glu Val Ala Glu Glu Val Gly Leu Glu Val
 115 120 125
 Glu Asn Ile Gln Tyr Ser Ala Ser Gln His Trp Pro Phe Pro Asn Ser
 130 135 140
 Ser Leu Met Ile Ala Cys His Ala Thr Val Lys Pro Gly His Thr Glu
 145 150 155 160
 Ile Gln Val Asn Leu Lys Glu Leu Glu Ala Ala Ala Trp Phe Ser Leu
 165 170 175
 Asp Glu Val Thr Thr Ala Leu Arg Arg Lys Gly Ser Leu Ala Leu Gln
 180 185 190
 Pro Ser Glu Ala Ser Pro Leu Leu Pro Pro Lys Leu Ala Ile Ala
 195 200 205
 His His Leu Ile Lys Lys Trp Val Glu Thr Arg Ser Cys Ser Ser Leu
 210 215 220
 Ala Ala
 225

<210> 668

<211> 781
 <212> PRT
 <213> Mouse

<400> 668

Met	Glu	Met	Met	Lys	Lys	Leu	Ile	Ala	Gly	Gln	Gly	Pro	Glu	Pro	Gln
1				5					10				15		
Pro	Ser	Asn	Arg	Pro	Thr	Ser	Arg	Leu	Gly	Gly	Ser	Leu	Leu	Phe	Gly
		20					25					30			
Asn	Leu	Val	Pro	Ala	Asn	Lys	Asp	Ala	Pro	Ala	Leu	Glu	Pro	Leu	Gly
	35					40					45				
Thr	Lys	Leu	Ser	Ala	Leu	Pro	His	Gly	Ala	Pro	Gly	Val	Arg	Lys	
	50				55					60					
Val	Pro	Gly	Gln	Leu	Pro	Leu	Leu	Cys	Ser	Gly	Arg	Pro	Pro	Pro	Glu
65				70					75						80
Lys	Pro	Ala	Pro	Ile	Glu	Pro	Pro	Glu	Gly	Trp	Ser	Pro	Ala	Pro	Lys
			85						90				95		
Thr	Gln	Gly	Lys	Leu	Asn	Thr	Arg	Pro	Gly	Lys	Val	Ile	Leu	Phe	Ser
	100						105					110			
Glu	Pro	Gly	Cys	Arg	Gly	Arg	Gly	Arg	Glu	Val	Trp	Gly	Asp	Ile	Ala
	115				120						125				
Asp	Ala	Ser	Ala	Trp	Asp	Pro	Val	Ala	Ser	Ile	Arg	Val	Ile	Arg	Gly
	130				135					140					
Cys	Trp	Ile	Leu	Tyr	Glu	Gln	Pro	Glu	Phe	Arg	Gly	Gln	Lys	Leu	Ser
145				150					155						160
Leu	Pro	Glu	Gly	Asp	Val	Glu	Leu	Arg	Ala	Leu	Ala	Cys	Ala	Trp	Ser
			165						170					175	
Leu	Gln	Gly	Phe	Gly	Ser	Leu	Arg	Arg	Ala	Val	Gln	Asp	Tyr	Cys	Thr
	180						185					190			
Pro	Thr	Ile	Ser	Leu	Phe	Ser	Glu	Glu	Gly	Leu	Lys	Gly	Lys	Pro	Val
	195					200					205				
Thr	Leu	Thr	Gly	Asp	Leu	Lys	Asp	Ser	Gln	Gly	Leu	Glu	Arg	Pro	Leu
	210				215						220				
Gln	Val	Ala	Ser	Ala	Thr	Val	Thr	Ala	Gly	Leu	Trp	Leu	Leu	Tyr	Pro
225				230					235						240
Lys	Pro	Phe	Phe	Glu	Asp	Thr	Pro	Tyr	Ile	Leu	Glu	Pro	Gly	Glu	Tyr
			245					250						255	
Pro	Thr	Leu	Glu	Ala	Trp	Gly	Thr	Ser	Gly	Pro	Ser	Val	Gly	Ser	Leu
	260						265					270			
Lys	Pro	Met	Arg	Leu	Gly	Cys	Pro	Ser	Val	Glu	Lys	Pro	Gly	Glu	Pro
	275					280						285			
Lys	Ala	Val	Val	Tyr	Glu	Ala	Pro	Gly	Phe	Gln	Gly	Gln	Ser	Trp	Glu
	290				295					300					
Val	Ser	Gly	Asp	Ile	Tyr	Asn	Leu	Gln	Gln	Pro	Glu	Asp	Ser	Gln	Ser
305				310					315						320
Pro	Gln	Leu	Thr	Ser	Val	Gly	Ser	Leu	Arg	Ile	Leu	Gly	Gly	Cys	Trp
			325						330					335	
Val	Gly	Tyr	Glu	Lys	Glu	Gly	Phe	Arg	Gly	His	Gln	Tyr	Leu	Leu	Glu
	340						345					350			
Glu	Gly	Glu	Tyr	Ala	Asp	Trp	Ser	His	Trp	Gly	Gly	Tyr	Asp	Glu	Leu
	355					360						365			
Leu	Thr	Ser	Leu	Arg	Val	Ile	Arg	Thr	Asp	Phe	Gly	Asp	Pro	Ala	Val
	370				375					380					
Val	Leu	Phe	Glu	Asp	Met	Asp	Phe	Gln	Gly	His	Arg	Val	Glu	Val	Ser
385				390					395						400
Ser	Ala	Leu	Pro	Asp	Val	Glu	Leu	Ala	Gln	His	Gly	Pro	Ser	Thr	Gln
			405					410					415		

Ala Ile His Val Leu Ser Gly Val Trp Val Ala Tyr Glu Arg Val Gly
 420 425 430
 Phe Ser Gly Glu Gln Tyr Ile Leu Glu Lys Gly Val Tyr Arg Asn Cys
 435 440 445
 Asp Asp Trp Gly Ser Gly Asn Cys Ala Leu Gly Ser Leu Gln Pro Val
 450 455 460
 Val Gln Val Gly Glu Ser Asp Leu His Phe Val Thr Lys Ile Gln Leu
 465 470 475 480
 Phe Ser Gly Pro Asn Phe Leu Gly Asp His Ile Ser Phe Glu Asp Asp
 485 490 495
 Gln Ala Ser Leu Pro Ala Ser Phe His Pro Gln Ser Cys Arg Val His
 500 505 510
 Gly Gly Ser Trp Val Leu Phe Glu Asp Lys Asn Phe Glu Ala Asp Gln
 515 520 525
 His Ile Val Ser Glu Gly Glu Phe Pro Thr Leu Thr Asp Met Gly Cys
 530 535 540
 Leu Ala Ser Thr Val Leu Gly Ser Leu Arg Lys Val Pro Leu His Phe
 545 550 555 560
 Ser Glu Pro Ser Leu Ser Leu Phe Gly Leu Glu Cys Phe Glu Gly Lys
 565 570 575
 Glu Ile Glu Leu Thr Gly Glu Val Arg Ser Leu Gln Ala Glu Gly Phe
 580 585 590
 Asn Asn His Val Leu Ser Val Arg Val Lys Gly Gly Val Trp Val Val
 595 600 605
 Cys Glu His Ser Asp Phe Arg Gly Arg Gln Trp Leu Val Gly Ser Cys
 610 615 620
 Glu Ile Thr Asn Trp Leu Thr Tyr Ser Gly Thr Gln Arg Val Gly Ser
 625 630 635 640
 Leu Tyr Pro Ile Lys Gln Arg Arg Ala Tyr Phe Arg Leu Trp Asn Ala
 645 650 655
 Ala Leu Gly Gly Phe Leu Ser Val Pro Asp His Val Glu Asp Met Lys
 660 665 670
 Ala Gly Arg Val Val Val Ser Glu Pro Arg Ala Gly Gly Ser Cys Ile
 675 680 685
 Trp Tyr Tyr Glu Asp Gly Leu Leu Lys Asn Gln Met Ala Pro Thr Met
 690 695 700
 Ser Leu Gln Val Ile Gly Pro Pro Ser Pro Gly Ser Lys Val Val Leu
 705 710 715 720
 Trp Ala Glu Ser Arg Leu Pro Arg Gln Thr Trp Ser Ile Asn Glu Leu
 725 730 735
 Gly His Ile Cys Ser Gln Met Phe Glu Gly Gln Ile Leu Asp Val Lys
 740 745 750
 Gly Gly Arg Gly Tyr Asp Arg Asp His Val Val Leu Trp Glu Pro Thr
 755 760 765
 Lys Asp Arg Leu Ser Gln Ile Trp Thr Val His Val Leu
 770 775 780

<210> 669

<211> 70

<212> PRT

<213> Mouse

<400> 669

Met Tyr Met Thr Met Arg Gly Lys Glu Pro Trp Gln Thr Ala Lys Leu
 1 5 10 15
 Gln Leu Gly Glu Leu Asn Arg Thr Ala Val Phe Thr Cys Arg Pro Ala
 20 25 30

Arg Val Lys Glu Gly Asp Ile Leu Tyr Ile His Ser Leu Gln Thr Val
 35 40 45
 Gly Ser Asn His Lys Pro Val Ala Ala Glu His Thr Tyr Trp Ala Trp
 50 55 60
 Pro Glu Glu Thr Asp Val
 65 70

<210> 670
 <211> 368
 <212> PRT
 <213> Mouse

<400> 670
 Leu Thr Asn Gly Ser Gln Ala Ser Asp Lys Ser Glu Glu Gly Ser Ala
 1 5 10 15
 Asp Thr Ala Asp Pro Gln Glu Asn Pro Leu Gln Pro Val Ser Val Gly
 20 25 30
 Glu Glu Pro Ser Ile Thr Glu His His Ser Val Gly Glu Gln Ala Trp
 35 40 45
 Asp Gly Thr Ser Gln Ser Cys Pro Ser Leu Pro Ala Thr Val Ser Phe
 50 55 60
 His Met Asp Ser Thr Asp Leu Glu Pro Gly Gln Gln Thr Ala Met Lys
 65 70 75 80
 Ser Cys Ser Arg Asp Asp Val Glu Met Val Glu Glu Phe Asp Glu Leu
 85 90 95
 Pro Thr Asp Ala Val Arg Arg Ile Arg Arg Glu Leu Val Thr Val Thr
 100 105 110
 Lys His Ser Pro Glu Gln Arg Gln Asp Pro Leu Cys Ile Ser Ile Thr
 115 120 125
 Val Cys Thr Val Glu Lys Asp Arg Pro Ala Ala Leu Asp Ser Leu Glu
 130 135 140
 Glu Pro Leu Pro Gly Met Leu Phe Phe Leu Ser Ser Gly Gln Asp Gln
 145 150 155 160
 Gln Ala His Pro Gln Leu Arg Glu His Pro Ala Pro Glu Ala Ser Glu
 165 170 175
 Ala Ser Gln Pro Gln Asp Ala Ala Glu Gly Ser Ser Ala Gly Glu Glu
 180 185 190
 Lys Asp Ala Ser Val Glu Pro Leu Leu Pro Ala Ala Ser Pro Gly Gly
 195 200 205
 Ser Thr Ser Gln Val Leu Glu Ala Ala Thr Cys Lys Lys Gln Val Ser
 210 215 220
 Gln Asp Phe Leu Glu Thr Arg Phe Lys Ile Gln Gln Leu Leu Glu Pro
 225 230 235 240
 Gln Gln Tyr Met Ala Cys Leu Pro His His Ile Ile Val Lys Ile Phe
 245 250 255
 Arg Leu Leu Pro Thr Leu Ser Leu Ala Ile Leu Lys Cys Thr Cys Arg
 260 265 270
 Tyr Phe Lys Ser Ile Ile Glu Tyr Tyr Asn Ile Arg Pro Ala Asp Ser
 275 280 285
 Arg Trp Val Arg Asp Pro Arg Tyr Arg Glu Asp Pro Cys Lys Gln Cys
 290 295 300
 Lys Lys Lys Tyr Val Lys Gly Asp Val Ser Leu Cys Arg Trp His Pro
 305 310 315 320
 Lys Pro Tyr Cys Gln Ala Leu Pro Tyr Gly Pro Gly Tyr Trp Met Cys
 325 330 335
 Cys Pro Pro Val Ser Glu Gly Leu Phe Cys Cys Lys Leu Gly Leu His
 340 345 350

Asp Asn His Trp Leu Pro Ala Cys His Ser Phe Asn Pro Gly Asn Pro
 355 360 365

<210> 671

<211> 293

<212> PRT

<213> Mouse

<400> 671

Thr His Phe Ile His Thr Leu Thr Arg Leu Gln Met Glu Gln Gly Ala
 1 5 10 15
 Glu Ser Leu Gly Asp Leu Glu Ser Pro Val Glu Asp Thr Pro Val Glu
 20 25 30
 Gln Ala Ala Leu Ser Pro Phe Pro Pro Ser Lys Pro Pro Val Ser Ser
 35 40 45
 Glu Leu Gly Asp Ser Ser Cys Ser Ser Asp Met Thr Asp Ser Ser Thr
 50 55 60
 Thr Leu Ser Ser Gly Ser Ser Glu Pro Pro Asn His Pro Ala His Pro
 65 70 75 80
 Ser Leu Pro Gly Pro Ser Phe Arg Ser Gly Val Asp Glu Asp Ser Leu
 85 90 95
 Glu Gln Ile Leu Asn Phe Ser Asp Ser Asp Leu Gly Ile Glu Glu Glu
 100 105 110
 Glu Glu Glu Gly Gly Gly Val Gly Asn Ser Asp Asn Leu Ser Cys Phe
 115 120 125
 His Leu Ala Asp Ile Phe Gly Thr Gly Asp Pro Gly Ser Leu Ala Ser
 130 135 140
 Trp Thr His Ser Gln Ser Gly Ser Ser Leu Ala Ser Gly Ile Leu Asp
 145 150 155 160
 Glu Asn Ala Asn Leu Asp Ala Ser Cys Phe Leu Asn Ser Gly Leu Gly
 165 170 175
 Gly Leu Arg Glu Gly Ser Leu Pro Gly Ser Ser Gly Ser Pro Glu Gly
 180 185 190
 Asp Ala Val Gln Ser Ser Ser Trp Asp Leu Ser Leu Ser Ser Cys Asp
 195 200 205
 Ser Phe Glu Leu Leu Gln Ala Leu Pro Asp Tyr Ser Leu Gly Pro His
 210 215 220
 Tyr Thr Ser Arg Arg Val Ser Gly Ser Pro Asp Ser Leu Glu Thr Phe
 225 230 235 240
 His Pro Leu Pro Ser Phe Ser Pro Pro Arg Asp Ala Ser Thr Cys Phe
 245 250 255
 Leu Glu Ser Leu Val Gly Leu Ser Glu Pro Val Thr Glu Val Leu Ala
 260 265 270
 Pro Leu Leu Glu Ser Gln Phe Glu Asp Ala Ala Leu Ala Pro Leu Leu
 275 280 285
 Glu Pro Val Pro Val
 290

<210> 672

<211> 904

<212> PRT

<213> Mouse

<400> 672

Met Glu Val Asn Cys Leu Thr Leu Lys Asp Leu Ile Ser Pro Arg Gln
 1 5 10 15
 Thr Arg Leu Asp Phe Ala Ile Glu Asp Ala Glu Asn Ala Gln Lys Glu

			20					25					30		
Asn	Ile	Phe	Val	Asp	Arg	Ser	Arg	Met	Thr	Pro	Lys	Thr	Pro	Met	Lys
		35					40					45			
Asn	Glu	Pro	Ile	Asp	Leu	Ser	Lys	Gln	Arg	Ile	Phe	Thr	Pro	Asp	Arg
	50					55					60				
Asn	Pro	Ile	Thr	Pro	Val	Lys	Pro	Val	Asp	Arg	Gln	Pro	Gln	Val	Glu
65					70				75						80
Pro	Trp	Thr	Pro	Thr	Ala	Asn	Leu	Lys	Met	Leu	Ile	Ser	Ala	Ala	Ser
				85					90					95	
Pro	Asp	Ile	Arg	Asp	Arg	Glu	Lys	Lys	Lys	Glu	Leu	Phe	Arg	Pro	Ile
			100					105					110		
Glu	Asn	Lys	Glu	Asp	Ala	Phe	Val	Asn	Ser	Leu	Gln	Leu	Asp	Val	Ala
		115					120					125			
Gly	Asp	Gly	Ala	Val	Asp	Glu	Tyr	Glu	Lys	Gln	Arg	Pro	Ser	Arg	Lys
		130				135					140				
Gln	Lys	Ser	Leu	Gly	Leu	Leu	Cys	Gln	Lys	Phe	Leu	Ala	Arg	Tyr	Pro
145					150					155					160
Ser	Tyr	Pro	Leu	Ser	Thr	Glu	Lys	Thr	Thr	Ile	Ser	Leu	Asp	Glu	Val
				165					170					175	
Ala	Val	Ser	Leu	Gly	Val	Glu	Arg	Arg	Arg	Ile	Tyr	Asp	Ile	Val	Asn
			180					185					190		
Val	Leu	Glu	Ser	Leu	His	Leu	Val	Ser	Arg	Val	Ala	Lys	Asn	Gln	Tyr
		195					200					205			
Gly	Trp	His	Gly	Arg	His	Ser	Leu	Pro	Lys	Thr	Leu	Arg	Thr	Leu	Gln
	210					215					220				
Arg	Leu	Gly	Glu	Glu	Gln	Lys	Tyr	Glu	Glu	Gln	Met	Ala	Cys	Leu	Gln
225					230					235					240
Gln	Lys	Glu	Leu	Asp	Leu	Met	Gly	Tyr	Arg	Phe	Gly	Glu	Arg	Arg	Lys
				245					250					255	
Asp	Gly	Ser	Pro	Asp	Pro	Arg	Asp	Pro	His	Leu	Leu	Asp	Phe	Ser	Glu
			260				265						270		
Ala	Asp	Tyr	Pro	Ser	Ser	Ser	Ala	Asn	Ser	Arg	Lys	Asp	Lys	Ser	Leu
			275				280					285			
Arg	Ile	Met	Ser	Gln	Lys	Phe	Val	Met	Leu	Phe	Leu	Val	Ser	Lys	Thr
	290					295					300				
Lys	Ile	Val	Thr	Leu	Asp	Val	Ala	Ala	Lys	Ile	Leu	Ile	Glu	Glu	Ser
305					310					315					320
Gln	Asp	Thr	Pro	Asp	His	Ser	Lys	Phe	Lys	Thr	Lys	Val	Arg	Arg	Leu
				325					330					335	
Tyr	Asp	Ile	Ala	Asn	Val	Leu	Thr	Ser	Leu	Ala	Leu	Ile	Lys	Lys	Val
			340					345					350		
His	Val	Thr	Glu	Glu	Arg	Gly	Arg	Lys	Pro	Ala	Phe	Lys	Trp	Ile	Gly
		355					360					365			
Pro	Val	Asp	Phe	Ser	Ser	Ile	Asp	Glu	Glu	Leu	Leu	Asp	Val	Ser	Ala
						375									

Leu Ser Met Asp Ser Glu Tyr Cys Val Lys Pro Leu Ala Gln Pro Val
 485 490 495
 Phe Ser Val Ala Gln Thr Asp Leu Pro Ala Phe Ser Ala Gln Asn Gly
 500 505 510
 Pro Ser Gly Gln Val Gly Val Pro Val Pro Ser Ala Ala Ser Asp Thr
 515 520 525
 Glu Asn Leu Lys Pro Ala Leu Leu Ala Gly Gln Pro Leu Val Tyr Val
 530 535 540
 Pro Ser Thr Gln Leu Phe Met Leu Tyr Gly Ser Val Gln Glu Gly Leu
 545 550 555 560
 Ser Pro Glu Ser Arg Ser Glu Glu Asp Gly Gly Gly Ser Asp Val Pro
 565 570 575
 Ala Asp Leu Ser Val Thr Pro Ser Ala Gln Lys Arg Leu Cys Glu Glu
 580 585 590
 Arg Asp Pro Gln Glu Glu Glu Asp Glu Pro Ala Met Lys Arg Gln Ser
 595 600 605
 Gln Glu Phe Glu Asp Ser Pro Leu Ser Leu Val Met Pro Lys Lys Pro
 610 615 620
 Ser Ser Ser Thr Asp Leu Ala Cys Pro Val Thr Met Gly Asn Gly Ser
 625 630 635 640
 Ser Pro Pro Leu Glu Asp Ala Cys Val Lys Gly Gln Leu Pro Ala Ala
 645 650 655
 Glu Glu Val Thr Gly Lys Ala Ala Pro Asn Cys Tyr Val Ala Ser Glu
 660 665 670
 Cys Gly Asn Pro Ala Arg Asn Pro Asp Thr Glu Lys Pro Ser Asn Glu
 675 680 685
 Asn Glu Ile Thr Lys Asp Pro Ser Leu Met Gln Tyr Leu Tyr Val Gln
 690 695 700
 Ser Pro Ala Gly Leu Asn Gly Phe Asn Met Val Leu Pro Gly Thr Gln
 705 710 715 720
 Thr Pro His Thr Val Ala Pro Ser Pro Ala Gln Leu Pro Ser Phe Gly
 725 730 735
 Val Pro Cys Met Phe Leu Gln Ser Pro Gly Leu Gly Pro Phe Pro Val
 740 745 750
 Leu Tyr Ser Pro Ala Ile Pro Gly Pro Ile Ser Ser Ala Pro Gly Thr
 755 760 765
 His Pro Asn Pro Gly Pro Met Asn Phe Gly Leu Ser Thr Leu Ala Ser
 770 775 780
 Ala Ser His Leu Leu Ile Ser Pro Ala Ala Met Val Asn Pro Lys Pro
 785 790 795 800
 Ser Thr Leu Pro Cys Thr Asp Pro Gln Leu Arg Cys Gln Pro Ser Leu
 805 810 815
 Asn Leu Asn Pro Val Met Pro Gly Ser His Gly Val Ile His Pro Glu
 820 825 830
 Ser Pro Cys Tyr Val Arg His Pro Val Ser Met Val Lys Ala Glu Gln
 835 840 845
 Ser Pro Ala Pro Ala Thr Pro Lys Ser Ile Gln Arg Arg His Arg Glu
 850 855 860
 Thr Phe Phe Lys Thr Pro Gly Ser Leu Gly Asp Pro Val Phe Arg Arg
 865 870 875 880
 Lys Glu Arg Asn Gln Ser Arg Asn Thr Ser Ser Ala Gln Arg Arg Leu
 885 890 895
 Glu Ile Ser Ser Ser Gly Pro Asp
 900

<210> 673

<211> 173

<212> PRT
<213> Mouse

<400> 673

```

Lys Arg Arg Lys Arg Lys Arg Ser Glu Gly Leu Ser Gln Glu Ala Thr
 1           5           10           15
Pro Ser Gln Asp Leu Ile Gln His Ser Cys Ser Pro Val Asp His Ser
      20           25           30
Glu Pro Glu Ala Arg Thr Glu Leu Gln Lys Lys Lys Lys Lys Arg
 35           40           45
Arg Lys Arg Lys Pro Glu Pro Gln Gln Asp Glu Glu Ser Lys His Pro
 50           55           60
Gly Asp Gln Arg Ser Pro Arg Pro Ser Val Thr Pro Val Pro Ala Leu
 65           70           75           80
Ser Val Asn Gly His Leu Pro Ser Asp Cys Leu Val Leu Thr Trp Asp
      85           90           95
Gly Glu Pro Ser Ala Ile Ser Gln Asp Ala Ile Lys Asp Ser Arg Leu
 100          105          110
Ala Arg Thr Gln Thr Val Val Asp Asp Trp Asp Glu Glu Phe Asp Arg
 115          120          125
Gly Lys Glu Lys Lys Ile Lys Lys Phe Lys Arg Glu Lys Lys Arg Asn
 130          135          140
Phe Asn Ala Phe Gln Lys Leu Gln Ser Arg Arg Asn Phe Trp Ser Val
 145          150          155          160
Thr His Pro Ala Lys Val Ala Ser Leu Ser Tyr Arg Arg
      165          170

```

<210> 674
<211> 470
<212> PRT
<213> Mouse

<400> 674

```

Glu Glu Thr Lys Pro Leu Leu Gly Ser Asp Val Ser Gly Pro Glu Gly
 1           5           10           15
Thr Lys Val Met Gly Ala Val Pro Cys Arg Arg Ala Leu Leu Leu Cys
      20           25           30
Asn Gly Met Arg Tyr Lys Leu Leu Gln Glu Gly Asp Ile Gln Val Cys
 35           40           45
Val Ile Arg His Pro Arg Thr Phe Leu Ser Lys Ile Leu Thr Ser Lys
 50           55           60
Phe Leu Arg Arg Trp Glu Pro His His Leu Thr Leu Ala Asp Asn Ser
 65           70           75           80
Leu Ala Ser Ala Thr Pro Ser Gly Tyr Met Glu Asn Ser Val Ser Tyr
      85           90           95
Ser Ala Ile Glu Asp Val Gln Pro Leu Ser Trp Glu Asn Ala Pro Lys
 100          105          110
Tyr Cys Leu Gln Leu Thr Ile Pro Gly Gly Thr Val Leu Leu Gln Ala
 115          120          125
Ala Asn Ser Tyr Leu Arg Asp Gln Trp Phe His Ser Leu Gln Trp Lys
 130          135          140
Lys Lys Ile Tyr Lys Tyr Lys Lys Val Leu Ser Asn Pro Ser Arg Trp
 145          150          155          160
Glu Val Val Leu Lys Glu Ile Arg Thr Leu Val Asp Met Ala Leu Thr
      165          170          175
Ser Pro Leu Gln Asp Asp Ser Ile Asn Gln Ala Pro Leu Glu Ile Val
 180          185          190

```

Ser Lys Leu Leu Ser Glu Asn Thr Asn Leu Thr Thr Gln Glu His Glu
 195 200 205
 Asn Ile Ile Val Ala Ile Ala Pro Leu Leu Glu Asn Asn His Pro Pro
 210 215 220
 Pro Asp Leu Cys Glu Phe Phe Cys Lys His Cys Arg Glu Arg Pro Arg
 225 230 235 240
 Ser Met Val Val Ile Glu Val Phe Thr Pro Val Val Gln Arg Ile Leu
 245 250 255
 Lys His Asn Met Asp Phe Gly Lys Cys Pro Arg Leu Arg Leu Phe Thr
 260 265 270
 Gln Glu Tyr Ile Leu Ala Leu Asn Glu Leu Asn Ala Gly Met Glu Val
 275 280 285
 Val Lys Lys Phe Ile Gln Ser Met His Gly Pro Thr Gly His Cys Pro
 290 295 300
 His Pro Arg Val Leu Pro Asn Leu Val Ala Val Cys Leu Ala Ala Ile
 305 310 315 320
 Tyr Ser Cys Tyr Glu Phe Ile Asn Ser Arg Asp Asn Ser Pro Ser
 325 330 335
 Leu Lys Glu Ile Arg Asn Gly Cys Gln Gln Pro Cys Asp Arg Lys Pro
 340 345 350
 Thr Leu Pro Leu Arg Leu Leu His Pro Ser Pro Asp Leu Val Ser Gln
 355 360 365
 Glu Ala Thr Leu Ser Glu Pro Arg Leu Lys Ser Val Val Val Ala Ser
 370 375 380
 Ser Glu Val His Val Glu Val Glu Arg Thr Ser Thr Ala Lys Pro Ala
 385 390 395 400
 Leu Thr Ala Ser Thr Gly Asn Asp Ser Glu Pro Asn Leu Ile Asp Cys
 405 410 415
 Leu Met Val Ser Pro Ala Cys Gly Thr Met Ser Ile Glu Leu Gly Pro
 420 425 430
 Gln Ala Gly Arg Thr Leu Gly Cys His Val Glu Ile Leu Lys Leu Leu
 435 440 445
 Ser Asp Tyr Asp Asp Trp Arg Pro Ser Leu Ala Ser Leu Leu Gln Pro
 450 455 460
 Ile Pro Phe Pro Lys Glu
 465 470

<210> 675

<211> 319

<212> PRT

<213> Mouse

<400> 675

Phe Ala Arg Thr Leu Pro Trp Ala Ser Val Leu Arg Val Trp Asp Met
 1 5 10 15
 Phe Phe Cys Glu Gly Val Lys Ile Ile Phe Arg Val Ala Leu Val Leu
 20 25 30
 Leu Arg His Thr Leu Gly Ser Val Glu Lys Leu Arg Ser Cys Gln Gly
 35 40 45
 Met Tyr Glu Thr Met Glu Gln Leu Arg Asn Leu Pro Gln Gln Cys Met
 50 55 60
 Gln Glu Asp Phe Leu Val His Glu Val Thr Asn Leu Pro Val Thr Glu
 65 70 75 80
 Ala Trp Ile Glu Arg Glu Asn Ala Ala Gln Leu Lys Lys Trp Arg Glu
 85 90 95
 Thr Arg Gly Glu Leu Gln Tyr Arg Pro Ser Arg Arg Leu His Gly Ser
 100 105 110

```

Arg Ala Ile His Glu Glu Arg Arg Arg Gln Gln Pro Pro Leu Gly Pro
      115      120      125
Ser Ser Ser Leu Leu Ser Leu Pro Ser Leu Lys Ser Arg Gly Ser Arg
      130      135      140
Ala Val Gly Gly Ala Pro Ser Pro Pro Pro Val Arg Arg Ala Ser
145      150      155      160
Ala Gly Pro Val Pro Gly Ala Val Val Ile Ala Glu Gly Leu His Pro
      165      170      175
Ser Leu Pro Ser Pro Thr Gly Asn Ser Thr Pro Leu Gly Thr Ser Lys
      180      185      190
Glu Ile Arg Arg Gln Glu Lys Glu Arg Gln Lys Gln Glu Lys Asp Arg
      195      200      205
Glu Lys Glu Arg Gln Arg Gln Glu Lys Glu Arg Glu Arg Gln Glu Arg
210      215      220
Ser Gly Arg Ser Gly Lys Arg Ser Lys Arg Arg Asn Ser Arg Ser Arg
225      230      235      240
Arg Arg Ser Gly Arg Ser Trp Arg Arg Lys Ala Lys Ala Gly Asn Cys
      245      250      255
Pro Cys Val Glu Gly Gln Met Gly Pro Arg His Pro Met Met Val Gly
      260      265      270
Thr Gly Gln Gln Leu Arg Pro Gly Arg Met Leu Thr Phe Asp Leu Trp
      275      280      285
Leu Asp Leu Asp Gly Met Ala Leu Leu Leu Pro Leu Ile Glu Ser Ser
      290      295      300
Pro Gly Arg Leu Ser Gln Leu Pro Leu Ala Gly Ser Ser Phe Phe
305      310      315

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<210> 676
 <211> 94
 <212> PRT
 <213> Mouse

```

<400> 676
Met Phe Ser Glu Lys Lys His Phe Leu His Thr Ile Gln Asn Pro Glu
 1      5      10      15
Ser Glu Lys Glu Arg Arg Arg Arg Arg Arg Arg Arg Arg Ser Arg Arg
      20      25      30
Arg Glu Arg Lys Lys Glu Arg Lys Lys Glu Arg Lys Lys Glu Arg Lys
      35      40      45
Gln Ala Ser Leu Pro Ser Val Lys Arg Glu Arg Ala Trp His Gly Glu
      50      55      60
Gln Thr Gln Gly Ser Leu Ser Thr Val Arg Gln Glu Ser Ser Pro Gly
65      70      75      80
His Arg Ala Lys Val Ile Ala Asp Leu Gly Lys Asn Asp Gln
      85      90

```

<210> 677
 <211> 137
 <212> PRT
 <213> Mouse

```

<400> 677
Val Arg Trp Lys Met Arg Arg Ser Leu Arg Ala Gly Arg Arg Arg Gln
 1      5      10      15
Thr Ala Gly Arg Lys Ser Lys Ser Pro Pro Lys Val Pro Ile Val Ile
      20      25      30
Gln Asp Asp Ser Leu Pro Thr Gly Pro Pro Pro Gln Ile Arg Ile Leu

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```

          35          40          45
Lys Arg Pro Thr Ser Asn Gly Val Val Ser Ser Pro Asn Ser Thr Ser
  50          55          60
Arg Pro Ala Leu Pro Val Lys Ser Leu Ala Gln Arg Glu Ala Glu Tyr
  65          70          75          80
Ala Glu Ala Arg Arg Arg Ile Leu Gly Ser Ala Ser Pro Glu Glu Glu
          85          90          95
Gln Glu Lys Pro Ile Leu Asp Arg Pro Thr Arg Ile Ser Gln Pro Glu
          100          105          110
Asp Ser Arg Gln Pro Ser Asn Val Ile Arg Gln Pro Leu Gly Pro Asp
          115          120          125
Gly Ser Gln Gly Phe Lys Gln Arg Arg
          130          135

```

<210> 678
 <211> 380
 <212> PRT
 <213> Mouse

```

<400> 678
Glu Thr Thr Ile Thr Thr Asp Ser Arg Asp Tyr Gln Met Ala Lys Gly
  1          5          10          15
Lys Arg Lys Asn Leu Thr Asn Arg Asn Gln Asp His Ser Leu Ser Ser
          20          25          30
Glu Pro Ser Thr Pro Thr Ser Ala Ser Pro Gly Tyr Pro Asp Thr Pro
          35          40          45
Glu Lys Gln Asp Ser Asn Leu Lys Ser Tyr Leu Met Met Leu Val Glu
          50          55          60
Asp Ile Lys Lys Gly Phe Asn Asn Ser Leu Lys Glu Val Lys Glu Asn
          65          70          75          80
Thr Ala Lys Glu Val Glu Val Leu Lys Glu Ile Gln Glu Asn Thr Thr
          85          90          95
Lys Gln Val Met Glu Leu Asn Lys Ile Ile Gln Asp Leu Lys Arg Glu
          100          105          110
Val Glu Thr Lys Lys Thr Gln Asn Glu Thr Thr Leu Glu Ile Glu Thr
          115          120          125
Leu Val Lys Lys Ser Gly Thr Ile Asp Val Ser Ile Ser Asn Arg Ile
          130          135          140
Gln Glu Met Glu Glu Arg Ile Ser Gly Ala Glu Asp Ser Ile Glu Asn
          145          150          155          160
Ile Gly Thr Thr Thr Lys Glu Asn Ala Lys Arg Lys Lys Ile Leu Thr
          165          170          175
Gln Asn Ile Gln Lys Ile Gln Asp Lys Met Arg Arg Pro Asn Leu Trp
          180          185          190
Ile Ile Gly Val Asp Glu Asn Glu Asp Ser Gln Leu Lys Gly Pro Ala
          195          200          205
Asn Ile Phe Asn Lys Phe Ile Glu Glu Asn Phe Pro Asn Leu Lys Lys
          210          215          220
Glu Met Ser Met Asn Arg Gln Glu Ala Tyr Arg Thr Pro Asn Arg Leu
          225          230          235          240
Asp Gln Lys Arg Asn Ser Ser Leu His Ile Ile Ile Arg Thr Thr Asn
          245          250          255
Ala Leu Asn Lys Asp Arg Ile Leu Lys Ala Val Arg Glu Lys Ser Gln
          260          265          270
Val Thr Tyr Lys Gly Arg Pro Ile Arg Ile Thr Pro Asp Phe Ser Pro
          275          280          285
Glu Thr Met Lys Ala Arg Arg Ser Trp Thr Asp Val Met Gln Thr Leu

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      290              295              300
Arg Glu His Lys Cys Gln Pro Arg Leu Leu Tyr Pro Ala Lys Leu Ser
305              310              315              320
Ile Thr Ile Asp Gly Glu Thr Lys Val Phe His Asp Lys Thr Lys Phe
      325              330              335
Thr Gln Tyr Leu Ser Met Asn Pro Gly Leu Gln Arg Ile Ile Lys Gly
      340              345              350
Lys His Gln His Lys Asp Gly Asn Tyr Thr Leu Glu Lys Ala Arg Lys
      355              360              365
Arg Ser Phe Asn Lys Pro Lys Arg Arg Gln Pro Lys
      370              375              380

```

<210> 679
 <211> 210
 <212> PRT
 <213> Mouse

```

<400> 679
Tyr Gly Thr His Asn His Cys Trp Leu Ser Leu His Arg Gly Phe Ile
1              5              10              15
Trp Ser Phe Leu Gly Pro Ala Ala Ala Ile Ile Leu Ile Asn Leu Val
      20              25              30
Phe Tyr Phe Leu Ile Ile Trp Ile Leu Arg Ser Lys Leu Ser Ser Leu
      35              40              45
Asn Lys Glu Val Ser Thr Leu Gln Asp Thr Lys Val Met Thr Phe Lys
      50              55              60
Ala Ile Val Gln Leu Phe Val Leu Gly Cys Ser Trp Gly Ile Gly Leu
      65              70              75              80
Phe Ile Phe Ile Glu Val Gly Lys Thr Val Arg Leu Ile Val Ala Tyr
      85              90              95
Leu Phe Thr Ile Ile Asn Val Leu Gln Gly Val Leu Ile Phe Met Val
      100              105              110
His Cys Leu Leu Asn Arg Gln Val Arg Met Glu Tyr Lys Lys Trp Phe
      115              120              125
His Arg Leu Arg Lys Glu Val Glu Ser Glu Ser Thr Glu Val Ser His
      130              135              140
Ser Thr Thr His Thr Lys Met Gly Leu Ser Leu Asn Leu Glu Asn Phe
      145              150              155              160
Cys Pro Thr Gly Asn Leu His Asp Pro Ser Asp Ser Ile Leu Pro Ser
      165              170              175
Thr Glu Val Ala Gly Val Tyr Leu Ser Thr Pro Arg Ser His Met Gly
      180              185              190
Ala Glu Asp Val Asn Ser Gly Thr His Ala Tyr Trp Ser Arg Thr Ile
      195              200              205
Ser Asp
      210

```

<210> 680
 <211> 373
 <212> PRT
 <213> Mouse

```

<400> 680
Met Lys Glu Tyr Val Met Leu Leu Leu Leu Ala Val Cys Ser Ala Lys
1              5              10              15
Pro Phe Phe Ser Pro Ser His Thr Ala Leu Lys Asn Met Met Leu Lys
      20              25              30

```


Asp Met Glu Asp Thr Asp Asp Asp Asp Asn Asp Asp Asp Asp Asn Ser
 35 40 45
 Leu Phe Pro Thr Lys Glu Pro Val Asn Pro Phe Phe Pro Phe Asp Leu
 50 55 60
 Phe Pro Thr Cys Pro Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His
 65 70 75 80
 Cys Ser Asp Leu Gly Leu Thr Ser Val Pro Asn Asn Ile Pro Phe Asp
 85 90 95
 Thr Arg Met Val Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu
 100 105 110
 Asn Asp Phe Lys Gly Leu Thr Ser Leu Tyr Ala Leu Ile Leu Asn Asn
 115 120 125
 Asn Lys Leu Thr Lys Ile His Pro Lys Thr Phe Leu Thr Thr Lys Lys
 130 135 140
 Leu Arg Arg Leu Tyr Leu Ser His Asn Gln Leu Ser Glu Ile Pro Leu
 145 150 155 160
 Asn Leu Pro Lys Ser Leu Ala Glu Leu Arg Ile His Asp Asn Lys Val
 165 170 175
 Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met Asn Ala Leu His Val
 180 185 190
 Leu Glu Met Ser Ala Asn Pro Leu Glu Asn Asn Gly Ile Glu Pro Gly
 195 200 205
 Ala Phe Glu Gly Val Thr Val Phe His Ile Arg Ile Ala Glu Ala Lys
 210 215 220
 Leu Thr Ser Ile Pro Lys Gly Leu Pro Pro Thr Leu Leu Glu Leu His
 225 230 235 240
 Leu Asp Phe Asn Lys Ile Ser Thr Val Glu Leu Glu Asp Leu Lys Arg
 245 250 255
 Tyr Arg Glu Leu Gln Arg Leu Gly Leu Gly Asn Asn Arg Ile Thr Asp
 260 265 270
 Ile Glu Asn Gly Thr Phe Ala Asn Ile Pro Arg Val Arg Glu Ile His
 275 280 285
 Leu Glu His Asn Lys Leu Lys Lys Ile Pro Ser Gly Leu Gln Glu Leu
 290 295 300
 Lys Tyr Leu Gln Ile Ile Phe Leu His Tyr Asn Ser Ile Ala Lys Val
 305 310 315 320
 Gly Val Asn Asp Phe Cys Pro Thr Val Pro Lys Met Lys Lys Ser Leu
 325 330 335
 Tyr Ser Ala Ile Ser Leu Phe Asn Asn Pro Met Lys Tyr Trp Glu Ile
 340 345 350
 Gln Pro Ala Thr Phe Arg Cys Val Leu Gly Arg Met Ser Val Gln Leu
 355 360 365
 Gly Asn Val Gly Lys
 370

<210> 681
 <211> 466
 <212> PRT
 <213> Mouse

<400> 681
 Met Trp Gly Cys Trp Leu Gly Leu Leu Leu Leu Leu Ala Gly Gln
 1 5 10 15
 Ala Ala Leu Glu Ala Arg Arg Ser Arg Trp Arg Arg Glu Leu Ala Pro
 20 25 30
 Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys Gln
 35 40 45

Glu Gln Asp Met Cys Cys Arg Gly Arg Ala Asp Glu Cys Ala Leu Pro
 50 55 60
 Tyr Leu Gly Ala Thr Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr Val
 65 70 75 80
 Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Ile Pro Pro
 85 90 95
 Pro Phe Pro Pro Val Gln Gly Cys Met His Gly Gly Arg Ile Tyr Pro
 100 105 110
 Val Phe Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys His Glu
 115 120 125
 Gly Gly His Trp Glu Cys Asp Gln Glu Pro Cys Leu Val Asp Pro Asp
 130 135 140
 Met Ile Lys Ala Ile Asn Arg Gly Asn Tyr Gly Trp Gln Ala Gly Asn
 145 150 155 160
 His Ser Ala Phe Trp Gly Met Thr Leu Asp Glu Gly Ile Arg Tyr Arg
 165 170 175
 Leu Gly Thr Ile Arg Pro Ser Ser Thr Val Met Asn Met Asn Glu Ile
 180 185 190
 Tyr Thr Val Leu Gly Gln Gly Glu Val Leu Pro Thr Ala Phe Glu Ala
 195 200 205
 Ser Glu Lys Trp Pro Asn Leu Ile His Glu Pro Leu Asp Gln Gly Asn
 210 215 220
 Cys Ala Gly Ser Trp Ala Phe Ser Thr Ala Ala Val Ala Ser Asp Arg
 225 230 235 240
 Val Ser Ile His Ser Leu Gly His Met Thr Pro Ile Leu Ser Pro Gln
 245 250 255
 Asn Leu Leu Ser Cys Asp Thr His His Gln Gln Gly Cys Arg Gly Gly
 260 265 270
 Arg Leu Asp Gly Ala Trp Trp Phe Leu Arg Arg Arg Gly Val Val Ser
 275 280 285
 Asp Asn Cys Tyr Pro Phe Ser Gly Arg Glu Gln Asn Glu Ala Ser Pro
 290 295 300
 Thr Pro Arg Cys Met Met His Ser Arg Ala Met Gly Arg Gly Lys Arg
 305 310 315 320
 Gln Ala Thr Ser Arg Cys Pro Asn Gly Gln Val Asp Ser Asn Asp Ile
 325 330 335
 Tyr Gln Val Thr Pro Ala Tyr Arg Leu Gly Ser Asp Glu Lys Glu Ile
 340 345 350
 Met Lys Glu Leu Met Glu Asn Gly Pro Val Gln Ala Leu Met Glu Val
 355 360 365
 His Glu Asp Phe Phe Leu Tyr Gln Arg Gly Ile Tyr Ser His Thr Pro
 370 375 380
 Val Ser Gln Gly Arg Pro Glu Gln Tyr Arg Arg His Gly Thr His Ser
 385 390 395 400
 Val Lys Ile Thr Gly Trp Gly Glu Glu Thr Leu Pro Asp Gly Arg Thr
 405 410 415
 Ile Lys Tyr Trp Thr Ala Ala Asn Ser Trp Gly Pro Trp Trp Gly Glu
 420 425 430
 Arg Gly His Phe Arg Ile Val Arg Gly Thr Asn Glu Cys Asp Ile Glu
 435 440 445
 Thr Phe Val Leu Gly Val Trp Gly Arg Val Gly Met Glu Asp Met Gly
 450 455 460
 His His
 465

<210> 682

<211> 210

<212> PRT
<213> Mouse

<400> 682

```

Met Arg Leu Arg Leu Leu Ala Leu Ala Ala Val Leu Leu Gly Pro
 1           5           10           15
Ala Pro Glu Val Cys Gly Ala Leu Asn Val Thr Val Ser Pro Gly Pro
          20           25           30
Val Val Asp Tyr Leu Glu Gly Glu Asn Ala Thr Leu Leu Cys His Val
          35           40           45
Ser Gln Lys Arg Arg Lys Asp Ser Leu Leu Ala Val Arg Trp Phe Phe
          50           55           60
Ala Pro Asp Gly Ser Gln Glu Ala Leu Met Val Lys Met Thr Lys Leu
          65           70           75           80
Arg Ile Ile Gln Tyr Tyr Gly Asn Phe Ser Arg Thr Ala Asn Gln Gln
          85           90           95
Arg Leu Arg Leu Leu Glu Glu Arg Arg Gly Val Leu Tyr Arg Leu Ser
          100          105          110
Val Leu Thr Leu Arg Pro Thr Asp Gln Gly Gln Tyr Val Cys Lys Val
          115          120          125
Gln Glu Ile Ser Lys His Arg Asn Lys Trp Thr Ala Trp Ser Asn Gly
          130          135          140
Ser Ser Ala Thr Glu Met Arg Val Ile Ser Leu Lys Ala Gly Glu Asp
          145          150          155          160
Ser Ser Phe Glu Lys Lys Lys Val Thr Trp Ala Phe Phe Glu Asp Leu
          165          170          175
Tyr Val Tyr Ala Val Leu Val Cys Cys Val Gly Ile Leu Ser Val Leu
          180          185          190
Leu Phe Thr Leu Val Ile Ala Cys Ser Leu Cys Phe Thr Arg Gly Asn
          195          200          205
Gln Glu
          210

```

<210> 683
<211> 255
<212> PRT
<213> Mouse

<400> 683

```

Met Asp Phe Trp Leu Trp Leu Leu Tyr Phe Leu Pro Val Ser Gly Ala
 1           5           10           15
Leu Arg Val Leu Pro Glu Val Gln Leu Asn Val Glu Trp Gly Gly Ser
          20           25           30
Ile Ile Ile Glu Cys Pro Leu Pro Gln Leu His Val Arg Met Tyr Leu
          35           40           45
Cys Arg Gln Met Ala Lys Pro Gly Ile Cys Ser Thr Val Val Ser Asn
          50           55           60
Thr Phe Val Lys Lys Glu Tyr Glu Arg Arg Val Thr Leu Thr Pro Cys
          65           70           75           80
Leu Asp Lys Lys Leu Phe Leu Val Glu Met Thr Gln Leu Thr Glu Asn
          85           90           95
Asp Asp Gly Ile Tyr Ala Cys Gly Val Gly Met Lys Thr Asp Lys Gly
          100          105          110
Lys Thr Gln Lys Ile Thr Leu Asn Val His Asn Glu Tyr Pro Glu Pro
          115          120          125
Phe Trp Glu Asp Glu Trp Thr Ser Glu Arg Pro Arg Trp Leu His Arg
          130          135          140

```

Phe Leu Gln His Gln Met Pro Trp Leu His Gly Ser Glu His Pro Ser
 145 150 155 160
 Ser Ser Gly Val Ile Ala Lys Val Thr Thr Pro Ala Ser Lys Thr Glu
 165 170 175
 Ala Pro Pro Val His Gln Pro Ser Ser Ile Thr Ser Val Thr Gln His
 180 185 190
 Pro Arg Val Tyr Arg Ala Phe Ser Val Ser Ala Thr Lys Ser Pro Ala
 195 200 205
 Leu Leu Pro Ala Thr Thr Ala Ser Lys Thr Ser Thr Gln Gln Ala Ile
 210 215 220
 Arg Pro Leu Glu Ala Ser Tyr Ser His His Thr Arg Leu His Glu Gln
 225 230 235 240
 Arg Thr Arg His His Gly Pro His Tyr Gly Arg Glu Asp Arg Gly
 245 250 255

<210> 684
 <211> 228
 <212> PRT
 <213> Mouse

<400> 684
 Met Lys Ala Leu Arg Ala Val Leu Leu Ile Leu Leu Leu Ser Gly Gln
 1 5 10 15
 Pro Gly Ser Gly Trp Ala Gln Glu Asp Gly Asp Ala Asp Pro Glu Pro
 20 25 30
 Glu Asn Tyr Asn Tyr Asp Asp Asp Asp Glu Glu Glu Glu Glu Glu
 35 40 45
 Thr Asn Met Ile Pro Gly Ser Arg Asp Arg Ala Pro Leu Gln Cys Tyr
 50 55 60
 Phe Cys Gln Val Leu His Ser Gly Glu Ser Cys Asn Gln Thr Gln Ser
 65 70 75 80
 Cys Ser Ser Ser Lys Pro Phe Cys Ile Thr Leu Val Ser His Ser Gly
 85 90 95
 Thr Asp Lys Gly Tyr Leu Thr Thr Tyr Ser Met Trp Cys Thr Asp Thr
 100 105 110
 Cys Gln Pro Ile Ile Lys Thr Val Gly Gly Thr Gln Met Thr Gln Thr
 115 120 125
 Cys Cys Gln Ser Thr Leu Cys Asn Ile Pro Pro Trp Gln Asn Pro Gln
 130 135 140
 Val Gln Asn Pro Leu Gly Gly Arg Ala Asp Ser Pro Leu Glu Ser Gly
 145 150 155 160
 Thr Arg His Pro Gln Gly Gly Lys Phe Ser His Pro Gln Val Val Lys
 165 170 175
 Ala Ala His Pro Gln Ser Asp Gly Ala Asn Leu Pro Lys Ser Gly Lys
 180 185 190
 Ala Asn Gln Pro Gln Gly Ser Gly Ala Gly Tyr Pro Ser Gly Trp Thr
 195 200 205
 Lys Phe Gly Asn Ile Ala Leu Leu Ser Phe Phe Thr Cys Leu Trp
 210 215 220
 Ala Ser Gly Ala
 225

<210> 685
 <211> 242
 <212> PRT
 <213> Mouse

<400> 685

```

Met Ala Ser Gly Trp Phe Tyr Leu Ser Cys Met Val Leu Gly Ser Leu
 1          5          10          15
Gly Ser Met Cys Ile Leu Phe Thr Ala Tyr Trp Met Gln Tyr Trp Arg
          20          25          30
Gly Gly Phe Ala Trp Asp Gly Thr Val Leu Met Phe Asn Trp His Pro
          35          40          45
Val Leu Met Val Ala Gly Met Val Val Leu Tyr Gly Ala Ala Ser Leu
          50          55          60
Val Tyr Arg Leu Pro Ser Ser Trp Val Gly Pro Arg Leu Pro Trp Lys
          65          70          75          80
Val Leu His Ala Ala Leu His Leu Leu Ala Phe Thr Cys Thr Val Val
          85          90          95
Gly Leu Ile Ala Val Phe Arg Phe His Asn His Ser Arg Ile Ala His
          100          105          110
Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr Thr Val Val Leu Phe
          115          120          125
Ala Cys Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala
          130          135          140
Ser Gln Trp Leu Arg Ser Leu Leu Lys Pro Leu His Val Phe Phe Gly
          145          150          155          160
Ala Cys Ile Leu Ser Leu Ser Ile Thr Ser Val Ile Ser Gly Ile Asn
          165          170          175
Glu Lys Leu Phe Phe Val Leu Lys Asn Ala Thr Lys Pro Tyr Ser Ser
          180          185          190
Leu Pro Gly Glu Ala Val Phe Ala Asn Ser Thr Gly Leu Leu Val Val
          195          200          205
Ala Phe Gly Leu Leu Val Leu Tyr Val Leu Leu Ala Ser Ser Trp Lys
          210          215          220
Arg Pro Asp Pro Gly Ala Leu Thr Asp Arg Gln Pro Leu Leu His Asp
          225          230          235          240
Arg Glu

```

<210> 686

<211> 188

<212> PRT

<213> Mouse

<400> 686

```

Met Arg Leu Pro Leu Pro Leu Leu Leu Phe Gly Cys Arg Ala Ile
 1          5          10          15
Leu Gly Ser Ala Gly Asp Arg Val Ser Leu Ser Ala Ser Ala Pro Thr
          20          25          30
Leu Asp Asp Glu Glu Lys Tyr Ser Ala His Met Pro Ala His Leu Arg
          35          40          45
Cys Asp Ala Cys Arg Ala Val Ala Phe Gln Met Gly Gln Arg Leu Ala
          50          55          60
Lys Ala Glu Ala Lys Ser His Thr Pro Asp Ala Ser Gly Leu Gln Glu
          65          70          75          80
Leu Ser Glu Ser Thr Tyr Thr Asp Val Leu Asp Gln Thr Cys Ser Gln
          85          90          95
Asn Trp Gln Ser Tyr Gly Val His Glu Val Asn Gln Met Lys Arg Leu
          100          105          110
Thr Gly Pro Gly Leu Ser Lys Gly Pro Glu Pro Arg Ile Ser Val Met
          115          120          125
Ile Ser Gly Gly Pro Trp Pro Asn Arg Leu Ser Lys Thr Cys Phe His

```

```

      130      135      140
Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala Tyr Arg Gln
145      150      155      160
Gly Gln Ala Asn Leu Glu Ala Leu Leu Cys Gly Gly Thr His Gly Pro
      165      170      175
Cys Ser Gln Glu Ile Leu Ala Gln Arg Glu Glu Leu
      180      185

```

<210> 687
 <211> 247
 <212> PRT
 <213> Mouse

```

<400> 687
Met Ile Pro Gln Val Val Thr Ser Glu Thr Val Thr Val Ile Ser Pro
  1      5      10      15
Asn Gly Ile Ser Phe Pro Gln Thr Asp Lys Pro Gln Pro Ser His Gln
      20      25      30
Ser Gln Asp Arg Leu Lys Lys His Leu Lys Ala Glu Ile Lys Val Met
      35      40      45
Ala Ala Ile Gln Ile Met Cys Ala Val Met Val Leu Ser Leu Gly Ile
      50      55      60
Ile Leu Ala Ser Val Pro Ser Asn Leu His Phe Thr Ser Val Phe Ser
      65      70      75      80
Ile Leu Leu Glu Ser Gly Tyr Pro Phe Val Gly Ala Leu Phe Phe Ala
      85      90      95
Ile Ser Gly Ile Leu Ser Ile Val Thr Glu Lys Lys Met Thr Lys Pro
      100      105      110
Leu Val His Ser Ser Leu Ala Leu Ser Ile Leu Ser Val Leu Ser Ala
      115      120      125
Leu Thr Gly Ile Ala Ile Leu Ser Val Ser Leu Ala Ala Leu Glu Pro
      130      135      140
Ala Leu Gln Gln Cys Lys Leu Ala Phe Thr Gln Leu Asp Thr Thr Gln
      145      150      155      160
Asp Ala Tyr His Phe Phe Ser Pro Glu Pro Leu Asn Ser Cys Phe Val
      165      170      175
Ala Lys Ala Ala Leu Thr Gly Val Phe Ser Leu Met Leu Ile Ser Ser
      180      185      190
Val Leu Glu Leu Gly Leu Ala Val Leu Thr Ala Thr Leu Trp Trp Lys
      195      200      205
Gln Ser Ser Ser Ala Phe Ser Gly Asn Val Ile Phe Leu Ser Gln Asn
      210      215      220
Ser Lys Asn Lys Ser Ser Val Ser Ser Glu Ser Leu Cys Asn Pro Thr
      225      230      235      240
Tyr Glu Asn Ile Leu Thr Ser
      245

```

<210> 688
 <211> 121
 <212> PRT
 <213> Mouse

```

<400> 688
Tyr Gln Arg Arg Ser Lys Thr Leu Glu Glu Leu Ala Asn Asp Ile Lys
  1      5      10      15
Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Thr Lys Gly Ser Asp
      20      25      30

```

```

Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala
  35          40          45
Leu Arg Pro Pro Lys Ala Ala Pro Pro Arg Pro Gly Thr Phe Thr Pro
  50          55          60
Thr Pro Ser Val Ser Ser Gln Ala Leu Ser Ser Pro Arg Leu Pro Arg
  65          70          75          80
Val Asp Glu Pro Pro Pro Gln Ala Val Ser Leu Thr Pro Gly Gly Val
          85          90          95
Ser Ser Ser Ala Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro
          100          105          110
Ala Gln Ser Gln Ala Gly Ser Leu Val
          115          120

```

<210> 689
 <211> 255
 <212> PRT
 <213> Mouse

```

<400> 689
Pro Ala Phe Ser Ser Ala Ala Met Ser Trp Ser Pro Ile Leu Pro Phe
  1          5          10          15
Leu Ser Leu Leu Leu Leu Phe Pro Leu Glu Val Pro Arg Ala Ala
          20          25          30
Thr Ala Ser Leu Ser Gln Ala Ser Ser Glu Gly Thr Thr Thr Cys Lys
          35          40          45
Val His Asp Val Cys Leu Leu Gly Pro Arg Pro Leu Pro Pro Ser Pro
          50          55          60
Pro Val Arg Val Ser Leu Tyr Tyr Glu Ser Leu Cys Gly Ala Cys Arg
          65          70          75          80
Tyr Phe Leu Val Arg Asp Leu Phe Pro Thr Trp Leu Met Val Met Glu
          85          90          95
Ile Met Asn Ile Thr Leu Val Pro Tyr Gly Asn Ala Gln Glu Arg Asn
          100          105          110
Val Ser Gly Thr Trp Glu Phe Thr Cys Gln His Gly Glu Leu Glu Cys
          115          120          125
Arg Leu Asn Met Val Glu Ala Cys Leu Leu Asp Lys Leu Glu Lys Glu
          130          135          140
Ala Ala Phe Leu Thr Ile Val Cys Met Glu Glu Met Asp Asp Met Glu
          145          150          155          160
Lys Lys Leu Gly Pro Cys Leu Gln Val Tyr Ala Pro Glu Val Ser Pro
          165          170          175
Glu Ser Ile Met Glu Cys Ala Thr Gly Lys Arg Gly Thr Gln Leu Met
          180          185          190
His Glu Asn Ala Gln Leu Thr Asp Ala Leu His Pro Pro His Glu Tyr
          195          200          205
Val Pro Trp Val Leu Val Asn Glu Lys Pro Leu Lys Asp Pro Ser Glu
          210          215          220
Leu Leu Ser Ile Val Cys Gln Leu Asp Gln Gly Thr Glu Lys Pro Asp
          225          230          235          240
Ile Cys Ser Ser Ile Ala Asp Ser Pro Arg Lys Val Cys Tyr Lys
          245          250          255

```

<210> 690
 <211> 255
 <212> PRT
 <213> Mouse

<400> 690

```

Met Val Trp Thr Gln Asp Arg Leu His Asp Arg Gln Arg Val Val His
 1          5          10          15
Trp Asp Leu Ser Gly Asp Pro Gly Ser Gln Arg Arg Arg Leu Val Asp
          20          25          30
Met Tyr Ser Ala Gly Glu Gln Arg Val Tyr Glu Pro Arg Asp Arg Asp
          35          40          45
Arg Leu Leu Leu Ser Pro Ser Ala Phe His Asp Gly Asn Phe Ser Leu
 50          55          60
Leu Ile Arg Ala Val Glu Arg Gly Asp Glu Gly Val Tyr Thr Cys Asn
 65          70          75          80
Leu His His His Tyr Cys His Leu Asp Glu Ser Leu Ala Val Arg Leu
          85          90          95
Glu Val Thr Asp Asp Pro Leu Leu Ser Arg Ala Tyr Trp Asp Gly Glu
          100          105          110
Lys Glu Val Leu Val Val Ala His Gly Ala Pro Ala Leu Met Thr Cys
          115          120          125
Ile Asn Arg Ala His Val Trp Thr Asp Arg His Leu Glu Glu Ala Gln
          130          135          140
Gln Val Val His Trp Asp Arg Gln Leu Pro Gly Val Ser His Asp Arg
          145          150          155          160
Ala Asp Arg Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr
          165          170          175
Gly Pro Pro Phe Leu Arg Asp Arg Val Ser Val Asn Thr Asn Ala Phe
          180          185          190
Ala Arg Gly Asp Phe Ser Leu Arg Ile Asp Glu Leu Glu Arg Ala Asp
          195          200          205
Glu Gly Ile Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu His
          210          215          220
Glu Arg Arg Val Phe His Leu Gln Val Thr Glu Pro Ala Phe Glu Pro
          225          230          235          240
Pro Ala Arg Ala Ser Pro Gly Asn Gly Ser Gly His Ser Ser Ala
          245          250          255

```

<210> 691

<211> 255

<212> PRT

<213> Mouse

<400> 691

```

Met Lys Leu Lys Gln Arg Val Val Leu Leu Ala Ile Leu Leu Val Ile
 1          5          10          15
Phe Ile Phe Thr Lys Val Phe Leu Ile Asp Asn Leu Asp Thr Ser Ala
          20          25          30
Ala Asn Arg Glu Asp Gln Arg Ala Phe His Arg Met Met Thr Gly Leu
          35          40          45
Arg Val Glu Leu Val Pro Lys Leu Asp His Thr Leu Gln Ser Pro Trp
          50          55          60
Glu Ile Ala Ala Gln Trp Val Val Pro Arg Glu Val Tyr Pro Glu Glu
          65          70          75          80
Thr Pro Glu Leu Gly Ala Ile Met His Ala Met Ala Thr Lys Lys Ile
          85          90          95
Ile Lys Ala Asp Val Gly Tyr Lys Gly Thr Gln Leu Lys Ala Leu Leu
          100          105          110
Ile Leu Glu Gly Gly Gln Lys Val Val Phe Lys Pro Lys Arg Tyr Ser
          115          120          125
Arg Asp Tyr Val Val Glu Gly Glu Pro Tyr Ala Gly Tyr Asp Arg His
          125          130          135

```



```

      130              135              140
Asn Ala Glu Val Ala Ala Phe His Leu Asp Arg Ile Leu Gly Phe Arg
145              150              155              160
Arg Ala Pro Leu Val Val Gly Arg Tyr Val Asn Leu Arg Thr Glu Val
      165              170              175
Lys Pro Val Ala Thr Glu Gln Leu Leu Ser Thr Phe Leu Thr Val Gly
      180              185              190
Asn Asn Thr Cys Phe Tyr Gly Lys Cys Tyr Tyr Cys Arg Glu Thr Glu
      195              200              205
Pro Ala Cys Ala Asp Gly Asp Met Met Glu Gly Ser Val Thr Leu Trp
      210              215              220
Leu Pro Asp Val Trp Pro Leu Gln Lys His Arg His Pro Trp Gly Arg
225              230              235              240
Thr Tyr Arg Glu Gly Lys Leu Ala Arg Trp Glu Tyr Asp Glu Ser
      245              250              255

```

<210> 692

<211> 255

<212> PRT

<213> Mouse

<400> 692

```

Met Gln Thr Met Trp Gly Ser Gly Glu Leu Leu Val Ala Trp Phe Leu
1      5      10      15
Val Leu Ala Ala Asp Gly Thr Thr Glu His Val Tyr Arg Pro Ser Arg
      20      25      30
Arg Val Cys Thr Val Gly Ile Ser Gly Gly Ser Ile Ser Glu Thr Phe
      35      40      45
Val Gln Arg Val Tyr Gln Pro Tyr Leu Thr Thr Cys Asp Gly His Arg
      50      55      60
Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser
65      70      75      80
Pro Gly Val Thr Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp
      85      90      95
Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln
      100      105      110
Pro Pro Cys Gly Asn Gly Gly Ser Cys Ile Arg Pro Gly His Cys Arg
      115      120      125
Cys Pro Val Gly Trp Gln Gly Asp Thr Cys Gln Thr Asp Val Asp Glu
      130      135      140
Cys Ser Thr Gly Glu Ala Ser Cys Pro Gln Arg Cys Val Asn Thr Val
145      150      155      160
Gly Ser Tyr Trp Cys Gln Gly Trp Glu Gly Gln Ser Pro Ser Ala Asp
      165      170      175
Gly Thr Arg Cys Leu Ser Lys Glu Gly Pro Ser Pro Val Ala Pro Asn
      180      185      190
Pro Thr Ala Gly Val Asp Ser Met Ala Arg Glu Glu Val Tyr Arg Leu
      195      200      205
Gln Ala Arg Val Asp Val Leu Glu Gln Lys Leu Gln Leu Val Leu Ala
      210      215      220
Pro Leu His Ser Leu Ala Ser Arg Ser Thr Glu His Gly Leu Gln Asp
225      230      235      240
Pro Gly Ser Leu Leu Ala His Ser Phe Gln Gln Leu Asp Arg Ile
      245      250      255

```

<210> 693

<211> 255

<212> PRT

<213> Mouse

<400> 693

```

Met Arg Leu Thr Val Gly Ala Leu Leu Ala Cys Ala Ala Leu Gly Leu
 1           5           10           15
Cys Leu Ala Val Pro Asp Lys Thr Val Lys Trp Cys Ala Val Ser Glu
          20           25           30
His Glu Asn Thr Lys Cys Ile Ser Phe Arg Asp His Met Lys Thr Val
          35           40           45
Leu Pro Pro Asp Gly Pro Arg Leu Ala Cys Val Lys Lys Thr Ser Tyr
          50           55           60
Pro Asp Cys Ile Lys Ala Ile Ser Ala Ser Glu Ala Asp Ala Met Thr
          65           70           75           80
Leu Asp Gly Gly Trp Val Tyr Asp Ala Gly Leu Thr Pro Asn Asn Leu
          85           90           95
Lys Pro Val Ala Ala Glu Phe Tyr Gly Ser Val Glu His Pro Gln Thr
          100          105          110
Tyr Tyr Tyr Ala Val Ala Val Val Lys Lys Gly Thr Asp Phe Gln Leu
          115          120          125
Asn Gln Leu Glu Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser
          130          135          140
Ala Gly Trp Val Ile Pro Ile Gly Leu Leu Phe Cys Lys Leu Ser Glu
          145          150          155          160
Pro Arg Ser Pro Leu Glu Lys Ala Val Ser Ser Phe Phe Ser Gly Ser
          165          170          175
Cys Val Pro Cys Ala Asp Pro Val Ala Phe Pro Lys Leu Cys Gln Leu
          180          185          190
Cys Pro Gly Cys Gly Cys Ser Ser Thr Gln Pro Phe Phe Gly Tyr Val
          195          200          205
Gly Ala Phe Lys Cys Leu Lys Asp Gly Gly Gly Asp Val Ala Phe Val
          210          215          220
Lys His Thr Thr Ile Phe Glu Val Leu Pro Glu Lys Ala Asp Arg Asp
          225          230          235          240
Gln Tyr Glu Leu Leu Cys Leu Asp Asn Thr Arg Lys Pro Val Asp
          245          250          255

```

<210> 694

<211> 255

<212> PRT

<213> Mouse

<400> 694

```

Gly Ala Pro Thr Pro Ala Tyr Val Arg Ser Ala Arg Arg Thr Glu Pro
 1           5           10           15
Leu Ala Ser Gly Ala Arg Ser Arg Leu Cys Gln Cys Arg Arg Val Pro
          20           25           30
Ala Arg Lys Gln Gly Pro Gln Glu Gln Gly Gly Ser Gly Glu Ser Thr
          35           40           45
Thr Ser Ser Pro Gln Trp Trp Arg Arg Trp Arg Arg Leu Trp Ser Thr
          50           55           60
Cys Ser Cys Ser Ala Asp Asp Arg His Thr Gly Ser His Thr Asp Leu
          65           70           75           80
Lys Glu Glu Thr Pro Ser Trp Thr Gln Ile Ser Val Val Phe Arg Lys
          85           90           95
Asp Gly Gln Asp Glu Leu Gln Ala Ala His Lys Ala His Gly Ser Gly
          100          105          110

```

```

Ser Pro Leu Thr Asn Gln Glu Ile Pro Ser Ser Ser Gly Ser Gly Phe
      115      120      125
Ile Val Ser Glu Asp Gly Leu Ile Val Thr Asn Ala His Val Leu Thr
      130      135      140
Asn Gln Gln Lys Ile Gln Val Glu Leu Gln Ser Gly Ala Arg Tyr Glu
      145      150      155      160
Ala Thr Val Lys Asp Ile Asp His Lys Leu Asp Leu Ala Leu Ile Lys
      165      170      175
Ile Glu Pro Asp Thr Glu Leu Pro Val Leu Leu Leu Gly Arg Ser Ser
      180      185      190
Asp Leu Arg Ala Gly Glu Phe Val Val Ala Leu Gly Ser Pro Phe Ser
      195      200      205
Leu Gln Asn Thr Val Thr Ala Gly Ile Val Ser Thr Thr Gln Arg Gly
      210      215      220
Gly Arg Glu Leu Gly Leu Lys Asn Ser Asp Ile Asp Tyr Ile Gln Thr
      225      230      235      240
Asp Ala Ile Ile Asn His Gly Asn Ser Gly Gly Pro Leu Val Asn
      245      250      255

```

<210> 695
 <211> 174
 <212> PRT
 <213> Mouse

```

<400> 695
Met Pro Ala Cys Arg Leu Cys Leu Leu Ala Ala Gly Leu Leu Leu Gly
  1      5      10      15
Leu Leu Leu Phe Thr Pro Ile Ser Ala Thr Gly Thr Asp Ala Glu Lys
      20      25      30
Pro Gly Glu Cys Pro Gln Leu Glu Pro Ile Thr Asp Cys Val Leu Glu
      35      40      45
Cys Thr Leu Asp Lys Asp Cys Ala Asp Asn Arg Lys Cys Cys Gln Ala
      50      55      60
Gly Cys Ser Ser Val Cys Ser Lys Pro Asn Gly Pro Ser Glu Gly Glu
      65      70      75      80
Leu Ser Gly Thr Asp Thr Lys Leu Ser Glu Thr Gly Thr Thr Thr Gln
      85      90      95
Ser Ala Gly Leu Asp His Thr Thr Lys Pro Pro Gly Gly Gln Val Ser
      100      105      110
Thr Lys Pro Pro Ala Val Thr Arg Glu Gly Leu Gly Val Arg Glu Lys
      115      120      125
Gln Gly Thr Cys Pro Ser Val Asp Ile Pro Lys Leu Gly Leu Cys Glu
      130      135      140
Asp Gln Cys Gln Val Asp Ser Gln Cys Ser Gly Asn Met Lys Cys Cys
      145      150      155      160
Arg Asn Gly Cys Gly Lys Met Ala Cys Thr Thr Pro Lys Phe
      165      170

```

<210> 696
 <211> 193
 <212> PRT
 <213> Mouse

```

<400> 696
Leu Ala Thr Leu Val Gln Val Ser Arg Ile Arg Ala Tyr Ser Gln Gly
  1      5      10      15
Gln Thr Gln Asp Gln Gln Gly Ser Ser Ser Leu Asp Lys Val Ala Val

```

```

                20                25                30
Pro Arg Glu Gln Thr His Ser Gly Leu Glu Gln Ile Gln Gln Ile Gln
      35                40                45
Gln Gln Leu Thr Gln Phe Asn Ala Ser Leu Ala Gly Leu Cys Arg Pro
      50                55                60
Cys Pro Trp Asp Trp Glu Leu Phe Gln Gly Ser Cys Tyr Leu Phe Ser
      65                70                75                80
Arg Thr Leu Gly Ser Trp Glu Thr Ser Ala Ser Ser Cys Glu Asp Leu
      85                90                95
Gly Ala His Leu Val Ile Val Asn Ser Val Ser Glu Gln Arg Phe Met
      100                105                110
Lys Tyr Trp Asn Val Arg Lys Asn Gln Arg Ser Trp Ile Gly Leu Ser
      115                120                125
Asp His Ile His Glu Gly Ser Trp Gln Trp Val Asp Gly Ser Ala Leu
      130                135                140
Lys Phe Ser Phe Trp Lys Glu Gly Glu Pro Asn Asn Asp Gly Asp Glu
      145                150                155                160
Asp Cys Val Glu Leu Phe Met Asp Asp Trp Asn Asp Asn Lys Cys Thr
      165                170                175
Glu Gln Asn Phe Trp Val Cys Glu Gln Pro Ser Ala Pro Cys Pro His
      180                185                190
His

```

<210> 697
 <211> 173
 <212> PRT
 <213> Mouse

```

<400> 697
Val Arg Asn Gly Asp Leu Phe Phe Lys Lys Val Gln Val Glu Asp Gly
  1                5                10                15
Gly Val Tyr Thr Cys Tyr Ala Met Gly Glu Thr Phe Asn Glu Thr Leu
      20                25                30
Ser Val Glu Leu Lys Val Tyr Asn Phe Thr Leu His Gly His His Asp
      35                40                45
Thr Leu Asn Thr Ala Tyr Thr Thr Leu Val Gly Cys Ile Leu Ser Val
      50                55                60
Val Leu Val Leu Ile Tyr Leu Tyr Leu Thr Pro Cys Arg Cys Trp Cys
      65                70                75                80
Arg Gly Val Glu Lys Pro Ser Ser His Gln Gly Asp Ser Leu Ser Ser
      85                90                95
Ser Met Leu Ser Thr Thr Pro Asn His Asp Pro Met Ala Gly Gly Asp
      100                105                110
Lys Asp Asp Gly Phe Asp Arg Arg Val Ala Phe Leu Glu Pro Ala Gly
      115                120                125
Pro Gly Gln Gly Gln Asn Gly Lys Leu Lys Pro Gly Asn Thr Leu Pro
      130                135                140
Val Pro Glu Ala Thr Gly Lys Gly Gln Arg Arg Met Ser Asp Pro Glu
      145                150                155                160
Ser Val Ser Ser Val Phe Ser Asp Thr Pro Ile Val Val
      165                170

```

<210> 698
 <211> 88
 <212> PRT
 <213> Mouse

<400> 698

```

Met Glu Glu Ile Thr Cys Ala Phe Leu Leu Leu Ala Gly Leu Pro
 1           5           10           15
Ala Leu Glu Ala Ser Asp Pro Val Asp Lys Asp Ser Pro Phe Tyr Tyr
 20           25           30
Asp Trp Glu Ser Leu Gln Leu Gly Gly Leu Ile Phe Gly Gly Leu Leu
 35           40           45
Cys Ile Ala Gly Ile Ala Met Ala Leu Ser Gly Lys Cys Lys Cys Arg
 50           55           60
Arg Thr His Lys Pro Ser Ser Leu Pro Gly Lys Ala Thr Pro Leu Ile
 65           70           75           80
Ile Pro Gly Ser Ala Asn Thr Cys
                        85

```

<210> 699

<211> 155

<212> PRT

<213> Mouse

<400> 699

```

Met Tyr Ser Glu Gly Ala Pro Phe Trp Thr Gly Ile Val Ala Met Leu
 1           5           10           15
Ala Gly Ala Val Ala Phe Leu His Lys Lys Arg Gly Gly Thr Cys Trp
 20           25           30
Ala Leu Met Arg Thr Leu Leu Val Leu Ala Ser Phe Cys Thr Ala Val
 35           40           45
Ala Ala Ile Val Ile Gly Ser Arg Glu Leu Asn Tyr Tyr Trp Tyr Phe
 50           55           60
Leu Gly Asp Asp Val Cys Gln Arg Asp Ser Ser Tyr Gly Trp Ser Thr
 65           70           75           80
Met Pro Arg Thr Thr Pro Val Pro Glu Glu Ala Asp Arg Ile Ala Leu
 85           90           95
Cys Ile Tyr Tyr Thr Ser Met Leu Lys Thr Leu Leu Met Ser Leu Gln
100           105           110
Ala Met Leu Leu Gly Ile Trp Val Leu Leu Leu Ala Ser Leu Thr
115           120           125
Pro Val Cys Val Tyr Ile Trp Lys Arg Phe Phe Thr Lys Ala Glu Thr
130           135           140
Glu Glu Lys Lys Leu Leu Gly Ala Ala Val Ile
145           150           155

```

<210> 700

<211> 255

<212> PRT

<213> Mouse

<400> 700

```

Met Leu Gln His Thr Ser Leu Val Leu Leu Leu Ala Ser Ile Trp Thr
 1           5           10           15
Thr Arg His Pro Val Gln Gly Ala Asp Leu Val Gln Asp Leu Ser Ile
 20           25           30
Ser Thr Cys Arg Ile Met Gly Val Ala Leu Val Gly Arg Asn Lys Asn
 35           40           45
Pro Gln Met Asn Phe Thr Glu Ala Asn Glu Ala Cys Lys Met Leu Gly
 50           55           60
Leu Thr Leu Ala Ser Arg Asp Gln Val Glu Ser Ala Gln Lys Ser Gly

```

```

65          70          75          80
Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Glu Gln Phe Ser Val Ile
      85          90
Pro Arg Ile Phe Ser Asn Pro Arg Cys Gly Lys Asn Gly Lys Gly Val
      100      105      110
Leu Ile Trp Asn Ala Pro Ser Ser Gln Lys Phe Lys Ala Tyr Cys His
      115      120      125
Asn Ser Ser Asp Thr Trp Val Asn Ser Cys Ile Pro Glu Ile Val Thr
      130      135      140
Thr Phe Tyr Pro Val Leu Asp Thr Gln Thr Pro Ala Thr Glu Phe Ser
145      150      155      160
Val Ser Ser Ser Ala Tyr Leu Ala Ser Ser Pro Asp Ser Thr Thr Pro
      165      170      175
Val Ser Ala Thr Thr Arg Ala Pro Pro Leu Thr Ser Met Ala Arg Lys
      180      185      190
Thr Lys Lys Ile Cys Ile Thr Glu Val Tyr Thr Glu Pro Ile Thr Met
      195      200      205
Ala Thr Glu Thr Glu Ala Phe Val Ala Ser Gly Ala Ala Phe Lys Asn
      210      215      220
Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu Leu Val Leu Ala
225      230      235      240
Leu Leu Phe Phe Gly Ala Ala Ala Val Leu Ala Val Cys Tyr Val
      245      250      255

```

<210> 701
 <211> 91
 <212> PRT
 <213> Mouse

```

<400> 701
Met Val Trp Ala Asn Leu Ala Val Phe Val Ile Cys Phe Leu Pro Leu
 1          5          10          15
His Val Val Leu Thr Val Gln Val Ser Leu Asn Leu Asn Thr Cys Ala
      20      25      30
Ala Arg Asp Thr Phe Ser Arg Ala Leu Ser Ile Thr Gly Lys Leu Ser
      35      40      45
Asp Thr Asn Cys Cys Leu Asp Ala Ile Cys Tyr Tyr Tyr Met Ala Arg
      50      55      60
Glu Phe Gln Glu Ala Ser Lys Pro Ala Thr Ser Ser Asn Thr Pro His
65          70          75          80
Lys Ser Gln Asp Ser Gln Ile Leu Ser Leu Thr
      85          90

```

<210> 702
 <211> 244
 <212> PRT
 <213> Mouse

```

<400> 702
Gly Trp Gln Gly Ala Pro Asp Pro Arg Gly Leu Gly Gln Leu Ser Gln
 1          5          10          15
Pro Tyr Met Gly Gly Glu Met Pro Trp Thr Ile Leu Leu Phe Ala Ser
      20      25      30
Gly Ser Leu Ala Ile Pro Ala Pro Ser Ile Ser Leu Val Pro Pro Tyr
      35      40      45
Pro Ser Ser His Glu Asp Pro Ile Tyr Ile Ser Cys Thr Ala Pro Gly
50          55          60

```

```

Asp Ile Leu Gly Ala Asn Phe Thr Leu Phe Arg Gly Gly Glu Val Val
65      70      75      80
Gln Leu Leu Gln Ala Pro Ser Asp Arg Pro Asp Val Thr Phe Asn Val
      85      90      95
Thr Gly Gly Gly Ser Gly Gly Gly Gly Glu Ala Ala Gly Gly Asn Phe
      100      105      110
Cys Cys Gln Tyr Gly Val Met Gly Glu His Ser Gln Pro Gln Leu Ser
      115      120      125
Asp Phe Ser Gln Gln Val Gln Val Ser Phe Pro Val Pro Thr Trp Ile
      130      135      140
Leu Ala Leu Ser Leu Ser Leu Ala Gly Ala Val Leu Phe Ser Gly Leu
      145      150      155      160
Val Ala Ile Thr Val Leu Val Arg Lys Ala Lys Ala Lys Asn Leu Gln
      165      170      175
Lys Gln Arg Glu Arg Glu Ser Cys Trp Ala Gln Ile Asn Phe Thr Asn
      180      185      190
Thr Asp Met Ser Phe Asp Asn Ser Leu Phe Ala Ile Ser Thr Lys Met
      195      200      205
Thr Gln Glu Asp Ser Val Ala Thr Leu Asp Ser Gly Pro Arg Lys Arg
      210      215      220
Pro Thr Ser Ala Ser Ser Pro Glu Pro Pro Glu Phe Ser Thr Phe
      225      230      235      240
Arg Ala Cys Gln

```

```

<210> 703
<211> 255
<212> PRT
<213> Mouse

```

```

<400> 703
Met Ala Gln Leu Ala Arg Ala Thr Arg Ser Pro Leu Ser Trp Leu Leu
1      5      10      15
Leu Leu Phe Cys Tyr Ala Leu Arg Lys Ala Gly Gly Asp Ile Arg Val
      20      25      30
Leu Val Pro Tyr Asn Ser Thr Gly Val Leu Gly Gly Ser Thr Thr Leu
      35      40      45
His Cys Ser Leu Thr Ser Asn Glu Asn Val Thr Ile Thr Gln Ile Thr
      50      55      60
Trp Met Lys Lys Asp Ser Gly Gly Ser His Ala Leu Val Ala Val Phe
      65      70      75      80
His Pro Lys Lys Gly Pro Asn Ile Lys Glu Pro Glu Arg Val Lys Phe
      85      90      95
Leu Ala Ala Gln Gln Asp Leu Arg Asn Ala Ser Leu Ala Ile Ser Asn
      100      105      110
Leu Ser Val Glu Asp Glu Gly Ile Tyr Glu Cys Gln Ile Ala Thr Phe
      115      120      125
Pro Arg Gly Ser Arg Ser Thr Asn Ala Trp Leu Lys Val Gln Ala Arg
      130      135      140
Pro Lys Asn Thr Ala Glu Ala Leu Glu Pro Ser Pro Thr Leu Ile Leu
      145      150      155      160
Gln Asp Val Ala Lys Cys Ile Ser Ala Asn Gly His Pro Pro Gly Arg
      165      170      175
Ile Ser Trp Pro Ser Asn Val Asn Gly Ser His Arg Glu Met Lys Glu
      180      185      190
Pro Gly Ser Gln Pro Gly Thr Thr Thr Val Thr Ser Tyr Leu Ser Met
      195      200      205

```

Val Pro Ser Arg Gln Ala Asp Gly Lys Asn Ile Thr Cys Thr Val Glu
 210 215 220
 His Glu Ser Leu Gln Glu Leu Asp Gln Leu Leu Val Thr Leu Ser Gln
 225 230 235 240
 Pro Tyr Pro Pro Glu Asn Val Ser Ile Ser Gly Tyr Asp Gly Asn
 245 250 255

<210> 704
 <211> 255
 <212> PRT
 <213> Mouse

<400> 704
 Met Phe Leu Val Gly Ser Leu Val Val Leu Cys Gly Leu Leu Ala His
 1 5 10 15
 Ser Thr Ala Gln Leu Ala Gly Leu Pro Leu Pro Leu Gly Gln Gly Pro
 20 25 30
 Pro Leu Pro Leu Asn Gln Gly Pro Pro Leu Pro Leu Asn Gln Gly Gln
 35 40 45
 Leu Leu Pro Leu Ala Gln Gly Leu Pro Leu Ala Val Ser Pro Ala Leu
 50 55 60
 Pro Ser Asn Pro Thr Asp Leu Leu Ala Gly Lys Phe Thr Asp Ala Leu
 65 70 75 80
 Ser Gly Gly Leu Leu Ser Gly Gly Leu Leu Gly Ile Leu Glu Asn Ile
 85 90 95
 Pro Leu Leu Asp Val Ile Lys Ser Gly Gly Gly Asn Ser Asn Gly Leu
 100 105 110
 Val Gly Gly Leu Leu Gly Lys Leu Thr Ser Ser Val Pro Leu Leu Asn
 115 120 125
 Asn Ile Leu Asp Ile Lys Ile Thr Asp Pro Gln Leu Leu Glu Leu Gly
 130 135 140
 Leu Val Gln Ser Pro Asp Gly His Arg Leu Tyr Val Thr Ile Pro Leu
 145 150 155 160
 Gly Leu Thr Leu Asn Val Asn Met Pro Val Val Gly Ser Leu Leu Gln
 165 170 175
 Leu Ala Val Lys Leu Asn Ile Thr Ala Glu Val Leu Ala Val Lys Asp
 180 185 190
 Asn Gln Gly Arg Ile His Leu Val Leu Gly Asp Cys Thr His Ser Pro
 195 200 205
 Gly Ser Leu Lys Ile Ser Leu Leu Asn Gly Val Thr Pro Val Gln Ser
 210 215 220
 Phe Leu Asp Asn Leu Thr Gly Ile Leu Thr Lys Val Leu Pro Glu Leu
 225 230 235 240
 Ile Gln Gly Lys Val Cys Pro Leu Val Asn Gly Ile Leu Ser Gly
 245 250 255

<210> 705
 <211> 255
 <212> PRT
 <213> Mouse

<400> 705
 Met Ala Thr Thr Thr Cys Gln Val Val Gly Leu Leu Leu Ser Leu Leu
 1 5 10 15
 Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
 20 25 30
 Gln Asp Leu Tyr Asp Asn Pro Val Thr Ala Val Phe Gln His Glu Gly


```

      35      40      45
Leu Trp Arg Ser Cys Val Gln Gln Ser Ser Gly Phe Thr Glu Cys Arg
 50      55      60
Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
 65      70      75      80
Ala Leu Met Ile Val Gly Ile Val Leu Gly Val Ile Gly Ile Leu Val
      85      90      95
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Asp Asp Ser
      100      105      110
Ala Lys Ala Lys Met Thr Leu Thr Ser Gly Ile Leu Phe Ile Ile Ser
      115      120      125
Gly Ile Cys Ala Ile Ile Gly Val Ser Val Phe Ala Asn Met Leu Val
      130      135      140
Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Ser Gly Met Gly Gly
 145      150      155      160
Met Gly Gly Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala
      165      170      175
Ala Leu Phe Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly
      180      185      190
Val Met Met Cys Ile Ala Cys Arg Gly Leu Thr Pro Asp Asp Ser Asn
      195      200      205
Phe Lys Ala Val Ser Tyr His Ala Ser Gly Gln Asn Val Ala Tyr Arg
      210      215      220
Pro Gly Gly Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Arg Asn
      225      230      235      240
Lys Lys Ile Tyr Asp Gly Gly Ala Arg Thr Glu Asp Asp Glu Gln
      245      250      255

```

<210> 706

<211> 255

<212> PRT

<213> Mouse

<400> 706

```

Met Gly Arg Phe Ala Ala Ala Leu Val Gly Ser Leu Phe Trp Leu Gly
 1      5      10      15
Leu Leu Leu Cys Gly Leu Gly Ser Leu Ala Ser Ala Glu Pro Arg Ala
      20      25      30
Pro Pro Asn Arg Ile Ala Ile Val Gly Ala Gly Ile Gly Gly Thr Ser
      35      40      45
Ser Ala Tyr Tyr Leu Arg Lys Lys Phe Gly Lys Asp Val Lys Ile Asp
      50      55      60
Val Phe Glu Arg Glu Glu Val Gly Gly Arg Leu Ala Thr Leu Lys Val
      65      70      75      80
Gln Gly His Asp Tyr Glu Ala Gly Gly Ser Val Ile His Pro Leu Asn
      85      90      95
Leu His Met Lys Arg Phe Val Lys Glu Leu Gly Leu Ser Ser Val Pro
      100      105      110
Ala Ser Gly Gly Leu Val Gly Val Tyr Asn Gly Lys Ser Leu Val Phe
      115      120      125
Glu Glu Ser Ser Trp Phe Val Ile Asn Val Ile Lys Leu Val Trp Arg
      130      135      140
Tyr Gly Phe Gln Ser Leu Arg Met His Met Trp Val Glu Asp Leu Leu
      145      150      155      160
Asp Lys Phe Met Arg Ile Tyr Arg Tyr Gln Ser His Asp Tyr Ala Phe
      165      170      175
Ser Ser Val Glu Lys Leu Met His Ala Ile Gly Gly Asp Asp Tyr Val

```

```

      180      185      190
Arg Leu Leu Asn Gln Thr Leu Arg Glu Asn Leu Lys Lys Ala Gly Phe
      195      200      205
Ser Glu Thr Phe Leu Asn Glu Met Ile Ala Pro Val Met Lys Val Asn
      210      215      220
Tyr Gly Gln Ser Thr Asp Ile Asn Ala Phe Val Gly Ala Val Ser Leu
      225      230      235      240
Thr Ala Ala Asp Ser Asn Leu Trp Ala Val Glu Gly Gly Asn Lys
      245      250      255

```

<210> 707
 <211> 150
 <212> PRT
 <213> Mouse

```

<400> 707
Met Ser Trp Trp Arg Asp Asn Phe Trp Ile Ile Leu Ala Met Ser Ile
  1      5      10      15
Ile Phe Ile Ser Leu Val Leu Gly Leu Ile Leu Tyr Cys Val Cys Arg
      20      25      30
Trp Gln Leu Arg Gln Gly Arg Asn Trp Glu Ile Ala Lys Pro Ser Lys
      35      40      45
Gln Asp Gly Arg Asp Glu Glu Lys Met Tyr Glu Asn Val Leu Asn Ser
      50      55      60
Ser Pro Gly Gln Leu Pro Ala Leu Pro Pro Arg Gly Ser Pro Phe Pro
      65      70      75      80
Gly Asp Leu Ala Pro Gln Glu Ala Pro Arg Gln Pro Ser Ala Trp Tyr
      85      90      95
Ser Ser Val Lys Lys Val Arg Asn Lys Lys Val Phe Ala Ile Ser Gly
      100      105      110
Ser Thr Glu Pro Glu Asn Asp Tyr Asp Asp Val Glu Ile Pro Ala Thr
      115      120      125
Thr Glu Thr Gln His Ser Lys Thr Thr Pro Phe Trp Gln Ala Glu Val
      130      135      140
Gly Leu His Ser Ser Phe
      145      150

```

<210> 708
 <211> 114
 <212> PRT
 <213> Mouse

```

<400> 708
Met Phe Leu Val Tyr Phe Ser Arg Arg Gly His Cys Ile Asn Tyr Val
  1      5      10      15
Lys Gly His Ala Asp Ser Leu Ala Pro Trp Cys Cys Gly Val Gly Leu
      20      25      30
Arg Ser Pro Leu Ala Arg Pro Gln His Gly His Val Ser Pro Lys Asp
      35      40      45
His Val Pro Gly Gly His Ala Pro Gly Pro Ser His Lys Trp Leu Cys
      50      55      60
Thr Ala Ala Leu Trp Arg Tyr Leu Glu His Ser Ala Val Thr His Gly
      65      70      75      80
Thr Ala Leu Pro Glu Ala His Ala Val Arg Gly Lys His Gly Lys Lys
      85      90      95
Gly Arg Arg Val Val Cys Cys Ser Val Asp Phe Pro Gln Ala Thr Ser
      100      105      110

```

Leu Phe

<210> 709
 <211> 132
 <212> PRT
 <213> Mouse

<400> 709

Ala His Pro Arg Pro Gly Ala Arg Arg Pro Arg Leu Leu Ala Phe Gln
 1 5 10 15
 Ala Ser Cys Ala Pro Ala Pro Gly Ser Arg Asp Arg Cys Pro Glu Glu
 20 25 30
 Gly Gly Pro Arg Cys Leu Arg Val Tyr Ala Gly Leu Ile Gly Thr Val
 35 40 45
 Val Thr Pro Asn Tyr Leu Asp Asn Val Ser Ala Arg Val Ala Pro Trp
 50 55 60
 Cys Gly Cys Ala Ala Ser Gly Asn Arg Arg Glu Glu Cys Glu Ala Phe
 65 70 75 80
 Arg Lys Leu Phe Thr Arg Asn Pro Cys Leu Asp Gly Ala Ile Gln Ala
 85 90 95
 Phe Asp Ser Leu Gln Pro Ser Val Leu Gln Asp Gln Thr Ala Gly Cys
 100 105 110
 Cys Phe Pro Arg Val Ser Trp Leu Tyr Ala Leu Thr Ala Leu Ala Leu
 115 120 125
 Gln Ala Leu Leu
 130

<210> 710
 <211> 255
 <212> PRT
 <213> Mouse

<400> 710

Met Arg Val Leu Trp Val Leu Gly Leu Cys Cys Val Leu Leu Thr Phe
 1 5 10 15
 Gly Phe Val Arg Ala Asp Asp Glu Val Asp Val Asp Gly Thr Val Glu
 20 25 30
 Glu Asp Leu Gly Lys Ser Arg Glu Gly Ser Arg Thr Asp Asp Glu Val
 35 40 45
 Val Gln Arg Glu Glu Glu Ala Ile Gln Leu Asp Gly Leu Asn Ala Ser
 50 55 60
 Gln Ile Arg Glu Leu Arg Glu Lys Ser Glu Lys Phe Ala Phe Gln Ala
 65 70 75 80
 Glu Val Asn Arg Met Met Lys Leu Ile Ile Asn Ser Leu Tyr Lys Asn
 85 90 95
 Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu
 100 105 110
 Asp Lys Ile Arg Leu Ile Ser Leu Thr Asp Glu Asn Ala Leu Ala Gly
 115 120 125
 Asn Glu Glu Leu Thr Val Lys Ile Lys Cys Asp Lys Glu Lys Asn Leu
 130 135 140
 Leu His Val Thr Asp Thr Gly Val Gly Met Thr Arg Glu Glu Leu Val
 145 150 155 160
 Lys Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Ser Glu Phe Leu Asn
 165 170 175
 Lys Met Thr Glu Ala Gln Glu Asp Gly Gln Ser Thr Ser Glu Leu Ile

```

      180      185      190
Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu Val Ala Asp Lys
      195      200      205
Val Ile Val Thr Ser Lys His Asn Asn Asp Thr Gln His Ile Trp Glu
      210      215      220
Ser Asp Ser Asn Glu Phe Ser Val Ile Ala Asp Pro Arg Gly Asn Thr
      225      230      235      240
Leu Gly Arg Gly Thr Thr Ile Thr Leu Val Leu Lys Glu Glu Ala
      245      250      255

```

<210> 711
 <211> 224
 <212> PRT
 <213> Mouse

```

<400> 711
Met Ala Leu Leu Ile Ser Leu Pro Gly Gly Thr Pro Ala Met Ala Gln
  1      5      10      15
Val Leu Leu Leu Leu Ser Ser Gly Cys Leu His Ala Gly Asn Ser Glu
      20      25      30
Arg Tyr Asn Arg Lys Asn Gly Phe Gly Val Asn Gln Pro Glu Arg Cys
      35      40      45
Ser Gly Val Gln Gly Gly Ser Ile Asp Ile Pro Phe Ser Phe Tyr Phe
      50      55      60
Pro Trp Lys Leu Ala Lys Asp Pro Gln Met Ser Ile Ala Trp Lys Trp
      65      70      75      80
Lys Asp Phe His Gly Glu Val Ile Tyr Asn Ser Ser Leu Pro Phe Ile
      85      90      95
His Glu His Phe Lys Gly Arg Leu Ile Leu Asn Trp Thr Gln Gly Gln
      100      105      110
Thr Ser Gly Val Leu Arg Ile Leu Asn Leu Lys Glu Ser Asp Gln Ala
      115      120      125
Gln Tyr Phe Ser Arg Val Asn Leu Gln Ser Thr Glu Gly Met Lys Leu
      130      135      140
Trp Gln Ser Ile Pro Gly Thr Gln Leu Asn Val Thr Gln Ala Leu Asn
      145      150      155      160
Thr Thr Met Arg Ser Pro Phe Ile Val Thr Ser Glu Phe Thr Thr Ala
      165      170      175
Gly Leu Glu His Thr Ser Asp Gln Arg Asn Pro Ser Leu Met Asn Leu
      180      185      190
Gly Ala Met Val Thr Met Leu Leu Ala Lys Val Leu Val Ile Val Leu
      195      200      205
Val Tyr Gly Trp Met Ile Phe Leu Arg Trp Lys Gln Arg Pro Ala His
      210      215      220

```

<210> 712
 <211> 133
 <212> PRT
 <213> Mouse

```

<400> 712
Met Ala Leu Pro Trp Thr Ile Leu Leu Ala Leu Ser Gly Ile Tyr Val
  1      5      10      15
Gln Gly Ala Gln Ala Trp Cys Ser Glu Glu Asp Thr Leu Glu Leu Asp
      20      25      30
Lys Leu Val Ser Glu Pro Asp Ile Val Lys Phe Ala Leu Ser Ala Phe
      35      40      45

```

His Lys Lys Ser Lys Asp Glu Tyr Ala Tyr Arg Val Ile His Ile Met
 50 55 60
 Asn Phe Leu Lys Val Gln Glu Glu Pro Pro Gln Thr Phe Phe Val Lys
 65 70 75 80
 Leu Arg Leu Thr Arg Thr Ile Cys Met Lys Phe Glu Lys Ser Leu Asp
 85 90 95
 Thr Cys Pro Leu Pro Glu Leu Gln Asn Ile Leu Ile Cys Ser Phe Ser
 100 105 110
 Ile Ser Ser Pro Gly Ser Lys Gln Phe Asn Leu Leu Lys Met Thr Cys
 115 120 125
 Ser Glu Gly Leu Leu
 130

<210> 713
 <211> 255
 <212> PRT
 <213> Mouse

<400> 713
 Glu Glu Glu Asp Leu Arg Arg Arg Leu Lys Tyr Phe Phe Met Ser Pro
 1 5 10 15
 Cys Asp Lys Phe Arg Ala Lys Gly Arg Lys Pro Cys Lys Leu Met Leu
 20 25 30
 Gln Val Val Lys Ile Leu Val Val Thr Val Gln Leu Ile Leu Phe Gly
 35 40 45
 Leu Ser Asn Gln Leu Val Val Thr Phe Arg Glu Glu Asn Thr Ile Ala
 50 55 60
 Phe Arg His Leu Phe Leu Leu Gly Tyr Ser Asp Gly Ser Asp Asp Thr
 65 70 75 80
 Phe Ala Ala Tyr Thr Gln Glu Gln Leu Tyr Gln Ala Ile Phe Tyr Ala
 85 90 95
 Val Asp Gln Tyr Leu Ile Leu Pro Glu Ile Ser Leu Gly Arg Tyr Ala
 100 105 110
 Tyr Val Arg Gly Gly Gly Gly Pro Trp Ala Asn Gly Ser Ala Leu Ala
 115 120 125
 Leu Cys Gln Arg Tyr Tyr His Arg Gly His Val Asp Pro Ala Asn Asp
 130 135 140
 Thr Phe Asp Ile Asp Pro Arg Val Val Thr Asp Cys Ile Gln Val Asp
 145 150 155 160
 Pro Pro Asp Arg Pro Pro Asp Ile Pro Ser Glu Asp Leu Asp Phe Leu
 165 170 175
 Asp Gly Ser Ala Ser Tyr Lys Asn Leu Thr Leu Lys Phe His Lys Leu
 180 185 190
 Ile Asn Val Thr Ile His Phe Gln Leu Lys Thr Ile Asn Leu Gln Ser
 195 200 205
 Leu Ile Asn Asn Glu Ile Pro Asp Cys Tyr Thr Phe Ser Ile Leu Ile
 210 215 220
 Thr Phe Asp Asn Lys Ala His Ser Gly Arg Ile Pro Ile Arg Leu Glu
 225 230 235 240
 Thr Lys Thr His Ile Gln Glu Cys Lys His Pro Ser Val Ser Arg
 245 250 255

<210> 714
 <211> 255
 <212> PRT
 <213> Mouse

<400> 714

```

Met Asn Ile Val Val Glu Phe Phe Val Val Thr Phe Lys Val Leu Trp
 1          5          10          15
Ala Phe Val Leu Ala Ala Ala Arg Trp Leu Val Arg Pro Lys Glu Lys
 20          25          30
Ser Val Ala Gly Gln Val Cys Leu Ile Thr Gly Ala Gly Ser Gly Leu
 35          40          45
Gly Arg Leu Phe Ala Leu Glu Phe Ala Arg Arg Arg Ala Leu Leu Val
 50          55          60
Leu Trp Asp Ile Asn Thr Gln Ser Asn Glu Glu Thr Ala Gly Met Val
 65          70          75          80
Arg His Ile Tyr Arg Asp Leu Glu Ala Ala Asp Ala Ala Leu Gln
 85          90          95
Ala Gly Lys Gly Glu Glu Glu Ile Leu Pro Pro Cys Asn Leu Gln Val
100          105          110
Phe Thr Tyr Thr Cys Asp Val Gly Lys Arg Glu Asn Val Tyr Leu Thr
115          120          125
Ala Glu Arg Val Arg Lys Glu Val Gly Glu Val Ser Val Leu Val Asn
130          135          140
Asn Ala Gly Val Gly Ser Gly His His Leu Leu Glu Cys Pro Asp Glu
145          150          155          160
Leu Ile Glu Arg Thr Met Met Val Asn Cys His Ala His Phe Trp Thr
165          170          175
Thr Lys Ala Phe Leu Pro Thr Met Leu Glu Ile Asn His Gly His Ile
180          185          190
Val Thr Val Ala Ser Ser Leu Gly Leu Phe Ser Thr Ala Gly Val Glu
195          200          205
Asp Tyr Cys Ala Ser Lys Phe Gly Val Val Gly Phe His Glu Ser Leu
210          215          220
Ser His Glu Leu Lys Ala Ala Glu Lys Asp Gly Ile Lys Thr Thr Leu
225          230          235          240
Val Cys Pro Tyr Leu Val Asp Thr Gly Met Phe Arg Gly Cys Arg
245          250          255

```

<210> 715

<211> 200

<212> PRT

<213> Mouse

<400> 715

```

Met Phe Pro Lys Asn Ser Arg Cys Pro Thr Cys Asp Leu Arg Lys Pro
 1          5          10          15
Ala Arg Ser Lys His Cys Arg Leu Cys Asp Arg Cys Val His Arg Phe
 20          25          30
Asp His His Cys Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Thr
 35          40          45
Arg Tyr Phe Leu Ile Tyr Leu Leu Thr Leu Thr Ala Ser Ala Ala Thr
 50          55          60
Ile Ala Thr Val Thr Ala Ala Phe Leu Leu Arg Leu Val Thr Val Ser
 65          70          75          80
Asp Leu Tyr Gln Glu Thr Tyr Leu Asp Asp Val Gly His Phe Gln Ala
 85          90          95
Val Asp Thr Val Phe Leu Ile Gln His Leu Phe Leu Ala Phe Pro Arg
100          105          110
Ile Val Phe Leu Leu Gly Phe Val Ile Val Leu Ser Met Leu Leu Ala
115          120          125
Gly Tyr Leu Cys Phe Ala Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr

```

130 135 140
 Asn Glu Trp Tyr Lys Gly Asp Trp Ala Trp Cys Gln Arg Trp Pro Leu
 145 150 155 160
 Val Ala Trp Ser Pro Ser Ala Glu Pro Arg Ile His Gln Asn Ile His
 165 170 175
 Ser His Gly Phe Arg Ser Asn Leu Arg Glu Ile Phe Leu Pro Ala Thr
 180 185 190
 Pro Ser Tyr Lys Lys Lys Glu Lys
 195 200

<210> 716
 <211> 115
 <212> PRT
 <213> Mouse

<400> 716
 Gly Glu Leu Arg Ala Leu Leu Ala Phe Thr His Leu Ser Ser Ala His
 1 5 10 15
 Phe Trp Leu Met Met Thr Leu Gly Gly Leu Phe Gly Phe Ala Ile Gly
 20 25 30
 Tyr Val Thr Gly Leu Leu Ile Lys Phe Thr Ser Pro Leu Thr His Asn
 35 40 45
 Val Ser Gly Thr Ala Lys Ala Cys Ala Gln Thr Val Leu Ala Val Leu
 50 55 60
 Tyr Tyr Glu Glu Ile Lys Ser Phe Leu Trp Trp Thr Ser Asn Leu Met
 65 70 75 80
 Val Leu Gly Gly Ser Ser Ala Tyr Thr Trp Val Arg Gly Trp Glu Met
 85 90 95
 Gln Lys Thr Gln Glu Asp Pro Ser Ser Lys Asp Gly Glu Lys Ser Ala
 100 105 110
 Ile Arg Val
 115

<210> 717
 <211> 88
 <212> PRT
 <213> Mouse

<400> 717
 Met Lys Ile Pro Ile Leu Pro Val Val Ala Leu Leu Ser Leu Leu Ala
 1 5 10 15
 Leu His Ala Val Gln Gly Ala Ala Leu Gly His Pro Thr Ile Tyr Pro
 20 25 30
 Glu Asp Ser Ser Tyr Asn Asn Tyr Pro Thr Ala Thr Glu Ala Phe Gln
 35 40 45
 Ser Glu Asn Phe Leu Asn Trp His Val Ile Thr Asp Met Phe Lys Asn
 50 55 60
 Ala Phe Pro Phe Ile Asn Trp Asp Phe Phe Pro Lys Val Lys Gly Leu
 65 70 75 80
 Arg Ser Ala Ala Pro Asp Ser Gln
 85

<210> 718
 <211> 84
 <212> PRT
 <213> Mouse

<400> 718

```

Met Arg Leu Pro Ile Phe His Ile Ile Ala Phe Phe Phe Leu Val Val
 1           5           10           15
Ser Met Gly Cys Thr Cys Ala His Gly Gly Gln Arg Ser Asp Leu Cys
          20           25           30
Thr Cys Gly Tyr Met Glu Val Arg Gly His Val Arg Arg Leu Leu Leu
          35           40           45
Leu Phe Ser Thr Phe Lys Arg Ile Val Ile Glu Ala Glu Gly Gly Gly
 50           55           60
Met Gly Trp Gly Gly Leu Gln Arg Gly Asn Arg Glu Gly Gly Gln His
65           70           75           80
Leu Lys Cys Lys

```

<210> 719

<211> 135

<212> PRT

<213> Mouse

<400> 719

```

Met Phe Val Ala Phe Tyr Ile Cys Thr Phe Leu Met Arg Phe Val Ser
 1           5           10           15
Thr Pro Val Thr Arg Met Cys Cys Pro Arg Gly Asp Ala Ala Trp Arg
          20           25           30
Arg Pro Tyr Pro Leu Pro Leu Asp Leu Phe Gly Gly Thr Pro Ser Pro
          35           40           45
Gly Pro Gly Ala Gly Arg Gly Ala Ser Cys Arg Pro Gln Ala Tyr Ser
 50           55           60
Glu Leu Val Phe Leu Lys Val Phe Leu Asp Pro Val Leu Val Asn Ile
65           70           75           80
Ser Ile Ile Leu Thr Arg Ala Ser Ser Cys Ser Leu Ser Leu Ser Leu
          85           90           95
Ser Leu Ser Leu Phe Asn Phe Ile Ile Ile Leu Ala Thr Cys Thr Phe
100           105           110
Leu Thr Lys Phe Ile Val Ala Ile Lys Val Phe Tyr Phe Pro Val His
115           120           125
Ile Thr Leu Val Ser Ser Pro
130           135

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<210> 720

<211> 129

<212> PRT

<213> Mouse

<400> 720

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          20           25           30
Lys Pro Asp Leu Leu His Pro Gln Ala Ile Pro Pro Ala Ser Leu Gly
          35           40           45
Gly Pro Leu Leu Gly Leu Pro Cys Ala Pro Val Cys Pro Gly Leu Ala
 50           55           60
Arg Leu Ser Pro Pro Ala Arg Gly Ser Ser Arg Ala Leu Met Val Leu
65           70           75           80
Lys Pro Ala Pro Leu Pro Tyr Val Leu His Phe Leu Gly Pro Val Pro
          85           90           95

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Pro Leu Pro Thr Gln Pro Arg Pro His Leu Arg Val Ser Asp Ser Cys
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 Thr Val Gly Glu Glu Val Gly Thr Glu Met Val Phe Cys Lys Lys Asn
 115 120 125
 Lys

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 <211> 255
 <212> PRT
 <213> Mouse

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 20 25 30
 Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu
 35 40 45
 Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
 50 55 60
 Glu Leu Ala Phe Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
 65 70 75 80
 Ala Arg Arg Ala Gln Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu
 85 90 95
 Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu
 100 105 110
 Thr Asp Thr Ser Ser His Glu Ala Ala Thr Lys Ala Val Leu Gln Glu
 115 120 125
 Phe Gly Lys Ile Asp Ile Leu Val Asn Asn Gly Gly Arg Ser Gln Arg
 130 135 140
 Ser Leu Val Leu Glu Thr Asn Leu Asp Val Phe Lys Glu Leu Ile Asn
 145 150 155 160
 Leu Asn Tyr Ile Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His
 165 170 175
 Met Ile Glu Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Ala
 180 185 190
 Gly Ile Ala Ser Val Ser Leu Ser Ser Gly Tyr Cys Ala Ser Lys His
 195 200 205
 Ala Leu Arg Gly Phe Phe Asn Ala Leu His Ser Glu Leu Gly Gln Tyr
 210 215 220
 Pro Gly Ile Thr Phe Cys Asn Val Tyr Pro Gly Pro Val Gln Ser Asp
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 Ile Val Lys Asn Ala Phe Thr Glu Glu Val Thr Lys Ser Met Arg
 245 250 255

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 <212> PRT
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 1 5 10 15
 His Gly Leu Pro Leu Ser Ser Lys Gln Ser Ser Phe Ile Val Met Val
 20 25 30
 Ser Thr Ser Phe Phe Ile Ala Leu Val Val Phe Tyr Ile Leu Phe Cys

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          35          40          45
Leu Leu Trp Pro Arg Ile Val Lys Ala Trp Val Ser Phe Arg Trp Lys
   50          55          60
Ile His Asn Met Met Ala Pro Glu Thr Tyr Ser Ser Ser Ser Ser
65          70          75          80
Gly Gly Phe Thr Leu His Ser His Ser Ser Glu Gly Ser Phe Glu Gly
          85          90          95
Pro Ser Arg Pro Gly Thr Lys Glu Asp Asn Val Gln Ala Lys Arg Ala
          100          105          110
Lys Val Ala
          115

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 <212> PRT
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          20          25          30
Gly Glu Thr Lys Tyr Ala Ser Glu Asn His Leu Ser Arg Phe Val Trp
          35          40          45
Phe Phe Ser Gly Ile Val Gly Gly Gly Leu Leu Met Leu Leu Pro Ala
          50          55          60
Phe Val Phe Ile Gly Leu Glu Gln Asp Asp Cys Cys Gly Cys Cys Gly
65          70          75          80
His Glu Asn Cys Gly Lys Arg Cys Ala Met Leu Ser Ser Val Leu Ala
          85          90          95
Ala Leu Ile Gly Ile Ala Gly Ser Gly Tyr Cys Val Ile Val Ala Ala
          100          105          110
Leu Gly Leu Ala Glu Gly Pro Leu Cys Leu Asp Ser Leu Gly Gln Trp
          115          120          125
Asn Tyr Thr Phe Ala Ser Thr Glu Gly Gln Tyr Leu Gly Arg Asp His
          130          135          140
Ala
145

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<210> 724
 <211> 217
 <212> PRT
 <213> Mouse

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          20          25          30
Arg Arg Tyr Asp Gly Gly Leu Asp Ser Gly Phe His Ser Val Asp Ser
          35          40          45
Gly Ser Lys Arg Trp Ser Gly Asn Glu Ser Thr Asp Asp Phe Ser Glu
          50          55          60
Leu Ser Phe Arg Ile Ser Glu Leu Ala Arg Asp Pro Arg Gly Pro Arg
65          70          75          80
Gln Pro Arg Glu Asp Gly Ala Gly Asp Gly Asp Leu Glu Gln Ile Asp
          85          90          95

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Phe Ile Asp Ser His Val Pro Gly Glu Asp Glu Asp Arg Ser Ala Ala
      100      105      110
Glu Glu Gln Leu Pro Ser Glu Leu Ser Leu Val Ala Gly Asp Val Glu
      115      120      125
Lys Pro Ser Ser Ser Arg Arg Glu Glu Pro Ala Gly Glu Glu Arg Arg
      130      135      140
Arg Pro Asp Thr Leu Gln Leu Trp Gln Glu Arg Glu Arg Lys Gln Gln
      145      150      155      160
Gln Gln Ser Gly Gly Trp Gly Ser Pro Arg Lys Asp Ser Val Leu Lys
      165      170      175
Arg Gly Ile Arg Ala Ala Gly Ala Gly Ala Ser Ala Pro Ser Thr Gln
      180      185      190
Ala Thr Cys Asn Gly Pro Pro Pro Arg Thr Pro Phe Leu Tyr Leu Asp
      195      200      205
Gln Val Leu Pro Leu Gln Ser Leu Phe
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<210> 725

<211> 255

<212> PRT

<213> Mouse

<400> 725

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  1      5      10      15
Leu Leu Leu Leu Val Val Gly Phe Leu Phe Gly Arg Asp Pro
      20      25      30
Asp Tyr Gly Leu Gly Thr Thr Ala Thr Leu Asp Glu Asp Pro Tyr Arg
      35      40      45
Ser Arg Asn Leu Ser Ala Ser Ser Pro Gln Leu Leu Leu Pro Pro Lys
      50      55      60
Cys Glu Met Leu His Val Ala Ile Val Cys Ala Gly Tyr Asn Ser Ser
      65      70      75      80
Arg Glu Ile Ile Thr Leu Thr Lys Ser Leu Leu Phe Tyr Arg Lys Asn
      85      90      95
Pro Leu His Leu His Leu Ile Thr Asp Ala Val Ala Arg Asn Ile Leu
      100      105      110
Glu Thr Leu Phe Arg Thr Trp Met Val Pro Ala Val Val Val Ser Phe
      115      120      125
Tyr Asp Ala Glu Glu Leu Lys Pro Leu Val Ser Trp Ile Pro Asn Lys
      130      135      140
His Tyr Ser Gly Leu Tyr Gly Leu Met Lys Leu Val Leu Pro Ser Ile
      145      150      155      160
Leu Pro Pro Ser Leu Ala Arg Val Ile Val Leu Asp Thr Asp Val Thr
      165      170      175
Phe Ser Ser Asp Ile Val Glu Leu Trp Ala Leu Phe Asp His Phe Ser
      180      185      190
Asp Lys Gln Val Val Gly Leu Val Glu Asn Gln Ser Asp Trp Tyr Leu
      195      200      205
Gly Asn Leu Trp Lys Asn His Arg Pro Trp Pro Ala Leu Gly Arg Gly
      210      215      220
Phe Asn Thr Gly Val Ile Leu Leu Trp Leu Asp Arg Leu Gln Gln Thr
      225      230      235      240
Gly Trp Glu Gln Met Trp Lys Val Thr Ala Lys Arg Glu Leu Leu
      245      250      255

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ01/00099

A. CLASSIFICATION OF SUBJECT MATTERInt. Cl. ⁷: C12N 15/12, 15/18, 15/19

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

AS BELOW

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

AS BELOW.

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Dgene, Swiss Prot, EMBL, Genebank, : SEQ ID. NOS. 1 - 10.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	EP 1 067 182 HELIX RESEARCH INSTITUTE (10 January 2001) See Sequence Id. 487, & GeneBank Accession Number AX136565.	1 - 3. (SEQ ID NO 1)
P, X	EP 1067 182 HELIX RESEARCH INSTITUTE (10 January 2001) See Sequence Id. 219, & GeneBank Accession Number AX136297.	1 - 3. (SEQ ID NO 1)
X	EMBL Accession Number AC008119 (9 October 1999) Homo sapiens 12q24.1-116.6-118.9 BAC RPC11-951111	1 - 3. (SEQ ID NO 1)

☒ Further documents are listed in the continuation of Box C
☒ See patent family annex

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

20 August 2001

Date of mailing of the international search report

21 SEPTEMBER 2001

Name and mailing address of the ISA/AU

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ01/00099

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US, A, 5 952 486 L. N. BLOKSBERG ET. AL. (14 September 1999) See SEQ ID 53. & GeneBank Accession number AR074144.	1 - 3. (SEQ ID NO 2)
X	WO, A, 2000 40752 THE NOTTINGHAM TRENT UNIVERSITY (13 July 2000) See SEQ ID NO. 2. & GeneBank Accession Number AX026540.	1 - 3. (SEQ ID NO 2)
X	EMBL Accession Number UCAJ4935 (2 March 1999.) Urechis caupo mRNA for cytoplasmic intermediate filament protein.	1 - 3. (SEQ ID NO 2)
X	WO, A, 99 53040 METAGEN GESELLSCHAFT FÜR GENOMFORSCHUNG MBH (21 October 1999) See SEQ ID 31. & GenBank Accession Number AX014842.	1 - 3. (SEQ ID NO 4)
P, X	WO, A, 2001 07612 INCYTE GENOMICS, INC. (1 February 2001) See SEQ ID 43 & Genebank Accession Number AX078375.	1 - 3. (SEQ ID NO 4)
P, X	WO, A, 2001 10902 CURAGEN CORPORATION (15 February 2001) See SEQ ID 5 & Genebank Accession Number AX084211.	1 - 3. (SEQ ID NO 5)
X	EMBL Accession Number AF169677 (29 JANUARY 2000) Homo sapiens leucine-rich repeat transmembrane protein FLRT3 (FLRT3) mRNA, complete cds.	1 - 3. (SEQ ID NO 5)
X	EMBL Accession Number RNMOG (20 August 1992) Rattus norvegicus myelin/oligodendrocyte glycoprotein (MOG) gene, complete cds.	1 - 3. (SEQ ID NO 7)
A	EMBL Accession Number D50030 (14 April 2000) Homo sapiens gene for hepatocyte growth factor activator, complete cds.	1 - 3. (SEQ ID NO 8)
X	WO, A, 99 55865 GENESIS RESEARCH AND DEVELOPMENT CORPORATION LIMITED (4 November 1999) See SEQ ID NOS 1 - 10, 147, 187, 196, 294, 295 and 395.	1 - 3, 8-17, 27-29 (SEQ ID NOS 1-10, 147, 196, 294, 295, 413-5, 417)
P, X	WO, A, 2000 69884 GENESIS RESEARCH AND DEVELOPMENT CORPORATION LIMITED (23 November 2000) See SEQ ID NOS 1 - 10, 147, 187, 196, 294, 295 and 395.	1 - 3, 8-17, 27-29 (SEQ ID NOS 1-10, 147, 196, 294, 295, 413-5, 417)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NZ01/00099

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
PX	WO, A, 00 63230 HUMAN GENOME SCIENCES, INC. (26 October 2000) See SEQ ID NO 68 and pages 16-29	1-3, 8-17, 27-29 (SEQ ID NOS 196, 413-5, 417)
X	WO, A, 00 29438 MILLENNIUM PHARMACEUTICALS, INC. (25 May 2000) See Figures 1, 3, 5, 7 and 8	1-3, 8-17, 27-29 (SEQ ID NOS 196, 413-5, 417)
PX	WO, A, 00 63377 ZYMOGENETICS, INC. (26 October 2000) See SEQ ID NOS 1 and 11	1-3 (SEQ ID NO 147, 294)
PX	WO, A, 01 49728 PROTOGENE, INC. (12 July 2001) See SEQ ID NO 59 and Table 1	1-3 (SEQ ID NO 147)
PX	WO, A, 00 73448 ZYMOGENETICS, INC. (7 December 2000) See SEQ ID NOS 1 and 14	1-3 (SEQ ID NO 294)
X	GenPept Accession No. CAB53702 (18 February 2000) Hypothetical Protein <i>Homo sapiens</i> Ottenwaelder B et al	1-3 (SEQ ID NO 295)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ01/00099

Box I Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos :
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos :
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos :
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box II Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
1-3, 8-17 and 27-29 (SEQ ID NOS 1-10, 147, 196, 294, 295, 413-415, 417)

More than one invention has been claimed. (continued in supplemental box)
4. ☐ No required additional search fees were timely paid by the applicant.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

Supplemental B x

(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: II

Rule 13.1 of the PCT states the principle that an International Application should relate to only one invention or, if there is more than one invention, that the inclusion of those inventions in one International Application is only permitted if all inventions are so linked to form a single general inventive concept. Rule 13.2 of the PCT defines the method for determining whether the requirement of unity of invention is satisfied in respect of a group of inventions claimed in the International application. Unity of invention exists only when there is a technical relationship among the claimed inventions involving one or more of the same or corresponding "special technical features." The expression "special technical features" is defined in Rule 13.2 as meaning those technical features that define a contribution which each of the inventions, considered as a whole, makes over the prior art. The determination is made on the contents of the claims as interpreted in the light of the description and drawings (if any).

There is no special technical feature which is common to all 725 sequences disclosed in the specification. It is well known in the art that for a given cell type, the cell will express a great many sequences, each having a different function from the others. That they are sourced from skin cells is not a special technical feature. For applications claiming nucleotides and peptides, there are two features which are to be considered for the purposes of determining the number of inventions in a specification.

1) If the polynucleotide has a corresponding peptide, then the two sequences may have a common special technical feature because the nucleotide encodes the peptide. Therefore they are regarded as a single invention.

In the present case, the specification does not disclose a complete concordance between the polynucleotides and corresponding polypeptides, other than those disclosed in Table 2. While Table 2 purports to provide a concordance between nucleotides and peptides for which they code, this is incomplete, as the majority of sequences are not referred to on this table. Therefore the ISA is unable to confidently determine the number of inventions, on the basis of a concordance between the polynucleotides and the peptides.

2) A group of two or more nucleotides, or two or more peptides, which share a significant structural element. A "significant structural element" is the structural element that defines the specific biological activity of an amino acid sequence or a nucleotide sequence or its encoded polypeptide and is disclosed as the feature that defines the contribution which each of the inventions, considered as a whole, makes over the prior art. If each of the inventions shares the same significant structural element, then it provides the special technical feature which is required to establish unity of invention.

In the present case, genes and their expressed proteins from skin cells have been sequenced. The applicant has provided no evidence that the nucleotide sequences of the present application, and the peptides they express, all form a group of protein types sharing a significant structural element. On the contrary, the putative peptides derived from the nucleotide sequences of the application have a wide range of functions based on their similarity to known proteins. (see Table 2) At best, it appears from Table 2 that there may be 76 distinct protein types which share a common function, and therefore may share a common significant structural element. However, most of the polynucleotides and peptides which do not appear on Table 2, have not have been identified in terms of their function, much less, whether any of them have a shared significant structural element. Therefore, the ISA is unable to confidently determine the number of inventions, on the basis of a shared significant structural element. Thus, at this stage, in the absence of a complete polynucleotide peptide concordance, or the definition of a special technical feature which is common to two or more sequences, this ISA considers that there are 72 groupings of sequences, which encompass the 725 sequences.

While the ISA is unable to determine the precise number of inventions in this application it is prepared, as a service, to search a first group of ten sequences for a single search fee. This offer is provided purely as a service to the applicant and should not be taken as having any bearing on the ISA's assessment of the number of inventions claimed in these 10 sequences. The ISA also agrees to search the two further inventions specified by the applicant in their letter of 30 August 2001, for two additional search fees. As such, the ISA has searched SEQ ID NOS 1-10, 147, 196, 294, 295, 413-5 and 417.